

**Search Notes**

Application No:

09/641,801

Applicant(s)

STANTON ET AL.

Examiner

Christopher Nichols, Ph.D.

Art Unit

1647

**SEARCHED**

Class	Subclass	Date	Examiner

**INTERFERENCE SEARCHED**

Class	Subclass	Date	Examiner

**SEARCH NOTES  
(INCLUDING SEARCH STRATEGY)**

	DATE	EXMR
SEQ ID NO: 11-20	12/5/2003	CJN

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 3.27128 Seconds  
(without alignments)  
38.802 Million cell updates/sec

**Title:** US-09-641-801-11

Perfect score: 3

Sequence: 1 DKE 3

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

**Word size :**

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

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4: /cgn2_6/ptodata/1/1aa/6B COMB.pcp:*
5: /cgn2_6/ptodata/1/1aa/6B COMB.pcp:*
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3: /cgn2_6/ptodata/1/1aa/PC1US COMB.rep:*
6: /cgn2_6/ptodata/1/1aa/backfl1en1.rep:*
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:testatv/bat/r/cacaa/\_a/:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3	100.0	3	4	US-09-641-803-11	Sequence 11, Appl
2	3	100.0	4	1	US-08-406-192-21	Sequence 21, Appl
3	3	100.0	4	2	US-08-546-151-21	Sequence 21, Appl
4	3	100.0	5	4	US-09-187-859-721	Sequence 721, Appl
5	3	100.0	4	5	US-09-305-927-131	Sequence 131, Appl
6	3	100.0	5	4	US-09-073-040-77	Sequence 77, Appl
7	3	100.0	5	4	US-09-839-542B-721	Sequence 721, Appl
8	3	100.0	6	4	US-09-187-859-722	Sequence 722, Appl
9	3	100.0	6	4	US-09-303-927-132	Sequence 132, Appl
10	3	100.0	6	4	US-09-073-040-78	Sequence 78, Appl
11	3	100.0	6	4	US-09-839-542B-722	Sequence 722, Appl
12	3	100.0	7	4	US-09-187-859-724	Sequence 724, Appl
13	3	100.0	7	4	US-09-480-993-10	Sequence 10, Appl
14	3	100.0	7	4	US-09-367-065A-15	Sequence 15, Appl
15	3	100.0	7	4	US-09-303-927-134	Sequence 134, Appl
16	3	100.0	7	4	US-09-073-040-80	Sequence 80, Appl
17	3	100.0	7	4	US-09-568-466-15	Sequence 15, Appl
18	3	100.0	7	4	US-09-839-542B-724	Sequence 724, Appl
19	3	100.0	8	1	US-08-266-514-13	Sequence 13, Appl
20	3	100.0	8	1	US-08-615-181-80	Sequence 80, Appl
21	3	100.0	8	2	US-08-654-604-13	Sequence 13, Appl
22	3	100.0	8	3	US-08-863-118-12	Sequence 12, Appl
23	3	100.0	8	3	US-09-082-279B-1446	Sequence 1446, Ap
24	3	100.0	8	4	US-09-315-304B-1599	Sequence 1599, Ap
25	3	100.0	8	4	US-09-187-859-730	Sequence 730, Appl
26	3	100.0	8	4	US-09-303-927-140	Sequence 140, Appl
27	3	100.0	8	4	US-09-073-040-86	Sequence 86, Appl

## ALIGNMENTS

## RESULT 1

US-09-641-803-11  
; Sequence 11, Application US/09641803  
; Patent No. 650798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641.803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149.310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-11

Query Match 100.0%; Score 3; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKE 3  
|||  
Db 1 DKE 3

## RESULT 2

US-08-406-192-21  
; Sequence 21, Application US/08406192  
; Patent No. 5739287  
; GENERAL INFORMATION:  
; APPLICANT: Wilbur, D. Scott  
; APPLICANT: Prathare, Pradip M  
; TITLE OF INVENTION: Biotinylated Cobalamins  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness  
; STREET: 1420 Fifth Avenue, Suite 2800  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: WA 98101-2333  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/406,192  
; FILING DATE: 16-MAR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/224,831  
; FILING DATE: 08-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Renzoni, George E  
; REGISTRATION NUMBER: 37,919  
; REFERENCE/DOCKET NUMBER: RECL18947  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 682 8100  
; TELEFAX: (206) 224 0779  
; TELEX: 4938023  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; TELEPHONE: (206) 682 8100  
; TELEFAX: (206) 224 0779  
; TELEX: 4938023  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-406-192-21

Query Match 100.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKE 3  
|||  
Db 1 DKE 3

## RESULT 3

US-08-545-151-21  
; Sequence 21, Application US/08545151  
; Patent No. 5840712  
; GENERAL INFORMATION:  
; APPLICANT: Morgan Jr, A. Charles  
; APPLICANT: Wilbur, D. Scott  
; APPLICANT: Prathare, Pradip M  
; TITLE OF INVENTION: Water Soluble Vitamin B12 Receptor  
; TITLE OF INVENTION: Modulating Agents and Methods Related Thereto  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen O'Connor-Johnson & KindnessPLLC  
; STREET: 1420 Fifth Avenue, Suite 2800  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: U.S.A.  
; ZIP: WA 98101-2333  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/545,151  
; FILING DATE: 19-OCT-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04404  
; FILING DATE: 07-APR-1995  
; APPLICATION NUMBER: US 08/406,192  
; FILING DATE: 16-MAR-1995  
; APPLICATION NUMBER: US 08/406,194  
; FILING DATE: 16-MAR-1995  
; APPLICATION NUMBER: US 08/406,191  
; FILING DATE: 16-MAR-1995  
; APPLICATION NUMBER: US 08/224,831  
; FILING DATE: 08-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Renzoni, George E  
; REGISTRATION NUMBER: 37,919  
; REFERENCE/DOCKET NUMBER: RECL18878  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 682 8100  
; TELEFAX: (206) 224 0779  
; TELEX: 4938023  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: peptide  
US-08-545-151-21

Query Match 100.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
DB 1 DKE 3

## RESULT 4

US-09-187-859-721  
; Sequence 721, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 721  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence  
US-09-187-859-721

Query Match 100.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
DB 3 DKE 5

## RESULT 5

US-09-305-927-131  
; Sequence 131, Application US/09305927  
; Patent No. 6433149  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING  
; TITLE OF INVENTION: CANCER METASTASIS  
; FILE REFERENCE: 100086.407C5  
; CURRENT APPLICATION NUMBER: US/09/305,927  
; CURRENT FILING DATE: 1999-05-05  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 131  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin  
; OTHER INFORMATION: cell adhesion recognition sequence  
US-09-305-927-131

Query Match 100.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3

DB 3 DKE 5  
|||

## RESULT 6

US-09-073-040-77  
; Sequence 77, Application US/09073040  
; Patent No. 6472367  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: OB-CADHERIN MEDIATED CELL ADHESION  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,040  
; FILING DATE: 05-MAY-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.407  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: circular  
US-09-073-040-77

Query Match 100.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
DB 3 DKE 5

## RESULT 7

US-09-839-542B-721  
; Sequence 721, Application US/09839542B  
; Patent No. 6569996  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407D1  
; CURRENT APPLICATION NUMBER: US/09/839,542B  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 721  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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;
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
US-09-839-542B-721

Query Match          100.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3
Db 3 DKE 5

RESULT 8
US-09-187-859-722
; Sequence 722, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 722
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
US-09-187-859-722

Query Match          100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3
Db 4 DKE 6

RESULT 9
US-09-305-927-132
; Sequence 132, Application US/09305927
; Patent No. 6433149
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
; TITLE OF INVENTION: CANCER METASTASIS
; FILE REFERENCE: 100086.407C5
; CURRENT APPLICATION NUMBER: US/09/305,927
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 132
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin
; OTHER INFORMATION: cell adhesion recognition sequence
US-09-305-927-132

Query Match          100.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 DKE 3  
Db 4 DKE 6

RESULT 10  
US-09-073-040-78  
; Sequence 78, Application US/09073040  
; Patent No. 6472367  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: OB-CADHERIN MEDIATED CELL ADHESION  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,040  
; FILING DATE: 05-MAY-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.407  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: circular  
US-09-073-040-78

Query Match 100.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 4 DKE 6

RESULT 11  
US-09-839-542B-722  
; Sequence 722, Application US/09839542B  
; Patent No. 6569996  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407D1  
; CURRENT APPLICATION NUMBER: US/09/839,542B  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 722  
; LENGTH: 6



Qy 1 DKE 3  
|||  
Db 5 DKE 7

## RESULT 16

US-09-073-040-80  
; Sequence 80, Application US/09073040  
; Patent No. 6472367  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: OB-CADHERIN MEDIATED CELL ADHESION  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073.040  
; FILING DATE: 05-MAY-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.407  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: circular  
US-09-073-040-80

Query Match 100.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 5 DKE 7

## RESULT 17

US-09-568-466-15  
; Sequence 15, Application US/09568466  
; Patent No. 6521417  
; GENERAL INFORMATION:  
; APPLICANT: Shokat, Kevan M.  
; TITLE OF INVENTION: Engineered Protein Kinases which Can Utilize Modified  
; TITLE OF INVENTION: Nucleotide Triphosphate Substrates  
; FILE REFERENCE: 51538-5002-US  
; CURRENT APPLICATION NUMBER: US/09/568.466  
; CURRENT FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: US/09/367.065  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: US 08/797,522  
; PRIOR FILING DATE: 1997-02-07  
; PRIOR APPLICATION NUMBER: US 60/046,727  
; PRIOR FILING DATE: 1997-05-16  
; PRIOR APPLICATION NUMBER: PCT/US98/02522

; PRIOR FILING DATE: 1998-02-09  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Example  
; OTHER INFORMATION: sequence for enzyme modification  
US-09-568-466-15

Query Match 100.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 5 DKE 7

## RESULT 18

US-09-839-542B-724  
; Sequence 724, Application US/09839542B  
; Patent No. 6569996  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407D1  
; CURRENT APPLICATION NUMBER: US/09/839,542B  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 724  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence  
US-09-839-542B-724

Query Match 100.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 5 DKE 7

## RESULT 19

US-08-266-514-13  
; Sequence 13, Application US/08266514  
; Patent No. 5594105  
; GENERAL INFORMATION:  
; APPLICANT: COMOGLIO, PAOLO  
; APPLICANT: PONZETTO, CAROLA  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF MITOGENESIS AND  
; TITLE OF INVENTION: MITOGENESIS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/266,514  
;; FILING DATE: 27-JUN-1994  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: GB 9313528  
;; FILING DATE: 30-JUN-1993  
;; PRIOR APPLICATION DATA: GB 9407673.4  
;; FILING DATE: 18-APR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Oblon, No. 5594105man F.  
;; REGISTRATION NUMBER: 24,618  
;; REFERENCE/DOCKET NUMBER: 769-323-0  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 413-3000  
;; TELEFAX: (703) 413-2220  
;; TELEX: 248855 OPAT UR  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 1  
;; OTHER INFORMATION: /note= "The Tyr residue at position 1 may  
;; OTHER INFORMATION: be phosphorylated."  
US-08-266-514-13

Query Match 100.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 2 DKE 4

RESULT 20  
US-08-615-181-80  
; Sequence 80, Application US/08615181  
; Patent No. 5758666  
; GENERAL INFORMATION:  
; APPLICANT: MASAFUMI, TAKIGUCHI  
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE  
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND  
; TITLE OF INVENTION: CURING AIDS  
; NUMBER OF SEQUENCES: 115  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/615,181  
; FILING DATE: 04-APR-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: PCT/JP94/01756  
;; FILING DATE: 19-OCT-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 261302/1993  
;; FILING DATE: 19-OCT-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OBLON, NORMAN F.  
;; REGISTRATION NUMBER: 24,618  
;; REFERENCE/DOCKET NUMBER: 10-796-0 PCT  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-413-3000  
;; TELEFAX: 703-413-2220  
;; INFORMATION FOR SEQ ID NO: 80:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; ORIGINAL SOURCE:  
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-08-615-181-80

Query Match 100.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 4 DKE 6

RESULT 21  
US-08-654-604-13  
; Sequence 13, Application US/08654604  
; Patent No. 5912183  
; GENERAL INFORMATION:  
; APPLICANT: COMOGGIO, PAOLO  
; APPLICANT: PONZETTO, CAROLA  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF MITOGENESIS AND  
; TITLE OF INVENTION: MOTOGENESIS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/654,604  
; FILING DATE: 29-MAY-1996  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/266,514  
; FILING DATE: 27-JUN-1994  
; APPLICATION NUMBER: GB 9313528  
; FILING DATE: 30-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9407673.4  
; FILING DATE: 18-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5912183man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 769-323-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000

; TELEFAX: (703) 413-2220  
; TELEX: 248955 OPAT UR  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The Tyr residue at position 1 may  
; be phosphorylated."  
US-08-654-604-13

Query Match 100.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
DB 2 DKE 4

## RESULT 22

US-08-863-118-12  
; Sequence 12, Application US/088631118A  
; Patent No. 6015893  
; GENERAL INFORMATION:  
; APPLICANT: CANCER, William G.  
; APPLICANT: LIU, Edison T.  
; APPLICANT: OWENS, Lewis V.  
; TITLE OF INVENTION: Oligonucleoside Compounds and Methods for Inhibiting  
; Tumor Growth, Invasion and Metastasis  
; FILE REFERENCE: 5470-90  
; CURRENT APPLICATION NUMBER: US/08/863,118A  
; CURRENT FILING DATE: 1997-05-27  
; EARLIER APPLICATION NUMBER: 08/276,843  
; EARLIER FILING DATE: 1994-07-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: portion of  
; focal adhesion kinase protein sequence  
US-08-863-118-12

Query Match 100.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
DB 2 DKE 4

## RESULT 23

US-09-082-279B-1446  
; Sequence 1446, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082,279B

; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1446  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HIV-1  
; ORGANISM: HIV-1446  
US-09-082-279B-1446

Query Match 100.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
DB 5 DKE 7

## RESULT 24

US-09-315-304B-1599  
; Sequence 1599, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; PROPERTIES  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1599  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HIV-1  
; ORGANISM: HIV-1599  
US-09-315-304B-1599

Query Match 100.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
DB 5 DKE 7

## RESULT 25

US-09-187-859-730  
; Sequence 730, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 730  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OB-cadherin cell adhesion recognition sequence  
US-09-187-859-730



## US-09-187-859-730

Query Match 100.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 6 DKE 8

## RESULT 26

US-09-305-927-140  
Sequence 140, Application US/09305927

Patent No. 6433149  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Byers, Stephen  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING  
TITLE OF INVENTION: CANCER METASTASIS  
FILE REFERENCE: 100086.407C5  
CURRENT APPLICATION NUMBER: US/09/305,927  
CURRENT FILING DATE: 1999-05-05  
NUMBER OF SEQ ID NOS: 319  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 140  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin  
OTHER INFORMATION: cell adhesion recognition sequence  
US-09-305-927-140

Query Match 100.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 6 DKE 8

## RESULT 27

US-09-073-040-86  
Sequence 86, Application US/09073040

Patent No. 6472367  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
TITLE OF INVENTION: OB-CADHERIN MEDIATED CELL ADHESION  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,040  
FILING DATE: 05-MAY-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392

## REFERENCE/DOCKET NUMBER: 100086.407

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: circular  
US-09-073-040-86

Query Match 100.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 6 DKE 8

## RESULT 28

US-09-834-784-1446  
Sequence 1446, Application US/09834784  
Patent No. 6562787  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/834,784  
CURRENT FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1446  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HIV-1  
US-09-834-784-1446

Query Match 100.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 5 DKE 7

## RESULT 29

US-09-839-542B-730  
Sequence 730, Application US/09839542B  
Patent No. 6569996  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Symonds, James Matthew  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
FILE REFERENCE: 100086.407D1  
CURRENT APPLICATION NUMBER: US/09/839,542B  
CURRENT FILING DATE: 2001-04-20  
NUMBER OF SEQ ID NOS: 4052  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 730  
LENGTH: 8  
TYPE: PRT

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
US-09-839-542B-730
Query Match 100.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;
Qy 1 DKE 3
Db 6 DKE 8
RESULT 30
US-08-322-707-4
; Sequence 4, Application US/08322707
; Patent No. 5510331
; GENERAL INFORMATION:
; APPLICANT: Gilles Hamon, et al.
; TITLE OF INVENTION: NOVEL PEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/322,707
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 795,426
; FILING DATE: 20-NOV-1991
; APPLICATION NUMBER: 5510331-1991
; FILING DATE: 20-NOV-1991
; APPLICATION NUMBER: France 90-14498
; FILING DATE: 21-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles A. Musierlian
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1119
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; FEATURE:
; LOCATION: 5
; OTHER INFORMATION: Xaa is Nle.
; FEATURE:
; OTHER INFORMATION: Optional disulfide bridge:
; OTHER INFORMATION: Cys (1) and Cys (9).
US-08-322-707-4
Query Match 100.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;
Qy 1 DKE 3
Db 6 DKE 8
```

```
RESULT 31
US-07-807-529A-55
; Sequence 55, Application US/07807529A
; Patent No. 5547669
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-Chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: One Kendall Square, Building 600
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,529A
; FILING DATE: 19911213
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Channing, Stacey L.
; REGISTRATION NUMBER: 31,095
; REFERENCE/DOCKET NUMBER: IPC-027/imi-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 494-0060
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-07-807-529A-55
Query Match 100.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;
Qy 1 DKE 3
Db 1 DKE 3
RESULT 32
US-08-986-234-52
; Sequence 52, Application US/08986234
; Patent No. 5981706
; GENERAL INFORMATION:
; APPLICANT: Wallen, et al.
; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
; FILE REFERENCE: UNME-0008-1
; CURRENT APPLICATION NUMBER: US/08/986,234
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
```

; SEQ ID NO 52  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-08-986-234-52

Query Match 100.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
|||  
Db 3 DXE 5

RESULT 33  
US-09-187-859-733  
; Sequence 733, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 733  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence  
US-09-187-859-733

Query Match 100.0%; Score 3; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
|||  
Db 7 DXE 9

RESULT 34  
US-09-305-927-143  
; Sequence 143, Application US/09305927  
; Patent No. 6433149  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING  
; TITLE OF INVENTION: CANCER METASTASIS  
; FILE REFERENCE: 100086.407C5  
; CURRENT APPLICATION NUMBER: US/09/305,927  
; CURRENT FILING DATE: 1999-05-05  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 143  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin  
; OTHER INFORMATION: cell adhesion recognition sequence  
US-09-305-927-143

Query Match 100.0%; Score 3; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
|||  
Db 7 DXE 9

RESULT 35  
US-09-259-478A-8  
; Sequence 8, Application US/09259478A  
; Patent No. 6465199  
; GENERAL INFORMATION:  
; APPLICANT: Colyer, Roger K  
; APPLICANT: Colyer, John  
; TITLE OF INVENTION: Compositions and methods for monitoring the  
; TITLE OF INVENTION: modification of natural binding partners  
; FILE REFERENCE: 10069/1100  
; CURRENT APPLICATION NUMBER: US/09/259,478A  
; CURRENT FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE  
; OTHER INFORMATION: SEQUENCE  
US-09-259-478A-8

Query Match 100.0%; Score 3; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
|||  
Db 7 DXE 9

RESULT 36  
US-09-259-478A-11  
; Sequence 11, Application US/09259478A  
; Patent No. 6465199  
; GENERAL INFORMATION:  
; APPLICANT: Colyer, Roger K  
; APPLICANT: Colyer, John  
; TITLE OF INVENTION: Compositions and methods for monitoring the  
; TITLE OF INVENTION: modification of natural binding partners  
; FILE REFERENCE: 10069/1100  
; CURRENT APPLICATION NUMBER: US/09/259,478A  
; CURRENT FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE  
; OTHER INFORMATION: SEQUENCE  
US-09-259-478A-11

Query Match 100.0%; Score 3; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
|||  
Db 7 DXE 9

RESULT 37  
US-09-073-040-89

; Sequence 89, Application US/09073040  
; Patent No. 6472367  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: OB-CADHERIN MEDIATED CELL ADHESION  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/073,040  
; FILING DATE: 05-MAY-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 100086.407  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 89:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: circular  
US-09-073-040-89

Query Match 100.0%; Score 3; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 7 DKE 9

RESULT 38  
US-09-839-542B-733  
; Sequence 733, Application US/09839542B  
; Patent No. 6569996  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407D1  
; CURRENT APPLICATION NUMBER: US/09/839,542B  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 733  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence  
US-09-839-542B-733

Query Match 100.0%; Score 3; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DKE 3  
Db 7 DKE 9

RESULT 39  
US-08-166-195A-37  
; Sequence 37, Application US/08166195A  
; Patent No. 5480799  
; GENERAL INFORMATION:  
; APPLICANT: O'Rand, Michael G.  
; APPLICANT: Widgren, Esther E.  
; APPLICANT: Richardson, Richard T.  
; APPLICANT: Lea, Isabel  
; TITLE OF INVENTION: Sperm Antigen Corresponding to a  
; TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth D. Sibley  
; STREET: P.O. Box 34009  
; CITY: Charlotte  
; STATE: No. 5480799th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/166,195A  
; FILING DATE: 10 DEC 1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5470/73  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-166-195A-37

Query Match 100.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 6 DKE 8

RESULT 40  
US-08-166-195A-38  
; Sequence 38, Application US/08166195A  
; Patent No. 5480799  
; GENERAL INFORMATION:  
; APPLICANT: O'Rand, Michael G.  
; APPLICANT: Widgren, Esther E.  
; APPLICANT: Richardson, Richard T.  
; APPLICANT: Lea, Isabel  
; TITLE OF INVENTION: Sperm Antigen Corresponding to a  
; TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope  
; NUMBER OF SEQUENCES: 51

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Kenneth D. Sibley  
;; STREET: P.O. Box 34009  
;; CITY: Charlotte  
;; STATE: No. 5480799th Carolina  
;; COUNTRY: USA  
;; ZIP: 28234  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: 10 DEC 1993  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sibley, Kenneth D.  
;; REGISTRATION NUMBER: 31,665  
;; REFERENCE/DOCKET NUMBER: 5470/73  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 919-881-3140  
;; TELEFAX: 919-881-3175  
;;  
;; INFORMATION FOR SEQ ID NO: 38:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;;  
;; US-08-166-195A-38

Query Match 100.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
Db |||  
3 DKE 5

RESULT 41  
US-08-199-776-8  
; Sequence 8, Application US/08199776  
; Patent No. 5594120  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. 5594120el integrin alpha subunit  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Plumer, Elizabeth R.  
; REGISTRATION NUMBER: 36,637  
; REFERENCE/DOCKET NUMBER: B0801/7020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-720-3500  
; TELEFAX: 617-720-2441

;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: YES  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: internal  
;; ORIGINAL SOURCE:  
;; ORGANISM: Homo sapiens  
;;  
;; US-08-199-776-8

Query Match 100.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
Db |||  
7 DKE 9

RESULT 42  
US-08-199-776-9  
; Sequence 9, Application US/08199776  
; Patent No. 5594120  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. 5594120el integrin alpha subunit  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/199,776  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Plumer, Elizabeth R.  
; REGISTRATION NUMBER: 36,637  
; REFERENCE/DOCKET NUMBER: B0801/7020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-720-3500  
; TELEFAX: 617-720-2441  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: YES  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-08-199-776-9

Query Match 100.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
Db 6 DKE 8

STATE: MA  
COUNTRY: USA  
ZIP: 02210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/199,776

FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7020  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE: Homo sapiens  
US-08-199-776-11

Query Match 100.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
Db 4 DKE 6

RESULT 45  
US-08-199-776-12  
Sequence 12, Application US/08199776  
Patent No. 5594120  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael B.  
APPLICANT: Parker, Christina M.  
TITLE OF INVENTION: No. 5594120e1 integrin alpha subunit  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/199,776

FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7020  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE: Homo sapiens  
US-08-199-776-11

QY 1 DKE 3  
Db 6 DKE 8

STATE: MA  
COUNTRY: USA  
ZIP: 02210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/199,776

FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7020  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE: Homo sapiens  
US-08-199-776-10

Query Match 100.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
Db 5 DKE 7

RESULT 44  
US-08-199-776-11  
Sequence 11, Application US/08199776  
Patent No. 5594120  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael B.  
APPLICANT: Parker, Christina M.  
TITLE OF INVENTION: No. 5594120e1 integrin alpha subunit  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston

```
TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-199-776-12

Query Match 100.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 3 DKE 5

RESULT 46
US-08-199-776-13
; Sequence 13, Application US/08199776
; Patent No. 5594120
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Parker, Christina M.
; TITLE OF INVENTION: No. 5594120e1 integrin alpha subunit
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,776
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-199-776-13

Query Match 100.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DKE 3
Db 2 DKE 4

RESULT 47
US-08-199-776-14
; Sequence 14, Application US/08199776
; Patent No. 5594120
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Parker, Christina M.
; TITLE OF INVENTION: No. 5594120e1 integrin alpha subunit
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,776
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-199-776-14

Query Match 100.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 1 DKE 3

RESULT 48
US-08-436-772-37
; Sequence 37, Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
```

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth D. Sibley  
; STREET: P.O. Box 34009  
; CITY: Charlotte  
; STATE: No. 5814456th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,772  
; FILING DATE: 08-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5470-73B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3175  
; TELEFAX: 919-881-3175  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-436-772-37

Query Match 100.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
Db 6 DKE 8

RESULT 49  
US-08-436-772-38  
; Sequence 38, Application US/08436772  
; Patent No. 5814456  
; GENERAL INFORMATION:  
; APPLICANT: O'Rand, Michael G.  
; APPLICANT: Widgren, Esther E.  
; APPLICANT: Richardson, Richard T.  
; APPLICANT: Lea, Isabel  
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm  
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth D. Sibley  
; STREET: P.O. Box 34009  
; CITY: Charlotte  
; STATE: No. 5814456th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,772  
; FILING DATE: 08-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5470-73B

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-436-772-38

Query Match 100.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
Db 3 DKE 5

RESULT 50  
US-08-436-883B-37  
; Sequence 37, Application US/08436883B  
; Patent No. 5820861  
; GENERAL INFORMATION:  
; APPLICANT: O'Rand, Michael G.  
; APPLICANT: Widgren, Esther E.  
; APPLICANT: Richardson, Richard T.  
; APPLICANT: Lea, Isabel  
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm  
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kenneth D. Sibley  
; STREET: P.O. Box 34009  
; CITY: Charlotte  
; STATE: No. 5820861th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,883B  
; FILING DATE: 08-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5470-73C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3175  
; TELEFAX: 919-881-3175  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-436-883B-37

Query Match 100.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
Db 6 DKE 8



```

RESULT 51
US-08-436-883B-38
; Sequence 38, Application US/08436883B
; Patent No. 5820861
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5820861th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,883B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-436-883B-38

Query Match 100.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 3 DKE 5

RESULT 52
US-08-617-929-20
; Sequence 20, Application US/08617929
; Patent No. 5885771
; GENERAL INFORMATION:
; APPLICANT: KUMAZAWA, Toshiaki
; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,929
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01823
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6/207695
; FILING DATE: 31-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5/272864
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 77384/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-617-929-20

Query Match 100.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 5 DKE 7

RESULT 53
US-08-663-731-8
; Sequence 8, Application US/08663731
; Patent No. 6057423
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Parker, Christina M.
; TITLE OF INVENTION: No. 6057423el integrin alpha subunit
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,731
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,776
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7020
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-663-731-8

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
DB 7 DKE 9

RESULT 54  
US-08-663-731-9  
Sequence 9, Application US/08663731  
Patent No. 6057423  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael B.  
APPLICANT: Parker, Christina M.  
TITLE OF INVENTION: No. 6057423el integrin alpha subunit  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/663,731  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/199,776  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7020  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-663-731-9

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DKE 3  
DB 6 DKE 8

RESULT 55  
US-08-663-731-10  
Sequence 10, Application US/08663731  
Patent No. 6057423  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael B.  
APPLICANT: Parker, Christina M.  
TITLE OF INVENTION: No. 6057423el integrin alpha subunit  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/663,731  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/199,776  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7020  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-663-731-10

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
DB 5 DKE 7

RESULT 56  
US-08-663-731-11  
Sequence 11, Application US/08663731  
Patent No. 6057423  
GENERAL INFORMATION:

APPLICANT: Brenner, Michael B.  
APPLICANT: Parker, Christina M.  
TITLE OF INVENTION: No. 6057423el integrin alpha subunit  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/663,731  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/199,776  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7020  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-663-731-11

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 DKE 3  
Db 4 DKE 6

RESULT 57  
US-08-663-731-12  
Sequence 12, Application US/08663731  
Patent No. 6057423  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael B.  
APPLICANT: Parker, Christina M.  
TITLE OF INVENTION: No. 6057423el integrin alpha subunit  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/663,731  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/199,776  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7020  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-663-731-12

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 DKE 3  
Db 3 DKE 5

RESULT 58  
US-08-663-731-13  
Sequence 13, Application US/08663731  
Patent No. 6057423  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael B.  
APPLICANT: Parker, Christina M.  
TITLE OF INVENTION: No. 6057423el integrin alpha subunit  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/663,731  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/199,776  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7020  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-663-731-13

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 2 DKE 4

## RESULT 59

US-08-663-731-14  
Sequence 14, Application US/08663731  
Patent No. 6057423  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael B.  
APPLICANT: Parker, Christina M.  
TITLE OF INVENTION: No. 6057423el integrin alpha subunit  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/663,731  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/199,776  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7020  
TELEPHONE: 617-720-2441  
TELEFAX: 617-720-3500  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-663-731-14

Query Match 100.0%; Score 3; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 1 DKE 3

## RESULT 60

US-08-879-338-8  
Sequence 8, Application US/08879338A  
Patent No. 6063906  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael B.  
APPLICANT: Parker, Christina M.  
TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha  
TITLE OF INVENTION: Subunit  
FILE REFERENCE: B0801/7080/ERP  
CURRENT APPLICATION NUMBER: US/08/879,338A  
CURRENT FILING DATE: 1997-06-20  
EARLIER APPLICATION NUMBER: US 08/663,731  
EARLIER FILING DATE: 1996-06-14  
EARLIER APPLICATION NUMBER: US 08/199,776  
EARLIER FILING DATE: 1994-02-18  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-08-879-338-8

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 7 DKE 9

## RESULT 61

US-08-879-338-9  
Sequence 9, Application US/08879338A  
Patent No. 6063906  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael B.  
APPLICANT: Parker, Christina M.  
TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha  
TITLE OF INVENTION: Subunit  
FILE REFERENCE: B0801/7080/ERP  
CURRENT APPLICATION NUMBER: US/08/879,338A  
CURRENT FILING DATE: 1997-06-20  
EARLIER APPLICATION NUMBER: US 08/663,731  
EARLIER FILING DATE: 1996-06-14  
EARLIER APPLICATION NUMBER: US 08/199,776  
EARLIER FILING DATE: 1994-02-18  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-08-879-338-9

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 6 DKE 8

RESULT 62  
US-08-879-338-10  
; Sequence 10, Application US/08879338A  
; Patent No. 6063906  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha  
; FILE REFERENCE: B0801/7080/ERP  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER FILING DATE: 1996-06-14  
; EARLIER FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-08-879-338-10

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
Db 5 DXE 7

RESULT 63  
US-08-879-338-11  
; Sequence 11, Application US/08879338A  
; Patent No. 6063906  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha  
; FILE REFERENCE: B0801/7080/ERP  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER FILING DATE: 1996-06-14  
; EARLIER FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-08-879-338-11

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
Db 4 DXE 6

RESULT 64  
US-08-879-338-12  
; Sequence 12, Application US/08879338A  
; Patent No. 6063906  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.

; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha  
; FILE REFERENCE: B0801/7080/ERP  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER FILING DATE: 1996-06-14  
; EARLIER FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-08-879-338-12

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
Db 3 DXE 5

RESULT 65  
US-08-879-338-13  
; Sequence 13, Application US/08879338A  
; Patent No. 6063906  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha  
; FILE REFERENCE: B0801/7080/ERP  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER FILING DATE: 1996-06-14  
; EARLIER FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-08-879-338-13

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
Db 2 DXE 4

RESULT 66  
US-08-879-338-14  
; Sequence 14, Application US/08879338A  
; Patent No. 6063906  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha  
; FILE REFERENCE: B0801/7080/ERP  
; CURRENT FILING DATE: 1997-06-20  
; EARLIER FILING DATE: 1994-02-18  
; EARLIER FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-08-879-338-14

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
Db 2 DXE 4

; EARLIER FILING DATE: 1996-06-14  
; EARLIER APPLICATION NUMBER: US 08/199,776  
; EARLIER FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-08-879-338-14

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
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Db 1 DKE 3

RESULT 67  
US-09-238-448-6  
; Sequence 6, Application US/09238448  
; Patent No. 6238925  
; GENERAL INFORMATION:  
; APPLICANT: Sampson, Hugh A.  
; TITLE OF INVENTION: Method for Determining Likelihood of Developing  
; TITLE OF INVENTION: Immunological Tolerance  
; FILE REFERENCE: HS 100  
; CURRENT APPLICATION NUMBER: US/09/238,448  
; EARLIER FILING DATE: 1999-01-28  
; EARLIER APPLICATION NUMBER: 60/073,171  
; EARLIER FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide.  
US-09-238-448-6

Query Match 100.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 7 DKE 9

RESULT 68  
US-09-293-238B-8  
; Sequence 8, Application US/09293238B  
; Patent No. 6455042  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis  
; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibody to Alpha E  
; TITLE OF INVENTION: Beta 7 Integrin  
; FILE REFERENCE: L0560/7005/ERP  
; CURRENT APPLICATION NUMBER: US/09/293,238B  
; CURRENT FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-293-238B-8

Query Match 100.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 7 DKE 9

RESULT 69  
US-09-293-238B-9  
; Sequence 9, Application US/09293238B  
; Patent No. 6455042  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis  
; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibody to Alpha E  
; TITLE OF INVENTION: Beta 7 Integrin  
; FILE REFERENCE: L0560/7005/ERP  
; CURRENT APPLICATION NUMBER: US/09/293,238B  
; CURRENT FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-293-238B-9

Query Match 100.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 6 DKE 8

RESULT 70  
US-09-293-238B-10  
; Sequence 10, Application US/09293238B  
; Patent No. 6455042  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis  
; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibody to Alpha E  
; TITLE OF INVENTION: Beta 7 Integrin  
; FILE REFERENCE: L0560/7005/ERP  
; CURRENT APPLICATION NUMBER: US/09/293,238B  
; CURRENT FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10

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; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-293-238B-10

Query Match 100.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
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Db 5 DKE 7

## RESULT 71

US-09-293-238B-11  
; Sequence 11, Application US/09293238B  
; Patent No. 6455042  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis  
; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibody to Alpha E  
; TITLE OF INVENTION: Beta 7 Integrin  
; FILE REFERENCE: L0560/7005/ERP  
; CURRENT APPLICATION NUMBER: US/09/293,238B  
; CURRENT FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-293-238B-11

Query Match 100.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
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Db 4 DKE 6

## RESULT 72

US-09-293-238B-12  
; Sequence 12, Application US/09293238B  
; Patent No. 6455042  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis  
; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibody to Alpha E  
; TITLE OF INVENTION: Beta 7 Integrin  
; FILE REFERENCE: L0560/7005/ERP  
; CURRENT APPLICATION NUMBER: US/09/293,238B  
; CURRENT FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 10  
; TYPE: PRT

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; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-293-238B-12

Query Match 100.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
   |||  
Db 3 DKE 5

## RESULT 73

US-09-293-238B-13  
; Sequence 13, Application US/09293238B  
; Patent No. 6455042  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis  
; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibody to Alpha E  
; TITLE OF INVENTION: Beta 7 Integrin  
; FILE REFERENCE: L0560/7005/ERP  
; CURRENT APPLICATION NUMBER: US/09/293,238B  
; CURRENT FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-293-238B-13

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
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Db 2 DKE 4

## RESULT 74

US-09-293-238B-14  
; Sequence 14, Application US/09293238B  
; Patent No. 6455042  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis  
; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibody to Alpha E  
; TITLE OF INVENTION: Beta 7 Integrin  
; FILE REFERENCE: L0560/7005/ERP  
; CURRENT APPLICATION NUMBER: US/09/293,238B  
; CURRENT FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 10  
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-293-2388-14
Query Match      100.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKE 3
Db      1 DKE 3

. RESULT 75
PCT-US95-02044-8
; Sequence 8, Application PC/TUS9502044
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel integrin alpha subunit
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02044
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,776
; FILING DATE: 18 February 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
PCT-US95-02044-8
Query Match      100.0%; Score 3; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKE 3
Db      7 DKE 9

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 5.96808 Seconds  
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92.715 Million cell updates/sec

Title: US-09-641-801-11

Perfect score: 3

Sequence: 1 DKE 3

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

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Minimum DB seq length: 3

Maximum DB seq length: 20

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	3	100.0	5	10	US-09-264-516A-131
5	3	100.0	5	15	US-10-006-869-721
6	3	100.0	5	15	US-10-141-357-131
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8	3	100.0	6	10	US-09-305-928-108
9	3	100.0	6	15	US-10-006-869-722
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Sequence 39, Appl  
Sequence 49, Appl  
Sequence 60, Appl  
Sequence 80, Appl  
Sequence 210, App  
Sequence 387, App  
Sequence 78, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 18, Appl  
Sequence 19, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 103, App  
Sequence 13, Appl  
Sequence 12, Appl  
Sequence 20, Appl  
Sequence 36, Appl  
Sequence 37, Appl  
Sequence 103, App  
Sequence 7, Appl  
Sequence 28, Appl  
Sequence 442, App  
Sequence 508, App  
Sequence 1096, App  
Sequence 1374, App  
Sequence 1471, App  
Sequence 47743, A

Sequence 124, App  
Sequence 124, App  
Sequence 25, Appli  
Sequence 1, Appli  
Sequence 108, App  
Sequence 358, App  
Sequence 345, App  
Sequence 1, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 207, App  
Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-10-281-652-11  
; Sequence 11, Application US/10281652  
; Publication No. US2003091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOSH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281.652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-11

Query Match 100.0%; Score 3; DB 15; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
DB 1 DKE 3

RESULT 2  
US-09-234-395-107  
; Sequence 107, Application US/09234395  
; Patent No. US20020123044A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER  
; FILE REFERENCE: 100086.407C2  
; CURRENT APPLICATION NUMBER: US/09/234,395  
; CURRENT FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 107  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: Synthesis and Cyclization based on Human  
; OTHER INFORMATION: OB-Cadherin  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-234-395-107

Query Match 100.0%; Score 3; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
DB 3 DKE 5

RESULT 3  
US-09-305-928-107  
; Sequence 107, Application US/09305928  
; Patent No. US20020146687A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER  
; FILE REFERENCE: 100086.407C4  
; CURRENT APPLICATION NUMBER: US/09/305,928  
; CURRENT FILING DATE: 1999-05-05  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 107  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: Synthesis and Cyclization based on Human  
; OTHER INFORMATION: OB-Cadherin  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-305-928-107

Query Match 100.0%; Score 3; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
DB 3 DKE 5

RESULT 4  
US-09-264-516A-131  
; Sequence 131, Application US/09264516A  
; Patent No. US20020169106A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING  
; TITLE OF INVENTION: CANCER METASTASIS  
; FILE REFERENCE: 100086.407C3  
; CURRENT APPLICATION NUMBER: US/09/264,516A  
; CURRENT FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/234,395  
; PRIOR FILING DATE: 1999-01-20  
; PRIOR APPLICATION NUMBER: 09/187,859  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: 09/073,040  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 131

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; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin
; OTHER INFORMATION: cell adhesion recognition sequence
US-09-264-516A-131

Query Match      100.0%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 3 DKE 5

RESULT 5
US-10-006-869-721
; Sequence 721, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 721
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
US-10-006-869-721

Query Match      100.0%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 3 DKE 5

RESULT 6
US-10-141-357-131
; Sequence 131, Application US/10141357
; Publication No. US20030096746A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
; FILE REFERENCE: 100086.407C8
; CURRENT APPLICATION NUMBER: US/10/141,357
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 131
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin
; OTHER INFORMATION: cell adhesion recognition sequence
```

```
US-10-141-357-131

Query Match      100.0%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 3 DKE 5

RESULT 7
US-09-234-395-108
; Sequence 108, Application US/09234395
; Patent No. US20020123044A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C2
; CURRENT APPLICATION NUMBER: US/09/234,395
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: OB-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-234-395-108

Query Match      100.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 4 DKE 6

RESULT 8
US-09-305-928-108
; Sequence 108, Application US/09305928
; Patent No. US20020146687A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C4
; CURRENT APPLICATION NUMBER: US/09/305,928
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: OB-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-305-928-108

Query Match      100.0%; Score 3; DB 10; Length 6;
```

Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

Qy 1 DKE 3  
|||  
Db 4 DKE 6

RESULT 9  
US-09-264-516A-132  
; Sequence 132, Application US/09264516A  
; Patent No. US20020169106A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING  
; TITLE OF INVENTION: CANCER METASTASIS  
; FILE REFERENCE: 100086.407C3  
; CURRENT APPLICATION NUMBER: US/09/264,516A  
; CURRENT FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/234,395  
; PRIOR FILING DATE: 1999-01-20  
; PRIOR APPLICATION NUMBER: 09/187,859  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: 09/073,040  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 132  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin  
; OTHER INFORMATION: cell adhesion recognition sequence  
US-09-264-516A-132

Query Match 100.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 4 DKE 6

RESULT 10  
US-10-006-869-722  
; Sequence 722, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 722  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence  
US-10-006-869-722

Query Match 100.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DKE 3  
|||  
Db 4 DKE 6

RESULT 11  
US-10-141-357-132  
; Sequence 132, Application US/10141357  
; Publication No. US20030096746A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING  
; TITLE OF INVENTION: CANCER METASTASIS  
; FILE REFERENCE: 100086.407C8  
; CURRENT APPLICATION NUMBER: US/10/141,357  
; CURRENT FILING DATE: 2002-05-07  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 132  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin  
; OTHER INFORMATION: cell adhesion recognition sequence  
US-10-141-357-132

Query Match 100.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 4 DKE 6

RESULT 12  
US-09-234-395-110  
; Sequence 110, Application US/09234395  
; Patent No. US20020123044A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER  
; FILE REFERENCE: 100086.407C2  
; CURRENT APPLICATION NUMBER: US/09/234,395  
; CURRENT FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 110  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: Synthesis and Cyclization based on Human  
; OTHER INFORMATION: OB-Cadherin  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide  
US-09-234-395-110

Query Match 100.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||

Db 5 DKE 7

## RESULT 13

US-09-305-928-110  
; Sequence 110, Application US/09305928  
; Patent No. US20020146687A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER  
; FILE REFERENCE: 100086.407C4  
; CURRENT APPLICATION NUMBER: US/09/305,928  
; CURRENT FILING DATE: 1999-05-05  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 110  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Product of  
; OTHER INFORMATION: Synthesis and Cyclization based on Human  
; OTHER INFORMATION: OB-Cadherin  
; FEATURE:  
; OTHER INFORMATION: Cyclic Peptide

US-09-305-928-110

Query Match 100.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 5 DKE 7

## RESULT 14

US-09-264-516A-134  
; Sequence 134, Application US/09264516A  
; Patent No. US20020169106A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING  
; TITLE OF INVENTION: CANCER METASTASIS  
; FILE REFERENCE: 100086.407C3  
; CURRENT APPLICATION NUMBER: US/09/264,516A  
; CURRENT FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/234,395  
; PRIOR FILING DATE: 1999-01-20  
; PRIOR APPLICATION NUMBER: 09/187,859  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: 09/073,040  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 134  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin  
; OTHER INFORMATION: cell adhesion recognition sequence

Query Match 100.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3

Db 5 DKE 7  
|||

## RESULT 15

US-09-972-656-12  
; Sequence 12, Application US/09972656  
; Publication No. US20030099647A1  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Tsai, Mei-Mei  
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
; TITLE OF INVENTION: Neutralizing Activity  
; FILE REFERENCE: A-799  
; CURRENT APPLICATION NUMBER: US/09/972,656  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-972-656-12

Query Match 100.0%; Score 3; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 2 DKE 4

## RESULT 16

US-10-044-967-10  
; Sequence 10, Application US/10044967  
; Publication No. US20030073218A1  
; GENERAL INFORMATION:  
; APPLICANT: Shokat, Kevan M.  
; TITLE OF INVENTION: High Affinity Kinase Inhibitors for Target Validation  
; TITLE OF INVENTION: and Uses Thereof  
; FILE REFERENCE: 51538-5001-US  
; CURRENT APPLICATION NUMBER: US/10/044,967  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 09/480,993  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/115,340  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-11  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Imaginary  
; OTHER INFORMATION: sequence for enzyme modelling

US-10-044-967-10

Query Match 100.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 5 DKE 7

## RESULT 17

US-10-006-869-724  
; Sequence 724, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:

```
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT FILING DATE: 2001-12-03
; CURRENT APPLICATION NUMBER: US/10/006.869
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 724
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
US-10-006-869-724

Query Match          100.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKE 3
        |||
Db      5 DKE 7

RESULT 18
US-10-141-357-134
; Sequence 134, Application US/10141357
; Publication No. US20030096746A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
; TITLE OF INVENTION: CANCER METASTASIS
; FILE REFERENCE: 100086.407C8
; CURRENT FILING DATE: 2002-05-07
; CURRENT APPLICATION NUMBER: US/10/141.357
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 134
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin
; OTHER INFORMATION: cell adhesion recognition sequence
US-10-141-357-134

Query Match          100.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKE 3
        |||
Db      5 DKE 7

RESULT 19
US-09-234-395-116
; Sequence 116, Application US/09234395
; Patent No. US20020123044A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C2
; CURRENT APPLICATION NUMBER: US/09/234.395
; - CURRENT APPLICATION NUMBER: US/09/234.395
```

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; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 116
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: OB-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-234-395-116

Query Match          100.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKE 3
        |||
Db      6 DKE 8

RESULT 20
US-09-305-928-116
; Sequence 116, Application US/09305928
; Patent No. US2002014687A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 100086.407C4
; CURRENT FILING DATE: 1999-05-05
; CURRENT APPLICATION NUMBER: US/09/305.928
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 116
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: OB-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-305-928-116

Query Match          100.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKE 3
        |||
Db      6 DKE 8

RESULT 21
US-09-264-516A-140
; Sequence 140, Application US/09264516A
; Patent No. US20020169106A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
; TITLE OF INVENTION: CANCER METASTASIS
; FILE REFERENCE: 100086.407C3
; CURRENT APPLICATION NUMBER: US/09/264.516A
; CURRENT FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/234.395
```

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; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 09/187,859
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/073,040
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 140
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin
; OTHER INFORMATION: cell adhesion recognition sequence
; US-09-264-516A-140

Query Match          100.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKE 3
Db      6 DKE 8

RESULT 22
US-10-239-313A-159
; Sequence 159, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-10-239-313A-159

Query Match          100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKE 3
Db      4 DKE 6

RESULT 23
US-10-351-641-1600
; Sequence 1600, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
```

```
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1600
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
; US-10-351-641-1600

Query Match          100.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKE 3
Db      5 DKE 7

RESULT 24
US-10-006-869-730
; Sequence 730, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 730
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence
; US-10-006-869-730

Query Match          100.0%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DKE 3
Db      6 DKE 8

RESULT 25
US-10-141-357-140
; Sequence 140, Application US/10141357
; Publication No. US20030096746A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
; TITLE OF INVENTION: CANCER METASTASIS
; FILE REFERENCE: 100086.407C8
; CURRENT APPLICATION NUMBER: US/10/141,357
; CURRENT FILING DATE: 2002-05-07
```

```
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 140
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin
; OTHER INFORMATION: cell adhesion recognition sequence
US-10-141-357-140

Query Match      100.0%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 6 DKE 8

RESULT 26
US-08-464-363-55
; Sequence 55, Application US/08464363
; Publication No. US20030035815A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBINANT PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal
US-08-464-363-55

Query Match      100.0%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 1 DKE 3

RESULT 27
US-09-234-395-119
; Sequence 119, Application US/09234395
; Patent No. US20020123044A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 10086.407C2
; CURRENT APPLICATION NUMBER: US/09/234,395
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-234-395-119

Query Match      100.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
Db 7 DKE 9

RESULT 28
US-09-305-928-119
; Sequence 119, Application US/09305928
; Patent No. US20020146687A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND EVALUATING CANCER
; FILE REFERENCE: 10086.407C4
; CURRENT APPLICATION NUMBER: US/09/305,928
; CURRENT FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Synthesis and Cyclization based on Human
; OTHER INFORMATION: OB-Cadherin
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-305-928-119

Query Match      100.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3
```



Db |||  
7 DKE 9

## RESULT 29

US-09-264-516A-143  
; Sequence 143, Application US/09264516A  
; Patent No. US20020169106A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING  
; TITLE OF INVENTION: CANCER METASTASIS  
; FILE REFERENCE: 100086.407C3  
; CURRENT APPLICATION NUMBER: US/09/264,516A  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/234,395  
; PRIOR FILING DATE: 1999-01-20  
; PRIOR APPLICATION NUMBER: 09/187,859  
; PRIOR FILING DATE: 1998-11-06  
; PRIOR APPLICATION NUMBER: 09/073,040  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 319  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 143  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin  
; OTHER INFORMATION: cell adhesion recognition sequence

Query Match 100.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 7 DKE 9

## RESULT 30

US-09-770-102A-24  
; Sequence 24, Application US/09770102A  
; Publication No. US20020197606A1  
; GENERAL INFORMATION:  
; APPLICANT: Cyclacel  
; TITLE OF INVENTION: Compositions and Methods for Monitoring the Modification of Modifi  
; TITLE OF INVENTION: Dependent Binding Partner Polypeptides  
; FILE REFERENCE: 10069/1062  
; CURRENT APPLICATION NUMBER: US/09/770,102A  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 60/179283  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
; NAME/KEY: DOMAIN  
; LOCATION: (1)...(9)  
; OTHER INFORMATION: Consensus sequence

Query Match 100.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 7 DKE 9

## RESULT 31

US-09-770-102A-27  
; Sequence 27, Application US/09770102A  
; Publication No. US20020197606A1  
; GENERAL INFORMATION:  
; APPLICANT: Cyclacel  
; TITLE OF INVENTION: Compositions and Methods for Monitoring the Modification of Modi  
; TITLE OF INVENTION: Dependent Binding Partner Polypeptides  
; FILE REFERENCE: 10069/1062  
; CURRENT APPLICATION NUMBER: US/09/770,102A  
; CURRENT FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 60/179283  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
; NAME/KEY: DOMAIN  
; LOCATION: (1)...(9)  
; OTHER INFORMATION: Consensus sequence

Query Match 100.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 7 DKE 9

## RESULT 32

US-10-308-967-24  
; Sequence 24, Application US/10308967  
; Publication No. US20030162237A1  
; GENERAL INFORMATION:  
; APPLICANT: Cyclacel, Ltd.  
; APPLICANT: Griffiths, Gary  
; TITLE OF INVENTION: Methods of Monitoring Enzyme Activity  
; FILE REFERENCE: 10069/2002  
; CURRENT APPLICATION NUMBER: US/10/308,967  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: PCT/GB01/02502  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: GB0013888.3  
; PRIOR FILING DATE: 2000-06-07  
; PRIOR APPLICATION NUMBER: 60/211,313  
; PRIOR FILING DATE: 2000-06-13  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fyn N-Myristoylation site

Query Match 100.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||

Db 7 DKE 9

## RESULT 33

US-10-308-967-27  
; Sequence 27, Application US/10308967  
; Publication No. US20030162237A1

; GENERAL INFORMATION:

; APPLICANT: Cyclacel, Ltd.

; TITLE OF INVENTION: Methods of Monitoring Enzyme Activity

; FILE REFERENCE: 10069/2002

; CURRENT APPLICATION NUMBER: US/10/308,967

; CURRENT FILING DATE: 2002-12-03

; PRIOR APPLICATION NUMBER: PCT/GB01/02502

; PRIOR FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: GB0013888.3

; PRIOR FILING DATE: 2000-06-07

; PRIOR APPLICATION NUMBER: 60/211,313

; PRIOR FILING DATE: 2000-06-13

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 27

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Fyn Palmitoylation site

US-10-308-967-27

Query Match 100.0%; Score 3; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3

Db 7 DKE 9

## RESULT 34

US-09-824-200-8

; Sequence 8, Application US/09824200

; Publication No. US20030167531A1

; GENERAL INFORMATION:

; APPLICANT: RUSSELL, DOUGLAS A.

; TITLE OF INVENTION: SCHLITTLER, MICHAEL

; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF BIOACTIVE, AUTHENTIC

; FILE REFERENCE: 16712.0031

; CURRENT APPLICATION NUMBER: US/09/824,200

; CURRENT FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 60/194,217

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-824-200-8

Query Match 100.0%; Score 3; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3

Db 5 DKE 7

## RESULT 35

US-10-006-869-733

; "Sequence 733, Application US/10006869

; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 733  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: OB-cadherin cell adhesion recognition sequence  
US-10-006-869-733

Query Match 100.0%; Score 3; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3

Db 7 DKE 9

## RESULT 36

US-10-141-357-143

; Sequence 143, Application US/10141357

; Publication No. US20030096746A1

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Symonds, James Matthew

; APPLICANT: Byers, Stephen

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING

; TITLE OF INVENTION: CANCER METASTASIS

; FILE REFERENCE: 100086.407C8

; CURRENT APPLICATION NUMBER: US/10/141,357

; CURRENT FILING DATE: 2002-05-07

; NUMBER OF SEQ ID NOS: 319

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 143

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthesized cyclic peptide with an OB-cadherin

; OTHER INFORMATION: cell adhesion recognition sequence

US-10-141-357-143

Query Match

Best Local Similarity 100.0%; Score 3; DB 15; Length 9;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3

Db 7 DKE 9

## RESULT 37

US-09-572-404B-1276

; Sequence 1276, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572.404B

; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1276  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in EZH1 at 391-400 and may interact with Sequen  
; OTHER INFORMATION: in this patent.  
US-09-572-404B-1276

Query Match 100.0%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 4 DKE 6

## RESULT 38

US-09-572-404B-1278  
; Sequence 1278, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1278  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in EZH1 at 390-399 and may interact with Sequen  
; OTHER INFORMATION: in this patent.  
US-09-572-404B-1278

Query Match 100.0%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 5 DKE 7

## RESULT 39

US-09-572-404B-1578  
; Sequence 1578, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1578  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in KIAA0052 at 26-35 and may interact with Sequen  
; OTHER INFORMATION: 1577 in this patent.  
US-09-572-404B-1578

Query Match 100.0%; Score 3; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 5 DKE 7

## RESULT 40

US-09-572-404B-1648  
; Sequence 1648, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1648  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in YARS at 295-304 and may interact with Sequen  
; OTHER INFORMATION: in this patent.  
US-09-572-404B-1648

Query Match 100.0%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 4 DKE 6

## RESULT 41

US-09-572-404B-1672  
; Sequence 1672, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1672  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in EPHA7 OR EH3 OR HEK11 at 302-311 and may in  
; OTHER INFORMATION: with Sequence 1671 in this patent.  
US-09-572-404B-1672

Query Match 100.0%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 2 DKE 4

## RESULT 42

US-09-572-404B-1682  
; Sequence 1682, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProPatent version 1.0  
; SEQ ID NO 1682  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in FER OR TYK3 at 37-46 and may interact with Se  
; OTHER INFORMATION: 1681 in this patent.  
US-09-572-404B-1682

Query Match 100.0%; Score 3; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 3 DKE 5

RESULT 43  
US-10-177-550-8  
; Sequence 8, Application US/10177550  
; Publication No. US20030133933A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. US20030133933A1e1 Integrin Alpha Subunit  
; FILE REFERENCE: L00560/70009(MAT/JAV)  
; CURRENT APPLICATION NUMBER: US/10/177,550  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 09/293,238  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-177-550-8

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 7 DKE 9

RESULT 44  
US-10-177-550-9  
; Sequence 9, Application US/10177550  
; Publication No. US20030133933A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. US20030133933A1e1 Integrin Alpha Subunit  
; FILE REFERENCE: L00560/70009(MAT/JAV)  
; CURRENT APPLICATION NUMBER: US/10/177,550  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 09/293,238

; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-177-550-9

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 6 DKE 8

RESULT 45  
US-10-177-550-10  
; Sequence 10, Application US/10177550  
; Publication No. US20030133933A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. US20030133933A1e1 Integrin Alpha Subunit  
; FILE REFERENCE: L00560/70009(MAT/JAV)  
; CURRENT APPLICATION NUMBER: US/10/177,550  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 09/293,238  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-177-550-10

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 5 DKE 7

RESULT 46  
US-10-177-550-11  
; Sequence 11, Application US/10177550  
; Publication No. US20030133933A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. US20030133933A1e1 Integrin Alpha Subunit  
; FILE REFERENCE: L00560/70009(MAT/JAV)  
; CURRENT APPLICATION NUMBER: US/10/177,550  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 09/293,238  
; PRIOR FILING DATE: 1999-04-16

; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-177-550-11

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 4 DKE 6

RESULT 47  
US-10-177-550-12  
; Sequence 12, Application US/10177550  
; Publication No. US20030133933A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. US20030133933A1e1 Integrin Alpha Subunit  
; FILE REFERENCE: L00560/70009 (MAT/JAV)  
; CURRENT APPLICATION NUMBER: US/10/177,550  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 09/293,238  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-177-550-12

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 3 DKE 5

RESULT 48  
US-10-177-550-13  
; Sequence 13, Application US/10177550  
; Publication No. US20030133933A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. US20030133933A1e1 Integrin Alpha Subunit  
; FILE REFERENCE: L00560/70009 (MAT/JAV)  
; CURRENT APPLICATION NUMBER: US/10/177,550  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 09/293,238  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338

; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-177-550-13

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 2 DKE 4

RESULT 49  
US-10-177-550-14  
; Sequence 14, Application US/10177550  
; Publication No. US20030133933A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. US20030133933A1e1 Integrin Alpha Subunit  
; FILE REFERENCE: L00560/70009 (MAT/JAV)  
; CURRENT APPLICATION NUMBER: US/10/177,550  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 09/293,238  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-177-550-14

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 1 DKE 3

RESULT 50  
US-10-350-258-1  
; Sequence 1, Application US/10350258  
; Publication No. US20030139345A1  
; GENERAL INFORMATION:  
; APPLICANT: MATTHIAS RATH  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND METHODS FOR TREATING CANCER INVASION AND  
; FILE REFERENCE: 11957/23  
; CURRENT APPLICATION NUMBER: US/10/350,258  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: 60/351,317  
; PRIOR FILING DATE: January 23, 2002  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1

LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-350-258-1

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 8 DKE 10

## RESULT 51

US-10-239-313A-158  
; Sequence 158, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 158  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-158

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 4 DKE 6

## RESULT 52

US-10-118-471-3  
; Sequence 3, Application US/10118471  
; Publication No. US20030190600A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN, KEMIN  
; APPLICANT: ZELUS, BRUCE D.  
; APPLICANT: MEIJERS, ROB  
; APPLICANT: HOLMES, KATHRYN V.  
; APPLICANT: WANG, JIA-HUAI  
; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN CELL ADHESION MOLECULE  
; TITLE OF INVENTION: (CEACAM1) STRUCTURE AND USES THEREOF IN DRUG  
; TITLE OF INVENTION: IDENTIFICATION AND SCREENING  
; FILE REFERENCE: 400425  
; CURRENT APPLICATION NUMBER: US/10/118,471  
; CURRENT FILING DATE: 2002-08-22  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-118-471-3

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 8 DKE 10

## RESULT 53

US-10-138-176-3  
; Sequence 3, Application US/10138176  
; Publication No. US20030211477A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN, KEMIN  
; APPLICANT: ZELUS, BRUCE D.  
; APPLICANT: MEIJERS, ROB  
; APPLICANT: HOLMES, KATHRYN V.  
; APPLICANT: WANG, JIA-HUAI  
; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN CELL ADHESION MOLECULE  
; TITLE OF INVENTION: (CEACAM1) STRUCTURE AND USES THEREOF IN DRUG  
; TITLE OF INVENTION: IDENTIFICATION AND SCREENING  
; FILE REFERENCE: 400425  
; CURRENT APPLICATION NUMBER: US/10/138,176  
; CURRENT FILING DATE: 2002-05-01  
; PRIOR APPLICATION NUMBER: 10/118,471  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-138-176-3

Query Match 100.0%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 8 DKE 10

## RESULT 54

US-08-464-363-27  
; Sequence 27, Application US/08464363  
; Publication No. US20030035815A1  
; GENERAL INFORMATION:  
; APPLICANT: ROGERS, BRUCE L.  
; APPLICANT: Morgenstern, Jay  
; APPLICANT: Bond, Julian F.  
; APPLICANT: Garman, Richard D.  
; APPLICANT: Greenstein, Julia L.  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Morvile, Malcolm  
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lahive & Cockfield  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,363

;  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/807,529  
; FILING DATE: 13-DEC-1991  
; APPLICATION NUMBER: US 07/662,276  
; FILING DATE: 28-FEB-1991  
; APPLICATION NUMBER: US 07/431,565  
; FILING DATE: 03-NOV-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amy E. Mandragouras  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: IM1-01SCN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-464-363-27

Query Match 100.0%; Score 3; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 3 DKE 5

RESULT 55  
US-09-883-825-21  
; Sequence 21, Application US/09883825  
; Patent No. US20020151024A1  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; Bentley, Kelley  
; Charbonneau, Harry  
; Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/883,825  
; FILING DATE: 18-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/123,783  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/297,494  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20020151024Aland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:

;  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-883-825-21  
  
Query Match 100.0%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DKE 3  
|||  
Db 9 DKE 11  
  
RESULT 56  
US-10-283-028-16  
; Sequence 16, Application US/10283028  
; Publication No. US20030143684A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerard, Craig J.  
; Gerard, No. US20030143684Alma P.  
; Mackay, Charles R.  
; Ponath, Paul D.  
; Post, Theodore W.  
; Qin, Shixin  
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND  
; ANTAGONISTS THEREOF  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/283,028  
; FILING DATE: 28-Oct-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/720,565  
; FILING DATE: 30-SEP-1996  
; APPLICATION NUMBER: PCT/US96/00608  
; FILING DATE: 19-JAN-1996  
; APPLICATION NUMBER: US 08/375,199  
; FILING DATE: 19-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: LKS94-05A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-10-283-028-16

Query Match 100.0%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
DB 8 DKE 10

RESULT 57  
US-10-020-269-25  
; Sequence 25, Application US/10020269  
; Publication No. US20030175310A1  
; GENERAL INFORMATION:  
; APPLICANT: Mitchell, William M.  
; APPLICANT: Stratton, Charles W.  
; TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE  
; FILE REFERENCE: SEQUENCES  
; CURRENT APPLICATION NUMBER: US/10/020,269  
; CURRENT FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/025,596  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/023,921  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-14  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-10-020-269-25

Query Match 100.0%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
DB 8 DKE 10

RESULT 58  
US-09-876-904A-414  
; Sequence 414, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 414  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Gallus sp.  
; FEATURE:  
; OTHER INFORMATION: Chicken VBP (vitellogenin gene-binding protein).  
US-09-876-904A-414

Query Match 100.0%; Score 3; DB 11; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||

DB 1 DKE 3

RESULT 59  
US-10-043-487-404  
; Sequence 404, Application US/10043487  
; Publication No. US20030055220A1  
; GENERAL INFORMATION:  
; APPLICANT: HYBRIGENICS  
; APPLICANT: Pierre, LEGRAIN  
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptides  
; FILE REFERENCE: B4778A  
; CURRENT APPLICATION NUMBER: US/10/043,487  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/261,130  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 561  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 404  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Shigella Flexneri  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(2)  
; OTHER INFORMATION: MISC FEATURE  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (4)-(6)  
; OTHER INFORMATION: MISC FEATURE  
US-10-043-487-404

Query Match 100.0%; Score 3; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
DB 8 DKE 10

RESULT 60  
US-10-094-401-159  
; Sequence 159, Application US/10094401  
; Publication No. US20030069395A1  
; GENERAL INFORMATION:  
; APPLICANT: DYAX CORP.  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Lev, Arthur C.  
; APPLICANT: Cohen, Edward H.  
; TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES  
; FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US  
; CURRENT APPLICATION NUMBER: US/10/094,401  
; CURRENT FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/331,352  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/292,975  
; PRIOR FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 271  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 159  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: albumin binding peptide  
US-10-094-401-159

Query Match 100.0%; Score 3; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 DKE 3  
|||  
Db 6 DKE 8

## RESULT 61

US-09-813-329-39  
; Sequence 39, Application US/09813329  
; Patent No. US20020012968A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole  
; FILE REFERENCE: D0016.np  
; CURRENT APPLICATION NUMBER: US/09/813,329  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/190,816  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 39  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-813-329-39

Query Match 100.0%; Score 3; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 1 DKE 3

## RESULT 62

US-09-813-329-49  
; Sequence 49, Application US/09813329  
; Patent No. US20020012968A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole  
; FILE REFERENCE: D0016.np  
; CURRENT APPLICATION NUMBER: US/09/813,329  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/190,816  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 49  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-813-329-49

Query Match 100.0%; Score 3; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 1 DKE 3

## RESULT 63

US-09-813-329-60  
; Sequence 60, Application US/09813329  
; Patent No. US20020012968A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole  
; FILE REFERENCE: D0016.np  
; CURRENT APPLICATION NUMBER: US/09/813,329  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/190,816  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 60  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-813-329-60

FILE REFERENCE: D0016.np  
; CURRENT APPLICATION NUMBER: US/09/813,329  
; CURRENT FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 60/190,816  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 60  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-813-329-60

Query Match 100.0%; Score 3; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 1 DKE 3

## RESULT 64

US-09-826-290-80  
; Sequence 80, Application US/09826290  
; Patent No. US2002016468A1  
; GENERAL INFORMATION:  
; APPLICANT: Durham, L. Kathryn  
; APPLICANT: Friedman, David L.  
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
; APPLICANT: Kimmel, Lida H.  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Potter, David M.  
; APPLICANT: Rohlf, Christian  
; APPLICANT: Silber, B. Michael  
; APPLICANT: Stiger, Thomas R.  
; APPLICANT: Sunderland, P. Trey  
; APPLICANT: Townsend, Robert Reid  
; APPLICANT: White, Frost  
; APPLICANT: Williams, Stephen A.  
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and  
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of  
; TITLE OF INVENTION: Alzheimer's Disease  
; FILE REFERENCE: 2572-1-001 N2  
; CURRENT APPLICATION NUMBER: US/09/826,290  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/194,504  
; PRIOR FILING DATE: 2000-04-03  
; PRIOR APPLICATION NUMBER: US 60/253,647  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 492  
; SOFTWARE: FastSeq for Windows, Version 4.0  
; SEQ ID NO 80  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-09-826-290-80

Query Match 100.0%; Score 3; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 6 DKE 8

## RESULT 65

US-09-876-904A-210  
; Sequence 210, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIORITY FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 210

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: DBD peptide

US-09-876-904A-210,

Query Match 100.0%; Score 3; DB 11; Length 13;

Best Local Similarity 100.0%; Pred. No. 8.1e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3

DB 6 DKE 8

RESULT 66

US-09-876-904A-387

; Sequence 387, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIORITY FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 387

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

; FEATURE:

; OTHER INFORMATION: C. elegans Sdc-3 protein.

US-09-876-904A-387

Query Match

Best Local Similarity 100.0%; Score 3; DB 11; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3

DB 6 DKE 8

RESULT 67

US-10-325-694-78

; Sequence 78, Application US/10325694

; Publication No. US20030148463A1

; GENERAL INFORMATION:

; APPLICANT: KUFER, PETER

; APPLICANT: RAUM, TORBAS

; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN

; TITLE OF INVENTION: RECEPTORS AND USES THEREOF

; FILE REFERENCE: 38164000

; CURRENT APPLICATION NUMBER: US/10/325,694

; CURRENT FILING DATE: 2002-12-19

; PRIOR APPLICATION NUMBER: US/09/403,107

; PRIOR FILING DATE: 1999-10-14

; NUMBER OF SEQ ID NOS: 152

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 78

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

US-10-325-694-78

Query Match

Best Local Similarity 100.0%; Score 3; DB 12; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3

DB 2 DKE 4

RESULT 68

US-10-118-471-4

; Sequence 4, Application US/10118471

; Publication No. US20030190600A1

; GENERAL INFORMATION:

; APPLICANT: TAN, KEMIN

; APPLICANT: ZELUS, BRUCE D.

; APPLICANT: MEIJERS, ROB

; APPLICANT: HOLMES, KATHRYN V.

; APPLICANT: WANG, JIA-HUAI

; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN CELL ADHESION MOLECULE

; TITLE OF INVENTION: (CEACAM1) STRUCTURE AND USES THEREOF IN DRUG

; TITLE OF INVENTION: IDENTIFICATION AND SCREENING

; FILE REFERENCE: 400425

; CURRENT APPLICATION NUMBER: US/10/118,471

; CURRENT FILING DATE: 2002-08-22

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Mus sp.

US-10-118-471-4

Query Match

Best Local Similarity 100.0%; Score 3; DB 12; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3

DB 10 DKE 12

RESULT 69

US-10-138-176-4

; Sequence 4, Application US/10138176

; Publication No. US20030211477A1

; GENERAL INFORMATION:

; APPLICANT: TAN, KEMIN

; APPLICANT: ZELUS, BRUCE D.

; APPLICANT: MEIJERS, ROB

; APPLICANT: HOLMES, KATHRYN V.

; APPLICANT: WANG, JIA-HUAI

; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN CELL ADHESION MOLECULE

; TITLE OF INVENTION: (CEACAM1) STRUCTURE AND USES THEREOF IN DRUG

; TITLE OF INVENTION: IDENTIFICATION AND SCREENING

; FILE REFERENCE: 400425

; CURRENT APPLICATION NUMBER: US/10/138,176

; CURRENT FILING DATE: 2002-05-01

; PRIOR APPLICATION NUMBER: 10/118,471

; PRIOR FILING DATE: 2002-04-05

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-138-176-4

Query Match 100.0%; Score 3; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 10 DKE 12

## RESULT 70

US-10-177-550-18  
; Sequence 18, Application US/10177550  
; Publication No. US20030133933A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. US20030133933A1e1 Integrin Alpha Subunit  
; FILE REFERENCE: L00560/70009 (MAT/JAV)  
; CURRENT APPLICATION NUMBER: US/10/177,550  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 09/293,238  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-177-550-18

Query Match 100.0%; Score 3; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 3 DKE 5

## RESULT 71

US-10-177-550-19  
; Sequence 19, Application US/10177550  
; Publication No. US20030133933A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenner, Michael B.  
; APPLICANT: Parker, Christina M.  
; TITLE OF INVENTION: No. US20030133933A1e1 Integrin Alpha Subunit  
; FILE REFERENCE: L00560/70009 (MAT/JAV)  
; CURRENT APPLICATION NUMBER: US/10/177,550  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 09/293,238  
; PRIOR FILING DATE: 1999-04-16  
; PRIOR APPLICATION NUMBER: US 08/879,338  
; PRIOR FILING DATE: 1997-06-20  
; PRIOR APPLICATION NUMBER: US 08/663,731  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: US 08/199,776  
; PRIOR FILING DATE: 1994-02-18  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19

; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-177-550-19

Query Match 100.0%; Score 3; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 9 DKE 11

## RESULT 72

US-10-221-125-1  
; Sequence 1, Application US/10221125  
; Publication No. US20030191058A1  
; GENERAL INFORMATION:  
; APPLICANT: The Walter and Eliza Hall Institute of Medical Research  
; TITLE OF INVENTION: A method and agents useful for same  
; FILE REFERENCE: 2392478/EJH  
; CURRENT APPLICATION NUMBER: US/10/221,125  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: AU PQ6147  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-221-125-1

Query Match 100.0%; Score 3; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 4 DKE 6

## RESULT 73

US-10-221-125-2  
; Sequence 2, Application US/10221125  
; Publication No. US20030191058A1  
; GENERAL INFORMATION:  
; APPLICANT: The Walter and Eliza Hall Institute of Medical Research  
; TITLE OF INVENTION: A method and agents useful for same  
; FILE REFERENCE: 2392478/EJH  
; CURRENT APPLICATION NUMBER: US/10/221,125  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: AU PQ6147  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-221-125-2

Query Match 100.0%; Score 3; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 4 DKE 6

## RESULT 74

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US-08-860-844-103
; Sequence 103, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-860-844-103

Query Match 100.0%; Score 3; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3
Db 7 DKE 9

RESULT 75
US-09-873-438-13
; Sequence 13, Application US/09873438
; Patent No. US20020115140A1
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; Gimeno, Carlos J.
; TITLE OF INVENTION: RATH GENES AND POLYPEPTIDES AND METHODS
; FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/873,438
FILING DATE: 04-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/870,815
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-873-438-13

Query Match 100.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3
Db 9 DKE 11

Search completed: November 25, 2003, 20:25:38
Job time : 6.96808 secs
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 9.71809 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-11

Perfect score: 3

Sequence: 1 DKE 3

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	100.0	3	22	Colostrin derive
2	3	100.0	4	19	Human HE4 epitope
3	3	100.0	5	21	OB-cadherin cell a
4	3	100.0	5	21	OB-cadherin cell a
5	3	100.0	5	23	OB-cadherin CAR pe
6	3	100.0	5	23	Human TRIP leucine
7	3	100.0	5	24	OB-cadherin cell a
8	3	100.0	5	24	OB-cadherin cell a
9	3	100.0	6	15	Mycoplasma cancer

10	3	100.0	6	15	AAE64051	Peptide which bind
11	3	100.0	6	16	AAE67583	Cancer metastasis
12	3	100.0	6	21	AAE73602	OB-cadherin cell a
13	3	100.0	6	21	AAE60688	OB-cadherin cell a
14	3	100.0	6	22	AAE55777	PDZ motif sequence
15	3	100.0	6	22	AAE57609	Neurexin C-termina
16	3	100.0	6	22	AAE58019	Neurexin C-termina
17	3	100.0	6	23	ABG92300	OB-cadherin CAR pe
18	3	100.0	6	23	ABJ05275	T-cell surface rec
19	3	100.0	6	23	ABP63503	PDZ motif (PL) pep
20	3	100.0	6	24	ABU60023	OB-cadherin cell a
21	3	100.0	6	24	ABE99805	Peptide derived fr
22	3	100.0	6	24	ABU55832	OB-cadherin cell a
23	3	100.0	7	4	AAE30278	Sequence of the H
24	3	100.0	7	15	AAE64049	Peptide which bind
25	3	100.0	7	18	AAE30416	HRE-1 affinity pep
26	3	100.0	7	19	AAE54301	Human cytohesin-1
27	3	100.0	7	19	AAE54302	Human cytohesin-1
28	3	100.0	7	19	AAE54303	Human cytohesin-1
29	3	100.0	7	19	AAE54308	Human cytohesin-1
30	3	100.0	7	19	AAE54309	Human cytohesin-1
31	3	100.0	7	21	AAE73604	OB-cadherin cell a
32	3	100.0	7	21	AAE60690	OB-cadherin cell a
33	3	100.0	7	22	AAU08769	Soybean trypsin in
34	3	100.0	7	22	AAE75097	Nucleotide-5'-phos
35	3	100.0	7	22	AAE55778	PDZ motif sequence
36	3	100.0	7	22	AAE57610	Neurexin C-termina
37	3	100.0	7	22	AAE58020	Neurexin C-termina
38	3	100.0	7	23	ABG92302	OB-cadherin CAR pe
39	3	100.0	7	23	ABU05276	T-cell surface rec
40	3	100.0	7	23	ABP63504	PDZ motif (PL) pep
41	3	100.0	7	24	ABU60025	OB-cadherin cell a
42	3	100.0	7	24	ABU55834	OB-cadherin cell a
43	3	100.0	8	10	AAE91025	Hapten for prodn.
44	3	100.0	8	16	AAE70803	HIV(B35)ARV2-1, hu
45	3	100.0	8	16	AAE69840	Peptide comprising
46	3	100.0	8	21	AAE08328	Epitope derived fr
47	3	100.0	8	21	AAE73610	OB-cadherin cell a
48	3	100.0	8	21	AAE60696	OB-cadherin cell a
49	3	100.0	8	22	ABE14450	HIV A03 super moti
50	3	100.0	8	22	ABE16692	HIV B07 super moti
51	3	100.0	8	22	ABE16693	HIV B07 super moti
52	3	100.0	8	22	ABE17146	HIV B27 super moti
53	3	100.0	8	22	ABE18709	HIV B62 super moti
54	3	100.0	8	22	ABE18750	HIV B62 super moti
55	3	100.0	8	22	ABE20342	HIV A03 motif gag
56	3	100.0	8	22	ABE20359	HIV A03 motif gag
57	3	100.0	8	22	ABE22624	HIV A11 motif gag
58	3	100.0	8	22	ABE22633	HIV A11 motif gag
59	3	100.0	8	22	AAE99056	Vaccine related MH
60	3	100.0	8	22	AAE78499	PDZ motif sequence
61	3	100.0	8	22	AAE55779	HIV-1 gp 41 enhanc
62	3	100.0	8	22	AAE57611	Neurexin C-termina
63	3	100.0	8	22	AAE58021	Neurexin C-termina
64	3	100.0	8	23	ABG92308	OB-cadherin CAR pe
65	3	100.0	8	23	ABJ05277	T-cell surface rec
66	3	100.0	8	23	ABE63505	PDZ motif (PL) pep
67	3	100.0	8	24	ABE48409	Peptide SEQ ID NO:
68	3	100.0	8	24	ABU60031	Peptide SEQ ID NO:
69	3	100.0	8	24	ABU55840	OB-cadherin cell a
70	3	100.0	8	24	ABU55840	OB-cadherin cell a
71	3	100.0	9	16	AAE21332	Glucagon precursor
72	3	100.0	9	16	AAE74191	Netrin domain V pe
73	3	100.0	9	20	AAE55530	HLA binding plu-1
74	3	100.0	9	20	AAE25228	HIV gag protein de
75	3	100.0	9	21	AAE22053	Fyn protein N-myri
76	3	100.0	9	21	AAE22092	Fyn protein N-myri
77	3	100.0	9	21	AAE73613	OB-cadherin cell a
78	3	100.0	9	21	AAE60699	OB-cadherin cell a
79	3	100.0	9	22	ABE12763	HIV A02 super moti
80	3	100.0	9	22	ABE12764	HIV A02 super moti
81	3	100.0	9	22	ABE12765	HIV A02 super moti
82	3	100.0	9	22	ABE12767	HIV A02 super moti

83 3 100.0 9 22 ABP15631 HIV A24 super moti  
84 3 100.0 9 22 ABP15632 HIV A24 super moti  
85 3 100.0 9 22 ABP17175 HIV B27 super moti  
86 3 100.0 9 22 AAU05236 Palmitoylation site  
87 3 100.0 9 22 AAB99456 Post-translational  
88 3 100.0 9 22 AAB83818 Amino acid sequenc  
89 3 100.0 9 23 ABG92311 OB-cadherin CAR pe  
90 3 100.0 9 23 ABB76331 Haemophilus influe  
91 3 100.0 9 23 ABG34937 Human bone marrow  
92 3 100.0 9 23 AAE13262 Fusion peptide #6  
93 3 100.0 9 23 AAU75533 Oncoprotein fyn, N  
94 3 100.0 9 23 AAU75536 Oncoprotein fyn, p  
95 3 100.0 9 24 ABR04717 Human cancer-relat  
96 3 100.0 9 24 ABR04762 Human cancer-relat  
97 3 100.0 9 24 ABR05332 Human cancer-relat  
98 3 100.0 9 24 ABU60034 OB-cadherin cell a  
99 3 100.0 9 24 ABP83691 HLA protein 121P2A  
100 3 100.0 9 24 ABP83702 HLA protein 121P2A

## ALIGNMENTS

## RESULT 1

AAB72256  
ID AAB72256 standard; peptide; 3 AA.

XX AAB72256;

XX 14-MAY-2001 (first entry)

XX Colostrin derived cytokine inducing peptide SEQ ID 11.

XX Colostrin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Stanton GU, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrin as an immunological  
PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,  
CC a proline rich polypeptide aggregate contained in colostrum. The  
CC peptides have immune response modulatory activity, and are capable of  
CC inducing cytokines. Colostrin and its derived peptides are useful for  
CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.

XX SQ Sequence 3 AA;

Query Match 100.0%; Score 3; DB 22; Length 3;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3

DB 1 DKE 3

## RESULT 2

AAW81781  
ID AAW81781 standard; Protein; 4 AA.

XX AAW81781;

XX 25-MAR-2003 (updated)

DT 23-FEB-1999 (first entry)

XX Human HE4 epitope peptide #1.

XX HE4; epididymis-specific; diagnosis; male infertility; treatment;  
KW sterility; immunosterilisation.

XX Homo sapiens.

XX EP878544A1.

XX 18-NOV-1998.

XX 29-JAN-1991; 98EP-0250131.

XX 01-FEB-1990; 90DE-4002981.

PR 30-NOV-1990; 90DE-4038189.

PR 29-JAN-1991; 91EP-0250021.

XX (IHFH-) IHF INST HORMON & FORTPFLANZUNGS.

XX Ivell R, Kirchhoff C;

WPI; 1998-585748/50.

XX DNA encoding human epididymis polypeptides - useful for, e.g.

PT diagnosis of male infertility

XX Example 9; Page 19; 29pp; German.

XX This sequence represents a novel human epididymis-specific protein, HE4  
CC epitope fragment. This protein may be used for cloning and for expression  
CC of human epididymis-specific polypeptides in prokaryotic or eukaryotic  
CC host cells. Such proteins and antibodies generated from them may be used  
CC for diagnosis of e.g. male infertility. The polypeptides and antibodies  
CC may also be used for treatment of male infertility and for  
CC immunosterilisation of mammals.

CC (Updated on 25-MAR-2003 to correct PF field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 3; DB 19; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3

DB 1 DKE 3

## RESULT 3

AAV73601

ID AAV73601 standard; Peptide; 5 AA.

XX AC AAY73601;  
 XX DT 07-MAR-2000 (first entry)  
 XX DE OB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:107.  
 XX KW Diagnosis; cancer; OB-cadherin; N-cadherin; E-cadherin; CAR; cyclic;  
 KW cell adhesion recognition sequence; leukaemia; metastasis;  
 KW prostate cancer; breast cancer; ovarian cancer; carcinoma.  
 XX OS Synthetic.  
 OS Homo sapiens.  
 XX PN WO9957565-A2.  
 XX PD 11-NOV-1999.  
 XX PF 05-MAY-1999; 99WO-CA00362.  
 XX PR 05-MAY-1998; 98US-0073040.  
 PR 06-NOV-1998; 98US-0187859.  
 PR 20-JAN-1999; 99US-0234395.  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX PA Blaschuk OW, Gour BJ, Byers S;  
 PI WPI; 2000-062165/05.  
 DR Detecting expression of OB-cadherin or N-cadherin used for diagnosing  
 PT and evaluating cancer  
 PT Disclosure; Page 19, 56pp; English.  
 XX The present invention describes methods which have been developed for  
 CC detecting and evaluating cancer that are based on the finding that  
 CC OB-cadherin and N-cadherin are expressed by metastatic carcinoma cells,  
 CC but not by highly differentiated, poorly invasive carcinomas. A method  
 CC for determining the presence or absence of a cancer in a patient  
 CC comprises: (1) contacting a biological sample from the patient with a  
 CC binding agent that specifically binds to OB- or N-cadherin OR with an  
 CC oligonucleotide that hybridises to a polynucleotide that encodes OB- or  
 CC N-cadherin; and (2) detecting in the sample an amount of polypeptide  
 CC that binds to the binding agent OR the amount of polynucleotide that  
 CC hybridises to the oligonucleotide, relative to a predetermined cut-off  
 CC value, and determining the presence or absence of cancer in the patient  
 CC from this. The methods from the present invention can be used to  
 CC determine the metastatic potential of a cancer. The methods may be used  
 CC to detect a metastatic cancer in a patient, to monitor progression of a  
 CC cancer, or to evaluate the metastatic potential of a cancer. Cancers  
 CC which may be evaluated using the methods include leukemia, prostate  
 CC cancer, breast cancer and ovarian cancer. AAY73501 to AAY73813 represent  
 CC peptide sequences used in the exemplification of the present invention.  
 CC Specifically, AAY73503 to AAY73789 represent OB-cadherin cell adhesion  
 CC recognition (CAR) peptides and AAY73790 to AAY73808 represent N-cadherin  
 CC CAR peptides. AAZ47906 to AAZ47915 represent PCR primers used in examples  
 CC from the present invention.  
 XX SQ Sequence 5 AA;  
 Query Match 100.0%; Score 3; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05; Indels 0;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;  
 Oy 1 DKE 3  
 Db |||  
 3 DKE 5  
 RESULT 4  
 AAY60687  
 ID AAY60687 standard; Peptide; 5 AA.

XX AAY60687;  
 XX AC 02-MAR-2000 (first entry)  
 XX DT OB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:721.  
 XX DE  
 XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;  
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;  
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;  
 KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;  
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;  
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;  
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;  
 KW neurological disease; cyclic.  
 XX OS Synthetic.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Modified-site 1..5  
 FT /note= "the terminal residues are condensed with each  
 FT other to form a cyclic peptide"  
 XX WO9957149-A2.  
 XX PD 11-NOV-1999.  
 XX PF 05-MAY-1999; 99WO-CA00363.  
 XX PR 05-MAY-1998; 98US-0073040.  
 PR 06-NOV-1998; 98US-0187859.  
 PR 20-JAN-1999; 99US-0234395.  
 PR 08-MAR-1999; 99US-0264516.  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX PA Blaschuk OW, Gour BJ, Byers S;  
 PI WPI; 2000-038791/03.  
 XX New cadherin modulating agents, used for modulating nonclassical  
 PT cadherin-mediated functions for treating e.g. cancers, obesity,  
 PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological  
 PT disease  
 XX Claim 18; Page 159; 252pp; English.  
 XX The present invention describes cadherin modulating agents (MA)  
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
 CC recognition (CAR) sequence. The MAs can be used for modulating  
 CC nonclassical cadherin-mediated functions. They can be used for e.g.  
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
 CC mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
 CC expressing cell, preventing or treating obesity in a mammal, stimulating  
 CC blood vessel regression in a mammal, enhancing drug delivery to the  
 CC central nervous system, treating a demyelinating neurological disease,  
 CC increasing vasopermeability in a mammal, enhancing adhesion of  
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
 CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue  
 CC in a mammal. They can also be used for treating e.g. psoriasis,  
 CC arthritis, age-related macular degeneration, multiple sclerosis and  
 CC diabetes. The products can also be used for detection and diagnosis and  
 CC in bioreactors AAY60592 to AAY64572 represent specifically claimed  
 CC peptides, and AAY64573 to AAY64643 and AAY633183 to AAY633186 represent  
 CC sequences used in the exemplification of the present invention.  
 XX SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 |||  
 Db 3 DKE 5

RESULT 5  
 ABG92299  
 ID ABG92299 standard; Peptide; 5 AA.

XX AC ABG92299;

XX DT 29-NOV-2002 (first entry)

XX DE OB-cadherin CAR peptide #95.

XX KW Cancer metastasis; osteoblast cadherin; OB-cadherin CAR; cytostatic;  
 protein therapy.

XX OS Synthetic.

XX PN US6433149-B1.

XX PD 13-AUG-2002.

XX PF 05-MAY-1999; 99US-0305927.

XX PR 05-MAY-1998; 98US-0073040.

XX PR 06-NOV-1998; 98US-0187859.

XX PR 20-JAN-1999; 99US-0234395.

XX PR 08-MAR-1999; 99US-0264516.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Symonds JM, Byers S, Gour BJ;

XX WPI; 2002-681212/73.

XX PT Inhibiting cancer metastasis, and the use of osteoblast (OB)-cadherin  
 peptides, and antibodies that bind them, to inhibit adhesion and  
 PT metastasis of circulating cancer cells -

XX PS Disclosure; Column 10; 82pp; English.

XX CC The present invention relates to new methods for inhibiting cancer  
 CC metastasis, and the use of osteoblast (OB)-cadherin peptides, and  
 CC antibodies that bind them, to inhibit adhesion and metastasis of  
 CC circulating cancer cells. The methods of the invention are used to  
 CC inhibit cancer metastasis. The present amino acid sequence represents  
 CC an OB-cadherin CAR peptide, as described in the invention.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 |||  
 Db 3 DKE 5

RESULT 6  
 AAE20132  
 ID AAE20132 standard; peptide; 5 AA.

XX AC AAE20132;

XX DT 18-JUN-2002 (first entry)

XX DE Human TRIP leucine zipper peptide #7.  
 XX KW Human; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;  
 KW TRAF interacting protein; TRIP; cell activation; cell proliferation;  
 KW cell death; therapy; cytostatic; leucine zipper.  
 XX OS Homo sapiens.  
 XX PN US6346605-B1.  
 XX PD 12-FEB-2002.  
 XX PF 31-MAR-1998; 98US-0052089.  
 XX PR 01-APR-1997; 97US-042293P.  
 XX PR 07-APR-1997; 97US-042747P.  
 XX PA (UYRQ ) UNIV ROCKEFELLER.  
 XX PI Lee SY, Choi Y;  
 XX WPI; 2002-225005/28.  
 XX PT New tumor necrosis factor receptor associated factor interacting  
 PT protein, useful for inhibiting NF-kappa B activation, and for  
 PT modulating signals responsible for cell activation, cell proliferation  
 PT and cell death -  
 XX Example 2; Fig 2E; 37pp; English.  
 XX CC The present invention relates to a tumour necrosis factor (TNF) receptor  
 CC associated factor (TRAF) interacting protein (TRIP), which is a regulator  
 CC capable of binding to TRAF2. TRIP is useful for inhibiting NF-kappa B  
 CC activation and for modulating signals responsible for cell activation,  
 CC cell proliferation and cell death. Thus, TRIP is useful for treating  
 CC diseases associated with altered cell proliferation and cell death. The  
 CC present sequence is human TRIP leucine zipper peptide.  
 XX SQ Sequence 5 AA;

Query Match 100.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 |||  
 Db 1 DKE 3

RESULT 7  
 ABU60022  
 ID ABU60022 standard; Peptide; 5 AA.

XX AC ABU60022;

XX DT 24-APR-2003 (first entry)

XX DE OB-cadherin cell adhesion recognition cyclic sequence #53.

XX KW Metastasis; cancer; binding agent; cell adhesion recognition; CAR;  
 KW OB-cadherin; N-cadherin; prostate cancer; ovarian cancer; breast cancer;  
 KW leukaemia; cyclic.

XX OS Synthetic.

XX PN US2002146687-A1.

XX PD 10-OCT-2002.

XX PF 05-MAY-1999; 99US-0305928.

XX PR 05-MAY-1998; 98US-0073040.



```

PR 06-NOV-1998; 98US-0187859.
XX 20-JAN-1999; 99US-0234395.
PA (BLAS/) BLASCHUK O W.
PA (SYMO/) SYMONDS J M.
PA (BYER/) BYERS S.
PA (GOUR/) GOUR B J.
XX
PI Blaschuk OW, Symonds JM, Byers S, Gour BJ;
XX
XX WPI; 2003-246575/25.
XX
XX Diagnosing or evaluating metastatic potential of cancer in patient by
XX contacting biological sample obtained from patient with specified
XX binding agent or oligonucleotide, and detecting polypeptide that binds
XX to the binding agent -
XX
XX Disclosure; Page 7; 94pp; English.
XX
XX The invention discloses a method for diagnosing or evaluating metastatic
XX potential of cancer in a patient. The method comprises contacting a
XX biological sample obtained from the patient with a binding agent
XX preferentially antibodies or cell adhesion recognition (CAR) sequences,
XX that specifically bind to OB-cadherin or N-cadherin or an oligonucleotide
XX that hybridises to a polynucleotide encoding OB-cadherin or N-cadherin
XX and then detecting the amount of polypeptide that binds to the binding
XX agent. The inventive method is useful for diagnosing or evaluating
XX metastatic potential of cancer, such as prostate, ovarian or breast
XX cancer, as well as leukaemia in a patient. It can also be employed for
XX monitoring the progression of cancer in a patient. The inventive method
XX provides accurate diagnosis or evaluation of metastatic potential of
XX cancer in a patient in a simple and economical manner. The sequences
XX presented in ABU59970-ABU60210 are the OB-cadherin cyclic CAR sequences.
XX
XX Sequence 5 AA;
XX
XX Query Match 100.0%; Score 3; DB 24; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DKE 3
DB 3 DKE 5
XX
RESULT 8
ABU55831
ID ABU55831 standard; Peptide; 5 AA.
XX
XX AC ABU55831;
XX
XX 21-MAR-2003 (first entry)
XX
XX OB-cadherin cell adhesion recognition sequence peptide analogue #75.
XX
XX OB-cadherin; cell adhesion recognition; CAR; cytostatic; vulnerary;
XX OB-cadherin mediated cell adhesion; cyclisation; central nervous system;
XX cancer; metastasis; tumour; blood vessel regression; wound healing;
XX vasopermeability; cell adhesion modulation; cyclic.
XX
XX Unidentified.
XX
XX US6472367-B1.
XX
XX 29-OCT-2002.
XX
XX 05-MAY-1998; 98US-0073040.
XX
XX 05-MAY-1998; 98US-0073040.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk OW, Symonds JM, Gour BJ;
XX
XX WPI; 2003-165425/16.
XX
XX Novel cell adhesion modulating agent useful for e.g. modulating cell
XX adhesion of OB-cadherin-expressing cells and enhancing the delivery of
XX a drug to a tumour, comprises a native OB-cadherin cell adhesion
XX recognition sequence -
XX
XX Disclosure; Column 3; 42pp; English.
XX
XX The invention relates to a cell adhesion modulating agent comprising a
XX peptide four to nine amino acids in length that detectably inhibits
XX OB-cadherin mediated cell adhesion, consisting of a native OB-cadherin
XX cell adhesion recognition (CAR) sequence that comprises the sequence DDK
XX and optionally a residue on one or both sides of the CAR sequence to
XX facilitate cyclisation. The modulating agent is useful for modulating
XX cell adhesion of OB-cadherin-expressing cells and for enhancing the
XX delivery of a drug to a tumour or to the central nervous system in a
XX mammal. The agent is also useful for treating cancer and/or inhibiting
XX invasion and metastasis of a cancer. The agent is further useful for
XX stimulating blood vessel regression, for enhancing wound healing in a
XX mammal, for enhancing adhesion of foreign tissue implanted within a
XX mammal, for increasing vasopermeability in a mammal, for disrupting cell
XX adhesion mediated by multiple adhesion molecules, to facilitate cell
XX identification, sorting in vitro or imaging in vivo and for permitting
XX the selection of cells expressing OB-cadherin. This sequence represents
XX an OB-cadherin CAR sequence cyclic peptide analogue, used as a cell
XX adhesion modulating agent.
XX
XX Sequence 5 AA;
XX
XX Query Match 100.0%; Score 3; DB 24; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DKE 3
DB 3 DKE 5
XX
RESULT 9
AAR45365
ID AAR45365 standard; peptide; 6 AA.
XX
XX AC AAR45365;
XX
XX 25-MAR-2003 (updated)
XX
XX 05-JUL-1994 (first entry)
XX
XX Mycoplasma cancer metastasis-promoting protein partial sequence.
XX
XX Cancer; metastases; metastasis; promotion; human colon cancer;
XX RPMI 4788 cell; cancer therapy.
XX
XX Mycoplasma arginini.
XX
XX EP578356-A2.
XX
XX 12-JAN-1994.
XX
XX 14-MAY-1993; 93EP-0303758.
XX
XX 14-MAY-1992; 92JP-0166659.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Iwaki K, Kurimoto M, Ushio S;
XX
XX WPI; 1994-010213/02.
XX
XX Protein isolated from mycoplasma with metastasis-promoting
XX activity - used experimentally to study mechanism of metastasis
XX

```

PS Claim 1; Page 8; 9pp; English.

XX Cells from a seed culture of M.arginini IFO 14476 were pelleted and  
CC sonicated. The lysate was filtered and subjected to affinity  
CC chromatography. A protein which promotes the metastasis of RPMI 4788  
CC cells (FERM-2429) derived from human colon cancer was isolated. The  
CC protein contains the partial amino acid sequences AAR45365 and AAR45366,  
CC has mol.wt. 40-50KD, is soluble in water, saline and phosphate  
CC buffer, has isoelectric point of 5.0-7.0 and is inactivated in aq.  
CC soln. (pH 7.2) at 100 deg.C for 10 min.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 6 AA;

Query Match 100.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 3 DKE 5

RESULT 10

AAR64051  
ID AAR64051 standard; peptide; 6 AA.

AC AAR64051;

XX 01-MAR-1995 (first entry)

XX Peptide which binds to endothelin-1 antigenic determinant.

XX Endothelin-1; antigen; antibody; immunogen.

XX Synthetic.

XX JP06157592-A.

XX 03-JUN-1994.

XX 24-NOV-1992; 92JP-0313269.

XX 24-NOV-1992; 92JP-0313269.

XX (HITB) HITACHI CHEM CO LTD.

XX WPI; 1994-221952/27.

XX New oligo.peptide(s) which bind to antigenic determinant of  
PT endothelin-1 - are used to purify or detect endothelin-1 or to  
PT conjugate with protein to form immunogen

XX Claim 3; Page 2; 8pp; Japanese.

XX The peptide binds specifically to the loop structure between Cys  
CC at the 3rd and Cys at the 11th position of endothelin-1. It can be  
CC used as a ligand to purify anti-endothelin-1 antibody, or as a  
CC detecting reagent, or as a starting material for an immunogenic  
CC protein for obtaining the antibody.

CC Also claimed in the patent are an anti-endothelin-1 antigen composed  
CC of the peptide bound to a protein, and an anti-endothelin-1 antibody  
CC prepared by immunising an animal with the antigen.

XX Sequence 6 AA;

Query Match 100.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 4 DKE 6

RESULT 11

AAR67583  
ID AAR67583 standard; Peptide; 6 AA.

XX AAR67583;

XX 06-OCT-1995 (first entry)

XX Cancer metastasis protein peptide fragment.

XX Cancer metastasis; clinical tests; detection; peptide fragment

XX Homo sapiens.

XX JP06319559-A.

XX 22-NOV-1994.

XX 12-MAY-1993; 93JP-0144165.

XX 12-MAY-1993; 93JP-0144165.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX WPI; 1995-040317/06.

XX DNA encoding polypeptide involved in cancer metastasis - useful  
PT for the study of the mechanism of metastasis and in clinical  
PT tests

XX Claim 2; Page 2; 13pp; Japanese.

XX AAR67583 and AAR67584 are peptide fragments of the protein AAR67582, a  
CC protein involved in cancer metastasis. The protein and fragments  
CC may be used for the study of metastatic mechanisms, and for  
CC clinical tests to determine the presence or absence of cancer  
CC metastasis.

XX Sequence 6 AA;

Query Match 100.0%; Score 3; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 3 DKE 5

RESULT 12

AAV73602  
ID AAV73602 standard; Peptide; 6 AA.

XX AAV73602;

XX 07-MAR-2000 (first entry)

XX OB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:108.

XX Diagnosis; cancer; OB-cadherin; N-cadherin; E-cadherin; CAR; cyclic;  
KW cell adhesion recognition sequence; leukaemia; metastasis;  
KW prostate cancer; breast cancer; ovarian cancer; carcinoma.

XX Synthetic.

XX Homo sapiens.

XX WO9957565-A2.

XX 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA00362.

XX 05-MAY-1998; 98US-0073040.  
 PR 06-NOV-1998; 98US-0187859.  
 PR 20-JAN-1999; 99US-0234395.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 PI Blaschuk OW, Gour BJ, Byers S;  
 XX WPI; 2000-062165/05.  
 DR  
 XX Detecting expression of OB-cadherin or N-cadherin used for diagnosing  
 PT and evaluating cancer -  
 XX  
 PS Disclosure; Page 19; 56pp; English.  
 XX  
 CC The present invention describes methods which have been developed for  
 CC detecting and evaluating cancer that are based on the finding that  
 CC OB-cadherin and N-cadherin are expressed by metastatic carcinoma cells,  
 CC but not by highly differentiated, poorly invasive carcinomas. A method  
 CC for determining the presence or absence of a cancer in a patient  
 CC comprises: (1) contacting a biological sample from the patient with a  
 CC binding agent that specifically binds to OB- or N-cadherin OR with an  
 CC oligonucleotide that hybridizes to a polynucleotide that encodes OB- or  
 CC N-cadherin; and (2) detecting in the sample an amount of polypeptide  
 CC that binds to the binding agent OR the amount of polynucleotide that  
 CC hybridizes to the oligonucleotide, relative to a predetermined cut-off  
 CC value, and determining the presence or absence of cancer in the patient  
 CC from this. The methods from the present invention can be used to  
 CC determine the metastatic potential of a cancer. The methods may be used  
 CC to detect a metastatic cancer in a patient, to monitor progression of a  
 CC cancer, or to evaluate the metastatic potential of a cancer. Cancers  
 CC which may be evaluated using the methods include leukemia, prostate  
 CC cancer, breast cancer and ovarian cancer. AAY73501 to AAY73813 represent  
 CC peptide sequences used in the exemplification of the present invention.  
 CC Specifically, AAY73503 to AAY73789 represent OB-cadherin cell adhesion  
 CC recognition (CAR) peptides and AAY73790 to AAY73808 represent N-cadherin  
 CC CAR peptides. AAZ47906 to AAZ47915 represent PCR primers used in examples  
 CC from the present invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 3; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DKE 3  
 DB |||  
 4 DKE 6  
 RESULT 13  
 AAY60688  
 ID AAY60688 standard; Peptide; 6 AA.  
 XX  
 AC AAY60688;  
 XX  
 XX 02-MAR-2000 (first entry)  
 DT  
 XX OB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:722.  
 DE  
 XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;  
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;  
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;  
 KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;  
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;  
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;  
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;  
 KW neurological disease; cyclic.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX

FH Key Location/Qualifiers  
 Modified-site 1..6  
 FT /note= "the terminal residues are condensed with each  
 FT other to form a cyclic peptide"  
 XX  
 PN WO9957149-A2.  
 XX  
 XX 11-NOV-1999.  
 XX  
 XX 05-MAY-1999; 99WO-CA00363.  
 XX  
 XX 05-MAY-1998; 98US-0073040.  
 PR 06-NOV-1998; 98US-0187859.  
 PR 20-JAN-1999; 99US-0234395.  
 PR 08-MAR-1999; 99US-0264516.  
 XX  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 PA  
 XX Blaschuk OW, Gour BJ, Byers S;  
 XX WPI; 2000-038791/03.  
 DR  
 XX New cadherin modulating agents, used for modulating nonclassical  
 PT cadherin-mediated functions for treating e.g. cancers, obesity,  
 PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological  
 PT disease -  
 XX  
 PS Claim 18; Page 159; 252pp; English.  
 XX  
 CC The present invention describes cadherin modulating agents (MA)  
 CC comprising peptides which comprise a nonclassical cadherin cell  
 CC recognition (CAR) sequence. The MAe can be used for modulating  
 CC nonclassical cadherin-mediated functions. They can be used for e.g.  
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
 CC mammal, enhancing delivery of a drug through the skin of a mammal,  
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
 CC expressing cell, preventing or treating obesity in a mammal, stimulating  
 CC blood vessel regression in a mammal, enhancing drug delivery to the  
 CC central nervous system, treating a demyelinating neurological disease,  
 CC increasing vasopermeability in a mammal, enhancing adhesion of  
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound tissue  
 CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue  
 CC in a mammal. They can also be used for treating e.g. psoriasis,  
 CC arthritis, age-related macular degeneration, multiple sclerosis and  
 CC diabetes. The products can also be used for detection and diagnosis and  
 CC in bioreactors. AAY60592 to AAY64572 represent specifically claimed  
 CC peptides, and AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 3; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DKE 3  
 DB |||  
 4 DKE 6  
 RESULT 14  
 AAB55777  
 ID AAB55777 standard; Peptide; 6 AA.  
 XX  
 AC AAB55777;  
 XX  
 XX 07-MAR-2001 (first entry)  
 DT  
 XX PDZ motif sequence #8.  
 DE

XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;  
 KW allergy; asthma; multiple sclerosis; cancer; infection.  
 KW Synthetic.  
 OS

PN WO200069896-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13161.

XX 14-MAY-1999; 99US-0134114.

XX 14-MAY-1999; 99US-0134117.

PR 14-MAY-1999; 99US-0134118.

PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.

PR 13-DEC-1999; 99US-0170453.

PR 14-JAN-2000; 2000US-0176195.

PR 14-FEB-2000; 2000US-0182296.

PR 11-APR-2000; 2000US-0196460.

PR 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-080245/09.

XX Modulating a biological function of an endothelial cell or  
 PT hematopoietic cell, useful for treating autoimmune diseases and  
 PT infectious diseases, by administering an antagonist that inhibits  
 PT binding between a PDZ protein and a PL protein -

XX Disclosure; Page 87-94; 141pp; English.

XX The present invention relates to a new method for modulating a  
 CC biological function of an endothelial cell or hematopoietic cell. The  
 CC method involves introducing into a cell, an antagonist that inhibits  
 CC binding between a PDZ protein and a PL protein. The inhibitor is used  
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune  
 CC disease. It may also be used to prevent transplantation rejection of  
 CC a solid organ transplant. The method may also be used in the treatment  
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative  
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,  
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,  
 CC graft rejection, transplantation rejection), atherosclerosis, cancers,  
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.

XX Sequence 6 AA;

Query Match 100.0%; Score 3; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.2e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DKE 3

Db 1 DKE 3

RESULT 15

AAB57609

ID AAB57609 standard; Peptide; 6 AA.

XX AAB57609;

XX 12-MAR-2001 (first entry)

XX Neurexin C-terminal core sequence #3.

XX Endothelial cell; hematopoietic cell; PDZ domain protein;

KW PL domain protein; leukocyte activation; T cell surface receptor;

KW synapse formation; transmembrane neurotransmitter receptor;  
 KW autoimmune disease; transplantation rejection; inflammation; allergy;  
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;  
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
 KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.

XX WO200069897-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13166.

XX 14-MAY-1999; 99US-0134114.

XX 14-MAY-1999; 99US-0134117.

PR 14-MAY-1999; 99US-0134118.

PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.

PR 13-DEC-1999; 99US-0170453.

PR 14-JAN-2000; 2000US-0176195.

PR 14-FEB-2000; 2000US-0182296.

PR 11-APR-2000; 2000US-0196460.

PR 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-025003/03.

XX New inhibitors of binding of a PDZ protein and PL protein for  
 PT inhibiting T cell-mediated response by hematopoietic cells, or for  
 PT treating diseases characterized by inflammatory and humoral immune  
 PT responses, e.g. inflammation, cancer -

XX Disclosure; Page 93; 139pp; English.

XX The present invention relates to a method for modulating a biological  
 CC function of an endothelial cell or hematopoietic cell, comprises  
 CC introducing into a cell an antagonist that inhibits binding between a  
 CC PDZ domain protein and a PL domain protein to result in inhibition of  
 CC leukocyte activation. The present sequence is a core sequence of a PL  
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are  
 CC named after three prototypical proteins: PSD95, Drosophila large disc  
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved  
 CC in synapse formation by organising transmembrane neurotransmitter  
 CC receptors through intracellular interactions. The inhibitors identified  
 CC by the present invention can be used to treat a disease mediated by  
 CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy  
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,  
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic  
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple  
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,  
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.  
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The  
 CC inhibitors can also be used to prevent transplantation rejection of a  
 CC solid organ transplant.

XX Sequence 6 AA;

Query Match 100.0%; Score 3; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.2e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DKE 3

Db 1 DKE 3

RESULT 16

AAB58019

ID AAB58019 standard; Peptide; 6 AA.

XX AAB58019;  
XX  
XX  
DT 12-MAR-2001 (first entry)  
XX  
XX Neurexin C-terminal core sequence #3.  
XX  
XX Endothelial cell; haematopoietic cell; PDZ domain protein;  
KW PL domain protein; leukocyte activation; T cell surface receptor;  
KW synapse formation; transmembrane neurotransmitter receptor;  
KW autoimmune disease; transplantation rejection; inflammation; allergy;  
KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;  
KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
KW ischaemia; vasculitis; Crohn's disease.  
XX  
XX Homo sapiens.  
XX  
XX WQ200069898-A2.  
XX  
XX 23-NOV-2000.  
XX  
XX 12-MAY-2000; 2000MO-US13205.  
XX  
XX 14-MAY-1999; 99US-0134114.  
XX 14-MAY-1999; 99US-0134117.  
XX 14-MAY-1999; 99US-0134118.  
XX 21-OCT-1999; 99US-0160860.  
XX 29-OCT-1999; 99US-0162498.  
XX 13-DEC-1999; 99US-0170453.  
XX 14-JAN-2000; 2000US-0176195.  
XX 14-FEB-2000; 2000US-0182296.  
XX 11-APR-2000; 2000US-0196460.  
XX 11-APR-2000; 2000US-0196527.  
XX  
XX (ARBO-) ARBOR VITA CORP.  
XX  
XX Lu PS;  
XX  
XX WPI; 2001-061214/07.  
XX  
XX Modulating a biological function of a hematopoietic cell for treating  
PT an allergic response, or diseases mediated by immune system cells,  
PT comprises introducing into the cell a PDZ-PL interaction enhancer or  
PT inhibitor -  
XX  
XX Disclosure; Page 95; 143pp; English.  
XX  
XX The present invention relates to a method for modulating a biological  
CC function of an endothelial cell or haematopoietic cell, comprises  
CC introducing into a cell an antagonist that inhibits binding between a  
CC PDZ domain protein and a PL domain protein to result in inhibition of  
CC leukocyte activation. The present sequence is a core sequence of a PL  
CC domain protein (a T cell surface receptor). PDZ domains of proteins are  
CC named after three prototypical proteins: PSD95, Drosophila large disc  
CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved  
CC in synapse formation by organising transmembrane neurotransmitter  
CC receptors through intracellular interactions. The inhibitors identified  
CC by the present invention can be used to treat a disease mediated by  
CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy  
CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,  
CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic  
CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple  
CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,  
CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.  
CC viral infection), ischaemia, vasculitis and Crohn's disease. The  
CC inhibitors can also be used to prevent transplantation rejection of a  
XX solid organ transplant.  
XX  
XX Sequence 6 AA;  
SQ

Query Match 100.0%; Score 3; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 1 DKE 3

RESULT 17  
ABG92300  
ID ABG92300 standard; Peptide; 6 AA.

XX  
AC ABG92300;  
XX  
DT 29-NOV-2002 (first entry)  
XX  
XX OB-cadherin CAR peptide #96.

XX  
XX Cancer metastasis; osteoblast cadherin; OB-cadherin CAR; cytostatic;  
KW protein therapy.

XX Synthetic.

XX US6433149-B1.

XX 13-AUG-2002.

XX 05-MAY-1999; 99US-0305927.

XX 05-MAY-1998; 98US-0073040.

XX 06-NOV-1998; 98US-0187859.

XX 20-JAN-1999; 99US-0234395.

XX 08-MAR-1999; 99US-0264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Symonds JM, Byers S, Gour BJ;

XX WPI; 2002-681212/73.

XX Inhibiting cancer metastasis, and the use of osteoblast (OB)-cadherin  
PT peptides, and antibodies that bind them, to inhibit adhesion and  
PT metastasis of circulating cancer cells -  
XX  
XX Disclosure; Column 10; 82pp; English.

XX The present invention relates to new methods for inhibiting cancer  
CC metastasis, and the use of osteoblast (OB)-cadherin peptides, and  
CC antibodies that bind them, to inhibit adhesion and metastasis of  
CC circulating cancer cells. The methods of the invention are used to  
CC inhibit cancer metastasis. The present amino acid sequence represents  
CC an OB-cadherin CAR peptide, as described in the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 3; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 4 DKE 6

RESULT 18  
ABJ05275  
ID ABJ05275 standard; Peptide; 6 AA.

XX AC ABJ05275;

XX DT 07-NOV-2002 (first entry)

XX  
XX T-cell surface receptor C-terminal core peptide SEQ ID No 270.  
XX Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;

KW ligand; Ki: inhibitor; K-enhancer; leukocyte; autoimmune disease;  
 KW inflammatory; humoral immune response; inflammation; C-terminal core;  
 KW T-cell surface receptor.  
 XX Unidentified.  
 OS WO200231512-A2.  
 PN  
 XX  
 PD 18-APR-2002.  
 XX  
 XX 11-OCT-2001; 2001WO-US32150.  
 PF  
 XX  
 XX 13-OCT-2000; 2000US-0688017.  
 PR  
 XX  
 XX (ARBO-) ARBOR VITA CORP.  
 PA  
 XX Rabinowitz JD, Lu PS, Schweizer J;  
 PI WPI; 2002-416878/44.  
 DR  
 XX  
 XX Assays for determining the affinity of binding between a PDZ domain and  
 PT a ligand, and determining the Ki of an inhibitor of the binding,  
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ  
 PT domain -  
 XX  
 XX Disclosure; Page 117; 164pp; English.  
 PS  
 XX The invention relates to methods and reagents for determining the  
 XX apparent affinity (Kd) of binding between a PDZ domain and a ligand. The  
 CC invention also relates to methods and reagents for determining the Ki of  
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an  
 CC agent that enhances binding of a PDZ domain and a ligand, and determining  
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by  
 CC determining the ligand bound with an immobilised polypeptide comprising a  
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,  
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a  
 CC disease characterised by leukocyte activation, e.g., an autoimmune  
 CC disease that is characterised by inflammatory or humoral immune response,  
 CC and for reducing inflammation in a subject. This sequence represents a 1-  
 CC cell surface receptor C-terminal core peptide relating to the PDZ  
 CC containing proteins of the invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 3; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DKE 3  
 |||  
 Db 1 DKE 3  
 RESULT 19  
 ABP63503  
 ID ABP63503 standard; Peptide; 6 AA.  
 AC ABP63503;  
 XX  
 XX 28-OCT-2002 (first entry)  
 DT  
 XX PDZ motif (PL) peptide SEQ ID NO:230.  
 DE  
 XX Molecular interaction; haematopoietic cell; immune response; T cell;  
 KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;  
 KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;  
 KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;  
 KW antiulcer; antipsoriatic; dermatological; antiasthmatic; cytosstatic;  
 KW antimicrobial; vasotropic; inflammatory immune response; inflammation;  
 KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;  
 KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;  
 KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;  
 KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;

KW angiogenesis-dependent disorder; infectious disease.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200242422-A2.  
 PN  
 XX 30-MAY-2002.  
 PD  
 XX  
 XX 09-NOV-2001; 2001WO-US44138.  
 PF  
 XX  
 XX 11-NOV-2000; 2000US-0710059.  
 -PR  
 XX 24-NOV-2000; 2000US-0721915.  
 PR  
 XX 24-NOV-2000; 2000US-0722069.  
 PR  
 XX 28-NOV-2000; 2000US-0724553.  
 PR  
 XX (ARBO-) ARBOR VITA CORP.  
 PA  
 XX  
 XX Lu P, Rabinowitz JD, Schweizer J;  
 PI WPI; 2002-608221/65.  
 DR  
 XX  
 XX Modulating the biological function of an endothelial cell or  
 PT haematopoietic cell e.g., a T-cell or B-cell comprises introducing into  
 PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ  
 PT ligand protein in the cell -  
 XX  
 XX Disclosure; Page 135; 207pp; English.  
 PS  
 XX The present invention describes a method (M1) for modulating a biological  
 CC function of an endothelial cell or haematopoietic cell. M1 comprises  
 CC introducing into the cell, an agent that inhibits binding of a PDZ  
 CC (PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein)  
 CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the  
 CC biological function. Also described is a method (M2) for determining  
 CC whether a test compound is an inhibitor of binding between a PDZ protein  
 CC and a PL protein. M1 is used for modulating a biological function of an  
 CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an  
 CC inflammatory or humoral immune response, or an autoimmune disease. An  
 CC inhibitor (I) is useful for treating a disease characterised by leukocyte  
 CC activation, where the disease is characterised by an inflammatory or  
 CC humoral immune response, e.g., an autoimmune disease. The compounds  
 CC e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating  
 CC symptoms of) a variety of diseases and conditions characterised by  
 CC inflammatory and humoral immune responses e.g., inflammation, allergy,  
 CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,  
 CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic  
 CC diseases such as asthma, allergic rhinitis, transplantation rejection  
 CC (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,  
 CC autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,  
 CC angiogenesis-dependent disorders, infectious diseases and ischaemia.  
 CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 3; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DKE 3  
 |||  
 Db 1 DKE 3  
 RESULT 20  
 ABU60023  
 ID ABU60023 standard; Peptide; 6 AA.  
 XX  
 AC ABU60023;  
 XX  
 XX 24-APR-2003 (first entry)  
 DT  
 XX

```

DE OB-cadherin cell adhesion recognition cyclic sequence #54.
XX Metastasis; cancer; binding agent; cell adhesion recognition; CAR;
KW OB-cadherin; N-cadherin; prostate cancer; ovarian cancer; breast cancer;
KW leukaemia; cyclic.
XX Synthetic.
OS
XX
XX US2002146687-A1.
XX
XX 10-OCT-2002.
XX
XX 05-MAY-1999; 99US-0305928.
XX
XX 05-MAY-1998; 98US-0073040.
XX 06-NOV-1998; 98US-0187859.
XX 20-JAN-1999; 99US-0234395.
XX
XX (BLAS/) BLASCHUK O W.
XX (SYMO/) SYMONDS J M.
XX (BYER/) BYERS S.
XX (GOUR/) GOUR B J.
XX
XX Blaschuk OW, Symonds JM, Byers S, Gour BJ;
XX WPI; 2003-246575/25.
XX
XX Diagnosing or evaluating metastatic potential of cancer in patient by
PT contacting biological sample obtained from patient with specified
PT binding agent or oligonucleotide, and detecting polypeptide that binds
PT to the binding agent
XX
XX Disclosure; Page 7; 94pp; English.
XX
XX The invention discloses a method for diagnosing or evaluating metastatic
CC potential of cancer in a patient. The method comprises contacting a
CC biological sample obtained from the patient with a binding agent,
CC preferentially antibodies or cell adhesion recognition (CAR) sequences,
CC that specifically bind to OB-cadherin or N-cadherin or an oligonucleotide
CC that hybridises to a polynucleotide encoding OB-cadherin or N-cadherin
CC and then detecting the amount of polypeptide that binds to the binding
CC agent. The inventive method is useful for diagnosing or evaluating
CC metastatic potential of cancer, such as prostate, ovarian or breast
CC cancer, as well as leukaemia in a patient. It can also be employed for
CC monitoring the progression of cancer in a patient. The inventive method
CC provides accurate diagnosis or evaluation of metastatic potential of
CC cancer in a patient in a simple and economical manner. The sequences
CC presented in ABUS9970-ABU60210 are the OB-cadherin cyclic CAR sequences.
XX
XX Sequence 6 AA;
XX
XX Query Match 100.0%; Score 3; DB 24; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DKE 3
XX |||
XX Db 4 DKE 6
XX
XX RESULT 21
XX ABB99805
XX ID ABB99805 standard; peptide; 6 AA.
XX
XX AC ABB99805;
XX
XX 07-APR-2003 (first entry)
XX
XX Peptide derived from Plasmodium falciparum antigen DG747.
XX
XX Antigen; DG747; interferon-gamma; sporozoite; immunogen; vaccine;
KW infection; malaria.
XX

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OS Plasmodium falciparum.
XX
XX WO200292628-A2.
XX
XX 21-NOV-2002.
XX
XX 15-MAY-2002; 2002WO-FR01637.
XX
XX 16-MAY-2001; 2001CA-2345206.
XX 23-MAY-2001; 2001CA-2346968.
XX
XX (INSP ) INST PASTEUR.
XX
XX Druilhe P, Gruener A;
XX WPI; 2003-129263/12.
XX
XX New polynucleotide from Plasmodium falciparum and derived protein,
PT useful as immunogen for antimalarial vaccines and for preparing
PT diagnostic or therapeutic antibodies
XX
XX Claim 6; Fig 1E; 115pp; French.
XX
XX ABB99803-06 represent peptides derived from a Plasmodium falciparum
CC antigen, designated DG747. This antigen generates an interferon-gamma
CC response. The protein is localised on the surface of sporozoites and on
CC the intra-hepatic stage of parasites. The antigen, as well as nucleic
CC acids encoding it, is useful as immunogens/vaccines for protection
CC against infection by Plasmodium falciparum. They are useful in treating
CC P. falciparum malaria and for in vitro diagnosis of infection.
XX
XX Sequence 6 AA;
XX
XX Query Match 100.0%; Score 3; DB 24; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DKE 3
XX |||
XX Db 1 DKE 3
XX
XX RESULT 22
XX ABUS5832
XX ID ABUS5832 standard; Peptide; 6 AA.
XX
XX AC ABUS5832;
XX
XX 21-MAR-2003 (first entry)
XX
XX OB-cadherin cell adhesion recognition sequence peptide analogue #76.
XX
XX OB-cadherin; cell adhesion recognition; CAR; cytostatic; vulnary;
KW OB-cadherin mediated cell adhesion; cyclisation; central nervous system;
KW cancer; metastasis; tumour; blood vessel regression; wound healing;
KW vasopermeability; cell adhesion modulation; cyclic.
XX
XX Unidentified.
XX
XX US6472367-B1.
XX
XX 29-OCT-2002.
XX
XX 05-MAY-1998; 98US-0073040.
XX
XX 05-MAY-1998; 98US-0073040.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk OW, Symonds JM, Gour BJ;
XX WPI; 2003-165425/16.
XX

```

PT Novel cell adhesion modulating agent useful for e.g. modulating cell  
 PT adhesion of OB-cadherin-expressing cells and enhancing the delivery of  
 PT a drug to a tumour, comprises a native OB-cadherin cell adhesion  
 PT recognition sequence -  
 XX  
 XX Disclosure; Column 3; 42pp; English.  
 XX  
 CC The invention relates to a cell adhesion modulating agent comprising a  
 CC peptide four to nine amino acids in length that detectably inhibits  
 CC OB-cadherin mediated cell adhesion, consisting of a native OB-cadherin  
 CC cell adhesion recognition (CAR) sequence that comprises the sequence DDK  
 CC and optionally a residue on one or both sides of the CAR sequence to  
 CC facilitate cyclisation. The modulating agent is useful for modulating  
 CC cell adhesion of OB-cadherin-expressing cells and for enhancing the  
 CC delivery of a drug to a tumour or to the central nervous system in a  
 CC mammal. The agent is also useful for treating cancer and/or inhibiting  
 CC invasion and metastasis of a cancer. The agent is further useful for  
 CC stimulating blood vessel regression, for enhancing wound healing in a  
 CC mammal, for enhancing adhesion of foreign tissue implanted within a  
 CC mammal, for increasing vasopermeability in a mammal, for disrupting cell  
 CC adhesion mediated by multiple adhesion molecules, to facilitate cell  
 CC identification, sorting in vitro or imaging in vivo and for permitting  
 CC the selection of cells expressing OB-cadherin. This sequence represents  
 CC an OB-cadherin CAR sequence cyclic peptide analogue, used as a cell  
 CC adhesion modulating agent.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 3; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 |||  
 Db 4 DKE 6

# RESULT 23

AAP30278  
 ID AAP30278 standard; Protein; 7 AA.

AC AAP30278;

DT 25-MAR-2003 (updated)  
 DT 20-APR-1992 (first entry)

DE Sequence of the H epitope for the Simian virus 40 VP1 protein  
 DE corresp. to AAs 77-83 of the protein.

XX Synthetic vaccine; antigen; allergen; immunological response;  
 KW antibody.

XX Simian virus.

OS EP93851-A.

PN 16-NOV-1983.

PD 11-MAR-1983; 83EP-0102392.

PF 15-MAR-1982; 82US-0358150.

PR 28-JAN-1983; 83US-0461802.

PR 12-JUN-1981; 81US-0272855.

PR 09-JAN-1981; 81US-0223559.

PR 16-DEC-1986; 86US-0942562.

PA (NYBL-) NEW YORK BLOOD CENTER INC.

XX Hopp TP;

XX WPI; 1983-822049/47.

PT Synthetic vaccine - contains peptide residue coupled to higher

PT alkyl or alkenyl Gps. and with 6 amino acids in residue  
 XX  
 XX Claim 33; Page 44; 54pp; English.

XX The inventors claim a synthetic vaccine which comprises a peptide  
 CC residue coupled to an alkyl or alkenyl gp. having at least 12C, or  
 CC other lipophilic substance. The residue contains a sequence of 6 AAs  
 CC corresp. to the SQ of such AAs in a protein antigen or allergen where  
 CC the greatest local average hydrophilicity is found. Pref. the AAs in  
 CC the peptide do not exceed 50 residues, and they esp. contain 12-18  
 CC residues. The alkyl or alkenyl gp. pref. contains 12-24C and it is  
 CC pref. coupled to the terminal amino gp. of the residue opt. via a CO  
 CC gp. If a lipophilic substance is used, it is pref. palmitic, stearic,  
 CC behenic, oleic or mycolic acid.  
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 |||  
 Db 5 DKE 7

# RESULT 24

AAR64049

ID AAR64049 standard; peptide; 7 AA.

AC AAR64049;

XX 01-MAR-1995 (first entry)

XX Peptide which binds to endothelin-1 antigenic determinant.

XX Endothelin-1; antigen; antibody; immunogen.

XX Synthetic.

XX JP06157592-A.

XX 03-JUN-1994.

XX 24-NOV-1992; 92JP-0313269.

XX 24-NOV-1992; 92JP-0313269.

XX (HITB ) HITACHI CHEM CO LTD.

XX WPI; 1994-221952/27.

XX New oligo:peptide(s) which bind to antigenic determinant of  
 PT endothelin-1 - are used to purify or detect endothelin-1 or to  
 PT conjugate with protein to form immunogen

XX Claim 1; Page 2; 8pp; Japanese.

XX The peptide binds specifically to the loop structure between Cys  
 CC at the 3rd and Cys at the 11th position of endothelin-1. It can be  
 CC used as a ligand to purify anti-endothelin-1 antibody, or as a  
 CC detecting reagent, or as a starting material for an immunogenic  
 CC protein for obtaining the antibody.

XX Also claimed in the patent are an anti-endothelin-1 antigen composed  
 CC of the peptide bound to a protein; and an anti-endothelin-1 antibody  
 CC prepared by immunising an animal with the antigen.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 15; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 DKE 3  
Db 5 DKE 7

RESULT 25  
AAW30416  
ID AAW30416 standard; peptide; 7 AA.

XX AC AAW30416;

XX DT 22-APR-1998 (first entry)

XX DE HRE-I affinity peptide SEQ ID NO:34.

XX KW Binding site; HRE-I; screening; H-Ras; target gene; plasmid;  
XX KW inhibition; affinity peptide.

XX OS Synthetic.

XX PN WO9737030-A1.

XX PD 09-OCT-1997.

XX PF 31-MAR-1997; 97WO-JP01105.

XX PR 03-OCT-1996; 96JP-0263345.

XX PR 01-APR-1996; 96JP-0101990.

XX PA (YAWH ) NIPPON STEEL CHEM CO.

XX PA (YAWA ) NIPPON STEEL CORP.

XX PI Kato T;

XX DR WPI; 1997-503115/46.

XX PT Plasmid for screening peptide(s) which bind target genes - for  
XX PT treatment of conditions associated with H-Ras

XX PS Claim 41; Page 69; 127pp; Japanese.

XX CC A novel plasmid has been developed for screening peptides which bind  
XX CC target genes. The plasmid comprises a sequence encoding the test  
XX CC peptide, a promoter comprising the target gene, and a reporter gene  
XX CC bound to the promoter. The present sequence represents a specifically  
XX CC claimed peptide with affinity to HRE-I. The plasmids are used for  
XX CC screening for peptides which bind to target genes. The identified  
XX CC peptides can be used for the treatment of conditions associated with  
XX CC the inhibition of the expression the genes, and treatment of conditions  
XX CC associated with H-Ras.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 18; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 4 DKE 6

RESULT 26  
AAW54301  
ID AAW54301 standard; Peptide; 7 AA.

XX AC AAW54301;

XX DT 28-AUG-1998 (first entry)

XX DE Human cytohesin-1 PH domain randomised CD loop (clone 1).

KW Pleckstrin homology domain; PH domain; peptide library;  
KW functional molecular surface; protein structural template;  
KW vaccine; gene therapy; cytohesin 1; human.

XX OS Synthetic.

XX PN WO9745538-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-EP02840.

XX PR 31-MAY-1996; 96EP-0108776.

XX PA (MEDI-) MEDIGENE AG.

XX PI Bruhn H, Funk M, Henkel T, Steipe B;

XX DR WPI; 1998-230215/20.

XX DR N-PSDB; AAV26504.

XX PT Vectors used to produce PH domain-like peptide libraries - which are  
XX PT screened for therapeutically useful peptide(s), e.g. to produce  
XX PT vaccines.

XX PS Example 5; Fig 12; 137pp; English.

XX CC This is a randomised CD loop encoded by clone 1 (see AAV26504) of a  
XX CC large peptide library (2 million clones) of synthetic Pleckstrin  
XX CC homology (PH) domains with randomised discontinuous surface  
XX CC epitopes. The progenitor CD sequence comprises amino acid residues  
XX CC 40-46 of a stabilised synthetic PH domain (see AAW54310) of human  
XX CC cytohesin 1. The peptide library was generated by randomisation of  
XX CC AB and CD loop regions using randomised oligonucleotide primers  
XX CC (see AAW26493-94). The randomised AB and CD loop regions of 9 clones  
XX CC (see AAW54292-309) of the peptide library are provided. Randomisation  
XX CC did not compromise the structural integrity and folding stability of  
XX CC the progenitor domain. The invention provides vectors that are used  
XX CC for the production of PH domain-like peptide libraries which can  
XX CC be screened to identify peptides that have desirable properties,  
XX CC especially novel binding or catalytic properties, and which may  
XX CC be of use in research or therapy, or as vaccines. Novel synthetic  
XX CC protein structural templates for the generation, screening and  
XX CC evolution of functional molecular surfaces are provided.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 19; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
Db 2 DKE 4

RESULT 27  
AAW54302  
ID AAW54302 standard; Peptide; 7 AA.

XX AC AAW54302;

XX DT 28-AUG-1998 (first entry)

XX DE Human cytohesin-1 PH domain randomised CD loop (clone 2).

XX KW Pleckstrin homology domain; PH domain; peptide library;  
XX KW functional molecular surface; protein structural template;  
XX KW vaccine; gene therapy; cytohesin 1; human.

XX OS Synthetic.

XX PN WO9745538-A1.



PT Vectors used to produce PH domain-like peptide libraries - which are  
PT screened for therapeutically useful peptide(s), e.g. to produce  
PT vaccines  
XX  
PS Example 5; Fig 12; 137pp; English.  
XX  
CC This is a randomised CD loop encoded by clone 8 (see AAV26511) of a  
CC large peptide library (2 million clones) of synthetic pleckstrin  
CC homology (PH) domains with randomised discontinuous surface  
CC epitopes. The progenitor CD sequence comprises amino acid residues  
CC 40-46 of a stabilised synthetic PH domain (see AAW54310) of human  
CC cytohesin 1. The peptide library was generated by randomisation of  
CC AB and CD loop regions using randomised oligonucleotide primers  
CC (see AAW26493-94). The randomised AB and CD loop regions of 9 clones  
CC (see AAW54292-309) of the peptide library are provided. Randomisation  
CC did not compromise the structural integrity and folding stability of  
CC the progenitor domain. The invention provides vectors that are used  
CC for the production of PH domain-like peptide libraries, which can  
CC be screened to identify peptides that have desirable properties,  
CC especially novel binding or catalytic properties, and which may  
CC be of use in research or therapy, or as vaccines. Novel synthetic  
CC protein structural templates for the generation, screening and  
CC evolution of functional molecular surfaces are provided.  
XX  
XX Sequence 7 AA;  
SQ  
Query Match 100.0%; Score 3; DB 19; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DXE 3  
DB 2 DXE 4  
  
RESULT 30  
AAW54309  
ID AAW54309 standard; Peptide; 7 AA.  
XX  
AC AAW54309;  
XX  
DT 28-AUG-1998 (first entry)  
XX  
DE Human cytohesin-1 PH domain randomised CD loop (clone 8).  
XX  
KW Pleckstrin homology domain; PH domain; peptide library;  
KW functional molecular surface; protein structural template;  
KW vaccine; gene therapy; cytohesin 1; human.  
XX  
OS Synthetic.  
XX  
XX WO9745538-A1.  
XX  
XX 04-DEC-1997.  
XX  
XX 30-MAY-1997; 97WO-EP02840.  
XX  
XX 31-MAY-1996; 96EP-0108776.  
XX  
XX (MEDI-) MEDIGENE AG.  
XX  
PI Bruhn H, Funk M, Henkel T, Steipe B;  
XX  
XX WPI; 1998-230215/20.  
XX  
XX N-PSDB; AAV26512.  
XX  
CC Vectors used to produce PH domain-like peptide libraries - which are  
CC screened for therapeutically useful peptide(s), e.g. to produce  
CC vaccines  
XX  
PS Example 5; Fig 12; 137pp; English.  
XX  
CC This is a randomised CD loop encoded by clone 9 (see AAV26512) of a

CC large peptide library (2 million clones) of synthetic pleckstrin  
CC homology (PH) domains with randomised discontinuous surface  
CC epitopes. The progenitor CD sequence comprises amino acid residues  
CC 40-46 of a stabilised synthetic PH domain (see AAW54310) of human  
CC cytohesin 1. The peptide library was generated by randomisation of  
CC AB and CD loop regions using randomised oligonucleotide primers  
CC (see AAW26493-94). The randomised AB and CD loop regions of 9 clones  
CC (see AAW54292-309) of the peptide library are provided. Randomisation  
CC did not compromise the structural integrity and folding stability of  
CC the progenitor domain. The invention provides vectors that are used  
CC for the production of PH domain-like peptide libraries, which can  
CC be screened to identify peptides that have desirable properties,  
CC especially novel binding or catalytic properties, and which may  
CC be of use in research or therapy, or as vaccines. Novel synthetic  
CC protein structural templates for the generation, screening and  
CC evolution of functional molecular surfaces are provided.  
XX  
XX Sequence 7 AA;  
SQ  
Query Match 100.0%; Score 3; DB 19; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DXE 3  
DB 2 DXE 4  
  
RESULT 31  
AAW73604  
ID AAW73604 standard; Peptide; 7 AA.  
XX  
AC AAW73604;  
XX  
DT 07-MAR-2000 (first entry)  
XX  
DE OB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:110.  
XX  
KW Diagnosis; cancer; OB-cadherin; N-cadherin; E-cadherin; CAR; cyclic;  
KW cell adhesion recognition sequence; leukaemia; metastasis;  
KW prostate cancer; breast cancer; ovarian cancer; carcinoma.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9957565-A2.  
XX  
XX 11-NOV-1999.  
XX  
XX 05-MAY-1999; 99WO-CA00362.  
XX  
XX 05-MAY-1998; 98US-0073040.  
XX  
XX 06-NOV-1998; 98US-0187859.  
XX  
XX 20-JAN-1999; 99US-0234395.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
XX Blaschuck OW, Gour BJ, Byers S;  
XX  
XX WPI; 2000-062165/05.  
XX  
XX Detecting expression of OB-cadherin or N-cadherin used for diagnosing  
XX and evaluating cancer -  
XX  
XX Disclosure; Page 19; 56pp; English.  
XX  
CC The present invention describes methods which have been developed for  
CC detecting and evaluating cancer that are based on the finding that  
CC OB-cadherin and N-cadherin are expressed by metastatic carcinoma cells,  
CC but not by highly differentiated, poorly invasive carcinomas. A method  
CC for determining the presence or absence of a cancer in a patient  
CC comprises: (1) contacting a biological sample from the patient with a  
CC binding agent that specifically binds to OB- or N-cadherin OR with an

CC oligonucleotide that hybridizes to a polynucleotide that encodes OB- or  
 CC N-cadherin; and (2) detecting in the sample an amount of polypeptide  
 CC that binds to the binding agent OR the amount of polynucleotide that  
 CC hybridizes to the oligonucleotide, relative to a predetermined cut-off  
 CC value, and determining the presence or absence of cancer in the patient  
 CC from this. The methods from the present invention can be used to  
 CC determine the metastatic potential of a cancer. The methods may be used  
 CC to detect a metastatic cancer in a patient, to monitor progression of a  
 CC cancer, or to evaluate the metastatic potential of a cancer. Cancers  
 CC which may be evaluated using the methods include leukemia, prostate  
 CC cancer, breast cancer and ovarian cancer. AAY73501 to AAY73813 represent  
 CC peptide sequences used in the exemplification of the present invention.  
 CC Specifically, AAY73503 to AAY73789 represent OB-cadherin cell adhesion  
 CC recognition (CAR) peptides and AAY73790 to AAY73808 represent N-cadherin  
 CC CAR peptides. AAY73906 to AAY74915 represent PCR primers used in examples  
 CC from the present invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 3; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 5 DKE 7

RESULT 32

AAY60690  
 ID AAY60690 standard; Peptide; 7 AA.

XX AC AAY60690;

XX DT 02-MAR-2000 (first entry)

XX DE OB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:724.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;  
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;  
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;  
 KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;  
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;  
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;  
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;  
 KW neurological disease; cyclic.

XX Synthetic.  
 OS Homo sapiens.

XX Key Location/Qualifiers

PH Modified-site 1.7  
 FT /note= "the terminal residues are condensed with each  
 FT other to form a cyclic peptide"

XX WO9957149-A2.

XX 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA00363.

XX 05-MAY-1998; 98US-0073040.

XX 06-NOV-1998; 98US-0187859.

XX 20-JAN-1999; 99US-0234395.

XX 08-MAR-1999; 99US-0264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical

PT cadherin-mediated functions for treating e.g. cancers, obesity,  
 PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological  
 PT disease

XX Claim 18; Page 159; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)  
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
 CC recognition (CAR) sequence. The MA can be used for modulating  
 CC nonclassical cadherin-mediated functions. They can be used for e.g.  
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
 CC mammal, enhancing delivery of a drug through the skin of a mammal,  
 CC mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
 CC expressing cell, preventing or treating obesity in a mammal, stimulating  
 CC blood vessel regression in a mammal, enhancing drug delivery to the  
 CC central nervous system, treating a demyelinating neurological disease,  
 CC increasing vasopermeability in a mammal, enhancing adhesion of  
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound  
 CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue  
 CC in a mammal. They can also be used for treating e.g. psoriasis,  
 CC arthritis, age-related macular degeneration, multiple sclerosis and  
 CC diabetes. The products can also be used for detection and diagnosis and  
 CC in bioreactors. AAY60592 to AAY64572 represent specifically claimed  
 CC peptides, and AAY64573 to AAY64643 and AAY33183 to AAY33186 represent  
 CC sequences used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 3; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 5 DKE 7

RESULT 33

AAU08769

ID AAU08769 standard; Peptide; 7 AA.

XX AC AAU08769;

XX DT 16-JAN-2002 (first entry)

XX DE Soybean trypsin inhibitor C-terminal peptide.

XX KW Surface imprinting; imprint cavity; solid matrix; semi-solid matrix;  
 KW expression profiling; binding capacity; binding specificity; soybean;  
 KW trypsin inhibitor.

XX OS Glycine max.

XX WO200161354-A1.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US05118.

XX 18-FEB-2000; 2000US-0507299.

XX 18-MAY-2000; 2000US-0507300.

XX 09-MAY-2000; 2000US-203082P.

XX (ASPI-) ASPIRA BIOSYSTEMS INC.

XX Huang C;

XX WPI; 2001-648198/74.

PT Surface imprint composition for capturing, isolating, detecting,  
 PT analysing and/or quantifying molecules, comprises fraction of imprint  
 PT cavities that are localised at or near surface of matrix material -  
 XX  
 PS Example 10; Page 40; 63pp; English.  
 XX  
 CC The invention relates to molecular surface imprint compositions, useful  
 CC for detecting, analysing or quantifying molecules in a sample. A surface  
 CC imprint composition comprises a matrix material with an imprint cavity of  
 CC a template molecule. A substantial fraction of the imprint cavities are  
 CC localised at or near the surface of the matrix material. The matrix  
 CC material comprises one or more compounds that are capable of undergoing a  
 CC change in physical state, to produce a solid or semi-solid matrix that is  
 CC capable of retaining cavities corresponding in shape to the template  
 CC molecules. Surface imprints can also be used for isolating novel  
 CC molecules from complex mixtures and samples, for example, in expression  
 CC profiling and in the discovery of new molecules or novel members of known  
 CC classes of molecules. Surfacing imprinting provides improved binding  
 CC capacity and improved binding specificity. This sequence represents a  
 CC soybean trypsin inhibitor C-terminal peptide template molecule.  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 3 DKE 5

RESULT 34  
 AAB75097  
 ID AAB75097 standard; Peptide; 7 AA.

AC AAB75097;

XX 23-JUL-2001 (first entry)

XX Nucleotide-5'-phosphate producing enzyme variant peptide L140F.

XX Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;  
 KW transphosphorylation; phosphatase; protein co-ordinate data;  
 KW X-ray structural analysis; three-dimensional structure.

XX Synthetic.

XX WO200118184-A1.

XX 15-MAR-2001.

XX 01-SEP-2000; 2000WO-JP05973.

XX 03-SEP-1999; 99JP-0249545.

XX (AJIN ) AJINOMOTO CO INC.

XX Ishikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H;  
 PI Kurahashi O, Kouda T, Shimaoka M, Kozutsumi R, Asano Y;  
 PI WPI; 2001-380914/40.

XX Variant enzyme having elevated nucleoside 5-prime phosphate producing  
 PT activity and having a specific three-dimensional structure for  
 PT production of nucleotides as pharmaceutical intermediates -  
 XX  
 PS Example 18; Fig 8D; 150pp; Japanese.

XX The present invention describes a variant nucleoside-5'-phosphate  
 CC producing enzyme which is a modification of a transphosphorylase or  
 CC phosphatase which contains a lysine, two arginine and two histidine  
 CC residues and in which the C-alpha distances between these residues are

CC enclosing a space which permits the binding of a nucleoside with these  
 CC residues. Also described are: (1) a gene encoding the variant enzyme;  
 CC (2) expression vectors containing the DNA; (3) host cells transformed  
 CC by the vectors; (4) preparation of the variant enzyme by culture of the  
 CC transformants; (5) crystals of the enzyme and of a complex of the enzyme  
 CC with molybdenic acid; and (6) selection of inhibitors of acid  
 CC phosphatase or transphosphorylase using the structural coordinates  
 CC derived from the enzyme. The variant enzymes with increased efficiency  
 CC for production of nucleoside 5-phosphates can be used as pharmaceutical  
 CC intermediates. AAH19701 to AAH19785 and AAB75064 to AAB75101 represent  
 CC sequences used in the exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 2 DKE 4

RESULT 35  
 AAB55778  
 ID AAB55778 standard; Peptide; 7 AA.

AC AAB55778;

XX 07-MAR-2001 (first entry)

XX PDZ motif sequence #9.

XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;  
 KW allergy; asthma; multiple sclerosis; cancer; infection.

XX Synthetic.

XX WO200069896-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13161.

XX 14-MAY-1999; 99US-0134114.

XX 14-MAY-1999; 99US-0134117.

XX 14-MAY-1999; 99US-0134118.

XX 21-OCT-1999; 99US-0160860.

XX 29-OCT-1999; 99US-0162498.

XX 13-DEC-1999; 99US-0170453.

XX 14-JAN-2000; 2000US-0176195.

XX 14-FEB-2000; 2000US-0182296.

XX 11-APR-2000; 2000US-0196460.

XX 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-080245/09.

XX Modulating a biological function of an endothelial cell or  
 PT hematopoietic cell, useful for treating autoimmune diseases and  
 PT infectious diseases, by administering an antagonist that inhibits  
 PT binding between a PDZ protein and a PL protein -  
 XX  
 PS Disclosure; Page 87-94; 141pp; English.

XX The present invention relates to a new method for modulating a  
 CC biological function of an endothelial cell or hematopoietic cell. The  
 CC method involves introducing into a cell, an antagonist that inhibits  
 CC binding between a PDZ protein and a PL protein. The inhibitor is used  
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune



PT an allergic response, or diseases mediated by immune system cells,  
 PT comprises introducing into the cell a PDZ-PL interaction enhancer or  
 PT inhibitor -  
 PS Disclosure; Page 95; 143pp; English.  
 XX  
 XX The present invention relates to a method for modulating a biological  
 CC function of an endothelial cell or haematopoietic cell, comprises  
 CC introducing into a cell an antagonist that inhibits binding between a  
 CC PDZ domain protein and a PL domain protein to result in inhibition of  
 CC leukocyte activation. The present sequence is a core sequence of a PL  
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are  
 CC named after three prototypical proteins: PSD95, Drosophila large disc  
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved  
 CC in synapse formation by organising transmembrane neurotransmitter  
 CC receptors through intracellular interactions. The inhibitors identified  
 CC by the present invention can be used to treat a disease mediated by  
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy  
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,  
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic  
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple  
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,  
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.  
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The  
 CC inhibitors can also be used to prevent transplantation rejection of a  
 CC solid organ transplant.  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 ||||  
 Db 2 DKE 4

RESULT 38  
 ABG92302  
 ID ABG92302 standard; Peptide; 7 AA.

XX ABG92302;

XX 29-NOV-2002 (first entry)

XX OB-cadherin CAR peptide #98.

XX Cancer metastasis; osteoblast cadherin; OB-cadherin CAR; cytostatic;  
 KW protein therapy.

XX Synthetic.

XX US6433149-B1.

XX 13-AUG-2002.

XX 05-MAY-1999; 99US-0305927.

XX 05-MAY-1998; 98US-0073040.

XX 06-NOV-1998; 98US-0187859.

XX 20-JAN-1999; 99US-0234395.

XX 08-MAR-1999; 99US-0264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Symonds JM, Byers S, Gour BJ;

XX WPI; 2002-681212/73.

XX Inhibiting cancer metastasis, and the use of osteoblast (OB)-cadherin

PT peptides, and antibodies that bind them, to inhibit adhesion and

PT metastasis of circulating cancer cells -

XX Disclosure; Column 10; 82pp; English.  
 PS  
 XX The present invention relates to new methods for inhibiting cancer  
 CC metastasis, and the use of osteoblast (OB)-cadherin peptides, and  
 CC antibodies that bind them, to inhibit adhesion and metastasis of  
 CC circulating cancer cells. The methods of the invention are used to  
 CC inhibit cancer metastasis. The present amino acid sequence represents  
 CC an OB-cadherin CAR peptide, as described in the invention.

SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 ||||  
 Db 5 DKE 7

RESULT 39

ABJ05276

ID ABJ05276 standard; Peptide; 7 AA.

XX ABJ05276;

XX 07-NOV-2002 (first entry)

XX T-cell surface receptor C-terminal core peptide SEQ ID No 271.

XX Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;  
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;  
 KW inflammatory; humoral immune response; inflammation; C-terminal core;

XX T-cell surface receptor.

XX Unidentified.

XX WO200231512-A2.

XX 18-APR-2002.

XX 11-OCT-2001; 2001WO-US32150.

XX 13-OCT-2000; 2000US-0688017.

XX (ARBO-) ARBOR VITA CORP.

XX Rabinowitz JD, Lu PS, Schweizer J;

XX WPI; 2002-416878/44.

XX Assays for determining the affinity of binding between a PDZ domain and  
 PT a ligand, and determining the Ki of an inhibitor of the binding,  
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ  
 PT domain -

XX Disclosure; Page 117; 164pp; English.

XX The invention relates to methods and reagents for determining the  
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The  
 CC invention also relates to methods and reagents for determining the Ki of  
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an  
 CC agent that enhances binding of a PDZ domain and a ligand, and determining  
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by  
 CC determining the ligand bound with an immobilised polypeptide comprising a  
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,  
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a  
 CC disease characterised by leukocyte activation, e.g., an autoimmune  
 CC disease that is characterised by inflammatory or humoral immune response,  
 CC and for reducing inflammation in a subject. This sequence represents a T-  
 CC cell surface receptor C-terminal core peptide relating to the PDZ  
 CC containing proteins of the invention.

XX SQ Sequence 7 AA;  
 Query Match 100.0%; Score 3; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 DB 2 DKE 4

RESULT 40  
 ABP63504  
 ID ABP63504 standard; Peptide; 7 AA.  
 AC ABP63504;  
 DT 28-OCT-2002 (first entry)  
 DE PDZ motif (PL) peptide SEQ ID NO:231.  
 XX Molecular interaction; haematopoietic cell; immune response; T cell;  
 KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;  
 KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;  
 KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;  
 KW antiulcer; antipsoriatic; dermatological; antiasthmatic; cyostatic;  
 KW antimicrobial; vasotropic; inflammatory immune response; inflammation;  
 KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;  
 KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;  
 KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;  
 KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;  
 KW angiogenesis-dependent disorder; infectious disease.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200242422-A2.  
 PN 30-MAY-2002.  
 XX 09-NOV-2001; 2001WO-US44138.  
 XX 11-NOV-2000; 2000US-0710059.  
 PR 24-NOV-2000; 2000US-0721915.  
 PR 24-NOV-2000; 2000US-0722069.  
 PR 28-NOV-2000; 2000US-0724553.  
 XX (ARBO-) ARBOR VITA CORP.  
 PA Lu P, Rabinowitz JD, Schweizer J;  
 PI WPI; 2002-608221/65.  
 DR Modulating the biological function of an endothelial cell or  
 PT hemopoietic cell e.g., a T-cell or B-cell comprises introducing into  
 PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ  
 PT ligand protein in the cell  
 XX Disclosure; Page 135; 207pp; English.

XX The present invention describes a method (M1) for modulating a biological  
 CC function of an endothelial cell or haematopoietic cell. M1 comprises  
 CC introducing into the cell, an agent that inhibits binding of a PDZ  
 CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the  
 CC biological function. Also described is a method (M2) for determining  
 CC whether a test compound is an inhibitor of binding between a PDZ protein  
 CC and a PL protein. M1 is used for modulating a biological function of an  
 CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an  
 CC inflammatory or humoral immune response, or an autoimmune disease. An  
 CC inhibitor (I1) is useful for treating a disease characterised by leukocyte  
 CC activation, where the disease is characterised by an inflammatory or

CC humoral immune response, e.g., an autoimmune disease. The compounds  
 CC e.g., PI-PDZ interaction inhibitors are useful for treating (ameliorating  
 CC symptoms of) a variety of diseases and conditions characterised by  
 CC inflammatory and humoral immune responses e.g., inflammation, allergy,  
 CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,  
 CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic  
 CC diseases such as asthma, allergic rhinitis, corneal transplantation rejection  
 CC (cardiac, kidney, lung, liver, small bowel, trachea, pancreas, cadaver,  
 CC autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,  
 CC angiogenesis-dependent disorders, infectious diseases and ischaemia.  
 CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used  
 CC in the exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 DB 2 DKE 4

# RESULT 41

ABU60025  
 ID ABU60025 standard; Peptide; 7 AA.

AC ABU60025;

DT 24-APR-2003 (first entry)

DE OB-cadherin cell adhesion recognition cyclic sequence #56.

XX Metastasis; cancer; binding agent; cell adhesion recognition; CAR;  
 KW OB-cadherin; N-cadherin; prostate cancer; ovarian cancer; breast cancer;  
 KW leukaemia; cyclic.

OS Synthetic.

XX US2002146687-A1.

XX 10-OCT-2002.

XX 05-MAY-1999; 99US-0305928.

XX 05-MAY-1998; 98US-0073040.

XX 06-NOV-1998; 98US-0187859.

XX 20-JAN-1999; 99US-0234395.

XX (BLAS/) BLASCHUK O W.

XX (SYM/) SYMONDS J M.

XX (BYER/) BYERS S.

XX (GOUR/) GOUR B J.

XX Blaschuk OW, Symonds JM, Byers S, Gour BJ;

XX WPI; 2003-246575/25.

XX Diagnosing or evaluating metastatic potential of cancer in patient by  
 PT contacting biological sample obtained from patient with specified  
 PT binding agent or oligonucleotide, and detecting polypeptide that binds  
 PT to the binding agent

XX Disclosure; Page 7; 94pp; English.

XX The invention discloses a method for diagnosing or evaluating metastatic  
 CC potential of cancer in a patient. The method comprises contacting a  
 CC biological sample obtained from the patient with a binding agent,  
 CC preferentially antibodies or cell adhesion recognition (CAR) sequences,  
 CC that specifically bind to OB-cadherin or N-cadherin or an oligonucleotide  
 CC that hybridises to a polynucleotide encoding OB-cadherin or N-cadherin  
 CC and then detecting the amount of polypeptide that binds to the binding



CC agent. The inventive method is useful for diagnosing or evaluating  
 CC metastatic potential of cancer, such as prostate, ovarian or breast  
 CC cancer, as well as leukaemia in a patient. It can also be employed for  
 CC monitoring the progression of cancer in a patient. The inventive method  
 CC provides accurate diagnosis or evaluation of metastatic potential of  
 CC cancer in a patient in a simple and economical manner. The sequences  
 CC presented in ABU59970-ABU60210 are the OB-cadherin cyclic CAR sequences.

XX SQ Sequence 7 AA;  
 Query Match 100.0%; Score 3; DB 24; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 5 DKE 7

## RESULT 42

ABU55834  
 ID ABU55834 standard; Peptide; 7 AA.

XX AC ABU55834;

XX DT 21-MAR-2003 (first entry)

XX OB-cadherin cell adhesion recognition sequence peptide analogue #78.

XX OB-cadherin; cell adhesion recognition; CAR; cytostatic; vulnery;  
 KW OB-cadherin mediated cell adhesion; cyclisation; central nervous system;  
 KW cancer; metastasis; tumour; blood vessel regression; wound healing;  
 KW vasopermeability; cell adhesion modulation; cyclic.

XX Unidentified.

XX US6472367-B1.

XX 29-OCT-2002.

XX 05-MAY-1998; 98US-0073040.

XX 05-MAY-1998; 98US-0073040.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Symonds JM, Gour BJ;

XX WPI; 2003-165425/16.

XX Novel cell adhesion modulating agent useful for e.g. modulating cell  
 PT adhesion of OB-cadherin-expressing cells and enhancing the delivery of  
 PT a drug to a tumour, comprises a native OB-cadherin cell adhesion  
 PT recognition sequence -

XX Disclosure; Column 3; 42pp; English.

XX The invention relates to a cell adhesion modulating agent comprising a  
 CC peptide four to nine amino acids in length that detectably inhibits  
 CC OB-cadherin mediated cell adhesion, consisting of a native OB-cadherin  
 CC cell adhesion recognition (CAR) sequence that comprises the sequence DDK  
 CC and optionally a residue on one or both sides of the CAR sequence to  
 CC facilitate cyclisation. The modulating agent is useful for modulating  
 CC cell adhesion of OB-cadherin-expressing cells and for enhancing the  
 CC delivery of a drug to a tumour or to the central nervous system in a  
 CC mammal. The agent is also useful for treating cancer and/or inhibiting  
 CC invasion and metastasis of a cancer. The agent is further useful for  
 CC stimulating blood vessel regression, for enhancing wound healing in a  
 CC mammal, for enhancing adhesion of foreign tissue implanted within a  
 CC mammal, for increasing vasopermeability in a mammal, for disrupting cell  
 CC adhesion mediated by multiple adhesion molecules, to facilitate cell  
 CC identification, sorting in vitro or imaging in vivo and for permitting  
 CC the selection of cells expressing OB-cadherin. This sequence represents

CC an OB-cadherin CAR sequence cyclic peptide analogue, used as a cell  
 CC adhesion modulating agent.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 3; DB 24; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 5 DKE 7

## RESULT 43

AAP91025  
 ID AAP91025 standard; peptide; 8 AA.

XX AC AAP91025;

XX 25-MAR-2003 (updated)

DT 10-MAR-2003 (updated)

DT 08-MAR-1990 (first entry)

XX Hapten for prodn. of anti-endothelin antibodies.

XX Hapten; antibodies; endothelin.

XX Synthetic.

XX JP01233297-A.

XX 19-SEP-1989.

XX 15-MAR-1988; 88JP-0061125.

XX 15-MAR-1988; 88JP-0061125.

XX (DAIN ) DAINIPPON PHARM CO LTD.

XX (PEPT-) PEPTIDE KENKYU-JO KK.

XX WPI; 1989-314152/43.

XX New peptide(s) as hapten(s) - used for producing antibody for recognising  
 PT endothelin.

XX Claim 2; page 723; 10pp; Japanese.

XX This peptide is an example of the generic peptide Cys-Ser-Ser-X, where  
 CC X is as shown, or successively lacks one C-terminal residue up to Leu-OH  
 CC or -OH. The peptide is used as a hapten for raising antibodies which  
 CC recognise endothelin and its analogues.  
 CC (Updated on 10-MAR-2003 to add missing OS field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 10; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 6 DKE 8

## RESULT 44

AAR70603  
 ID AAR70603 standard; Peptide; 8 AA.

XX AC AAR70603;

XX 14-FEB-1996 (first entry)

XX DE HIV(B35)ARV2-1, human immunodeficiency virus epitope.  
 XX KW HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;  
 XX KW binding peptide; induce killer cell; prevention; treatment; AIDS;  
 KW KW autoimmune disease syndrome; vaccine.  
 XX OS Human immunodeficiency virus.  
 XX PN WO9511255-A1.  
 XX PD 27-APR-1995.  
 XX PF 19-OCT-1994; 94WO-JP01756.  
 XX PR 19-OCT-1993; 93JP-0261302.  
 XX PA (AJIN ) AJINOMOTO CO INC.  
 XX PA (AJIN ) AJINOMOTO KK.  
 XX PI Miwa K, Takiguchi M;  
 XX DR WPI; 1995-170188/22.  
 XX CC HLA-binding peptide fragments from HIV proteins - induce killer  
 PT cells which target HIV-infected cells and can be incorporated into  
 PT anti-HIV vaccines  
 XX PS Example 1; Page 10; 61pp; Japanese.  
 XX CC AAR70603 is a peptide fragment derived from an HIV (Human  
 CC Immunodeficiency Virus) gag protein (residues 479-486) and is capable of  
 CC binding to a human lymphocyte antigen. The peptide can induce killer  
 CC cells which target HIV-infected cells. It is also useful in the  
 CC prevention and treatment of HIV and AIDS. Anti-HIV vaccines may  
 CC incorporate the peptides, or may incorporate a vector (such as vaccinia  
 CC or BCG) contg. DNA encoding the peptides.  
 XX SQ Sequence 8 AA;  
 Query Match 100.0%; Score 3; DB 16; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DKE 3  
 DB 4 DKE 6  
 RESULT 45  
 AAR69840  
 ID AAR69840 standard; Peptide; 8 AA.  
 XX AC AAR69840;  
 XX DT 25-MAR-2003 (updated)  
 XX DT 20-SEP-1995 (first entry)  
 XX DE Peptide comprising a part of hHGF/SF receptor intracellular region.  
 XX KW intracellular region; human hepatocyte growth factor; hHGF; SF;  
 KW scatter factor; receptor; cytosolic signal transducer binding;  
 KW cell proliferation; movement; extracellular matrix invasion.  
 XX OS Synthetic.  
 XX PH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "H-Tyr; optionally phosphorylated"  
 FT Modified-site 8  
 FT /note= "Val-OH"  
 XX PN WO9501376-A1.

XX PD 12-JAN-1995.  
 XX PF 15-JUN-1994; 94WO-EP01943.  
 XX PR 30-JUN-1993; 93GB-0013528.  
 XX PR 18-APR-1994; 94GB-0007673.  
 XX PA (FARM ) FARMITALIA ERBA SRL CARLO.  
 XX PI Comoglio P, Ponzetto C;  
 XX DR WPI; 1995-060954/08.  
 XX CC New peptide(s) which bind to a cytosolic signal transducer - used  
 PT for interfering with pathways leading to cell proliferation and  
 PT motility, for treating neoplastic disease  
 XX PS Claim 17; Page 66; 19pp; English.  
 XX CC The peptides of the invention comprise a portion of the intracellular  
 CC region of the human hepatocyte growth factor/scatter factor (HGF/SF)  
 CC receptor. The tyrosine residue of this peptide is at position 1230  
 CC in the HGF/SF receptor. The peptides can generally reproduce potential  
 CC recognition motifs for the SH2 domains of intracellular (cytosolic)  
 CC signal inducers. The peptides can interfere with pathways leading to  
 CC cell proliferation, movement and extracellular matrix invasion. They  
 CC can be used to inhibit growth of neoplastic cells and to prevent  
 CC metastatic spreading.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 8 AA;  
 Query Match 100.0%; Score 3; DB 16; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DKE 3  
 DB 2 DKE 4  
 RESULT 46  
 AAB08328  
 ID AAB08328 standard; Peptide; 8 AA.  
 XX AC AAB08328;  
 XX DT 04-DEC-2000 (first entry)  
 XX DE Epitope derived from a hlamydia pneumoniae protein.  
 XX KW Chlamydia pneumoniae protein; infection; atherosclerosis;  
 KW coronary atherosclerosis; epitope.  
 XX OS Chlamydia pneumoniae.  
 XX PN WO200046359-A2.  
 XX PD 10-AUG-2000.  
 XX PF 28-JAN-2000; 2000WO-GB00237.  
 XX PR 05-FEB-1999; 99GB-0002555.  
 XX PA (NEUT-) NEUTEC PHARMA PLC.  
 XX PI Burnie JP, Matthews RC;  
 XX DR WPI; 2000-543485/49.  
 XX PT New Chlamydia pneumoniae protein of 496 amino acids for diagnosing,  
 PT preventing and treating C. pneumoniae infection and atherosclerosis,

PT including coronary atherosclerosis -  
 XX  
 PS Claim 5; Page 33; 35pp; English.

CC AAB08324-36 represent epitopes derived from a Chlamydia pneumoniae  
 CC protein. The protein, immunogenic fragments of it, nucleotide sequences  
 CC encoding it, or inhibitor specific against it are used to manufacturing  
 CC a medicament for the treatment of infection due to C. pneumoniae.  
 CC An antibody specific against the protein can diagnose a C. pneumoniae  
 CC infection. C. pneumoniae infection can be prevented. Artherosclerosis,  
 CC including coronary atherosclerosis, caused by C. pneumoniae can also  
 CC be prevented or treated.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 |||  
 Db 5 DKE 7

#### RESULT 47

AAV73610  
 ID AAY73610 standard; Peptide; 8 AA.

XX AC AAY73610;

XX DT 07-MAR-2000 (first entry)

XX DE OB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:116.

XX KW Diagnosis; cancer; OB-cadherin; N-cadherin; E-cadherin; CAR; cyclic;  
 KW cell adhesion recognition sequence; leukaemia; metastasis;  
 KW prostate cancer; breast cancer; ovarian cancer; carcinoma.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9957565-A2.

XX PD 11-NOV-1999.

XX PF 05-MAY-1999; 99WO-CA00362.

XX PR 05-MAY-1998; 98US-0073040.

XX PR 06-NOV-1998; 98US-0187859.

XX PR 20-JAN-1999; 99US-0234395.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Gour BJ, Byers S;

XX XX WPI; 2000-062165/05.

XX DR Detecting expression of OB-cadherin or N-cadherin used for diagnosing  
 XX PT and evaluating cancer -

XX PS Disclosure; Page 19; 56pp; English.

XX CC The present invention describes methods which have been developed for  
 CC detecting and evaluating cancer that are based on the finding that  
 CC OB-cadherin and N-cadherin are expressed by metastatic carcinoma cells,  
 CC but not by highly differentiated, poorly invasive carcinomas. A method  
 CC for determining the presence or absence of a cancer in a patient  
 CC comprises: (1) contacting a biological sample from the patient with a  
 CC binding agent that specifically binds to OB- or N-cadherin OR with an  
 CC oligonucleotide that hybridises to a polynucleotide that encodes OB- or  
 CC N-cadherin; and (2) detecting in the sample an amount of polypeptide  
 CC that binds to the binding agent OR the amount of polynucleotide that  
 CC hybridises to the oligonucleotide, relative to a predetermined cut-off

CC value, and determining the presence or absence of cancer in the patient  
 CC from this. The methods from the present invention can be used to  
 CC determine the metastatic potential of a cancer. The methods may be used  
 CC to detect a metastatic cancer in a patient, to monitor progression of a  
 CC cancer, or to evaluate the metastatic potential of a cancer. Cancers  
 CC which may be evaluated using the methods include leukemia, prostate  
 CC cancer, breast cancer and ovarian cancer. AAY73501 to AAY73813 represent  
 CC peptide sequences used in the exemplification of the present invention.  
 CC Specifically, AAY73503 to AAY73789 represent OB-cadherin cell adhesion  
 CC recognition (CAR) peptides and AAY73790 to AAY73808 represent N-cadherin  
 CC CAR peptides. AAY73906 to AAY73915 represent PCR primers used in examples  
 CC from the present invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 |||  
 Db 6 DKE 8

#### RESULT 48

AAV60696

ID AAY60696 standard; Peptide; 8 AA.

XX AC AAY60696;

XX DT 02-MAR-2000 (first entry)

XX DE OB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:730.

XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;  
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;  
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;  
 KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;  
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;  
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;  
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;  
 KW neurological disease; cyclic.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Modified-site 1..8

XX FT /note= "the terminal residues are condensed with each  
 XX other to form a cyclic peptide"

XX PN WO9957149-A2.

XX XX 11-NOV-1999.

XX XX 05-MAY-1999; 99WO-CA00363.

XX XX 05-MAY-1998; 98US-0073040.

XX PR 06-NOV-1998; 98US-0187859.

XX PR 20-JAN-1999; 99US-0234395.

XX PR 08-MAR-1999; 99US-0264516.

XX XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Gour BJ, Byers S;

XX XX WPI; 2000-038791/03.

XX CC New cadherin modulating agents, used for modulating nonclassical  
 XX cadherin-mediated functions for treating e.g. cancers, obesity,  
 XX rheumatoid arthritis, multiple sclerosis, diabetes or a neurological  
 XX disease -

PS Claim 18; Page 159; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)

CC comprising peptides which comprise a nonclassical cadherin cell adhesion

CC recognition (CAR) sequence. The MAs can be used for modulating

CC nonclassical cadherin-mediated functions. They can be used for e.g.

CC inhibiting adhesion of nonclassical-cadherin expressing cells in a

CC mammal, enhancing delivery of a drug through the skin of a mammal,

CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in

CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting

CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-

CC expressing cell, preventing or treating obesity in a mammal, stimulating

CC blood vessel regression in a mammal, enhancing drug delivery to the

CC central nervous system, treating a demyelinating neurological disease,

CC increasing vasopermeability in a mammal, enhancing adhesion of

CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in

CC a mammal, or preventing pregnancy in a mammal. They can also be used for

CC e.g. enhancing or directing neurite outgrowth, facilitating wound

CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue

CC in a mammal. They can also be used for treating e.g. psoriasis,

CC arthritis, age-related macular degeneration, multiple sclerosis and

CC diabetes. The products can also be used for detection and diagnosis and

CC in bioreactors. AAY60592 to AAY64572 represent specifically claimed

CC peptides, and AAY64573 to AAY64643 and AA233183 to AA233186 represent

CC sequences used in the exemplification of the present invention.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 21; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.2e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3

Db 6 DKE 8

RESULT 49

ABP14450

ID ABP14450 standard; Peptide; 8 AA.

XX

AC ABP14450;

XX

DT 15-JUL-2002 (first entry)

XX

DE HIV A03 super motif gag peptide #12.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus type 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US27766.

XX

PR 05-OCT-1999; 99US-0412863.

XX

PA (EPIM-) EPIMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1 -

XX

PS Claim 32; Page 164; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP23397). (I) has virucide activity and can be used in vaccines. (I)

CC may be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP1501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

CC invention.

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.2e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3

Db 5 DKE 7

RESULT 50

ABP16692

ID ABP16692 standard; Peptide; 8 AA.

XX

AC ABP16692;

XX

DT 15-JUL-2002 (first entry)

XX

DE HIV B07 super motif gag peptide #25.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus type 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US27766.

XX

PR 05-OCT-1999; 99US-0412863.

XX

PA (EPIM-) EPIMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1 -

XX

PS Claim 32; Page 210; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 8 AA;  
 Query Match 100.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
 |||  
 Db 4 DXE 6

RESULT 51  
 ABP16693  
 ID ABP16693 standard; Peptide; 8 AA.

XX AC ABP16693;

XX DT 15-JUL-2002 (first entry)

XX DE HIV B07 super motif gag peptide #26.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 XX peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 210; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
 |||  
 Db 4 DXE 6

RESULT 52  
 ABP17146  
 ID ABP17146 standard; Peptide; 8 AA.

XX AC ABP17146;

XX DT 15-JUL-2002 (first entry)

XX DE HIV B27 super motif gag peptide #22.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 XX peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 220; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 |||  
 Db 3 DKE 5

#### RESULT 53

ABP18709  
 ID ABP18709 standard; Peptide; 8 AA.

XX AC

XX ABP18709;

DT 15-JUL-2002 (first entry)

XX HIV B62 super motif gag peptide #2.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 PS Claim 32; Page 252; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
 |||  
 Db 4 DKE 6

#### RESULT 54

ABP18750

ID ABP18750 standard; Peptide; 8 AA.

XX AC

XX ABP18750;

DT 15-JUL-2002 (first entry)

XX HIV B62 super motif gag peptide #43.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -

PS Claim 32; Page 253; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 8 AA;  
 SQ Query Match 100.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 4 DKE 6

## RESULT 55

ABP20342  
 ID ABP20342 standard; Peptide; 8 AA.

XX  
 AC ABP20342;

DT 15-JUL-2002 (first entry)

DE HIV A03 motif gag peptide #5.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX WO200124810-A1.

PN 12-APR-2001.

PD 05-OCT-2000; 2000WO-US27766.

PF 05-OCT-1999; 99US-0412863.

PR (EPIM-) EPIMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 286; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 4 DKE 6

## RESULT 56

ABP20359  
 ID ABP20359 standard; Peptide; 8 AA.

XX  
 AC ABP20359;

DT 15-JUL-2002 (first entry)

DE HIV A03 motif gag peptide #22.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 287; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present

CC invention.  
 XX Sequence 8 AA;  
 SQ

Query Match 100.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 5 DKE 7

RESULT 57  
 ABP22624  
 ID ABP22624 standard; Peptide; 8 AA.  
 AC  
 XX ABP22624;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A11 motif gag peptide #3.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200124810-A1.  
 PD  
 XX  
 PP 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 PS Claim 32; Page 332; 448pp; English.  
 XX

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (AB25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX Sequence 8 AA;  
 SQ

Query Match 100.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 Db 4 DKE 6

RESULT 58  
 ABP22633  
 ID ABP22633 standard; Peptide; 8 AA.  
 XX  
 AC ABP22633;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A11 motif gag peptide #12.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200124810-A1.  
 PD  
 XX  
 PP 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 PS Claim 32; Page 333; 448pp; English.  
 XX

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (AB25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX Sequence 8 AA;  
 SQ

Query Match 100.0%; Score 3; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;



Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 5 DKE 7

RESULT 59  
AAM99056  
ID AAM99056 standard; Peptide; 8 AA.  
XX  
AC AAM99056;  
XX  
DT 07-DEC-2001 (first entry)  
XX  
DE Vaccine related MHC ligand peptide SEQ ID NO:159.  
XX  
KW Glutamic acid; glutamine; vaccine; major histocompatibility complex;  
KW MHC; immunomodulator; antiallergic; endocrine; neuroprotectant;  
KW virucidal; bactericidal; antiparasitic; fungicidal; cytostatic;  
KW medicine; pharmaceutical; immune disorder; immune deficiency;  
KW autoimmune; hypersensitivity; allergy; graft rejection; infection;  
KW hormonal disorder; central nervous system disease; cancer; melanoma;  
KW anti-melanoma vaccine; human immunodeficiency virus.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO200170772-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 22-MAR-2001; 2001WO-FR00872.  
XX  
PR 23-MAR-2000; 2000FR-0003711.  
XX  
PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX  
PI Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;  
XX WPI; 2001-611470/70.  
XX  
DR Stabilized pharmaceutical containing N-terminal glutamic acid or  
PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt  
PT with strong acid -  
XX  
PS Claim 9; Page 58; 149pp; French.  
XX  
CC The present invention describes a pharmaceutical compound (I) that  
CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue  
CC in the form of an addition salt with a strong, physiologically  
CC acceptable acid (II). Also described are: (a) a pharmaceutical  
CC composition containing at least one (I); (b) a vaccine containing at  
CC least one (I) where this is a major histocompatibility complex (MHC)  
CC ligand (Ia); (c) a method for in vitro diagnosis of diseases associated  
CC with the presence of (Ia); (d) a kit for method (c) that includes a (Ia);  
CC and (e) a process for preparing (I). (I) has immunomodulator, endocrine,  
CC antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic,  
CC fungicidal and cytostatic activities. (I) are useful, in human or  
CC veterinary medicine, in pharmaceutical compositions (for treating immune  
CC disorders, e.g. immune deficiency, autoimmune states, hypersensitivity,  
CC allergy, graft rejection, infection, hormonal disorders and central  
CC nervous system diseases), also, where (I) is a MHC ligand (Ia), in  
CC vaccines for treatment or prevention of: (i) viral, bacterial, parasitic  
CC or fungal infections; or (ii) of cancers. A particular application is in  
CC anti-melanoma vaccines. (I) are also useful for in vitro diagnosis of  
CC diseases associated with interactions between MHC and (I), e.g. melanoma  
CC and human immunodeficiency virus infection. AAM98898 to AAM99592  
CC represent peptides which can be used in pharmaceutical compounds from  
CC the present invention.  
XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 5 DKE 7

Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
|||  
Db 4 DKE 6

RESULT 60  
AAB78499  
ID AAB78499 standard; Peptide; 8 AA.  
XX  
AC AAB78499;  
XX  
DT 19-APR-2001 (first entry)  
XX  
DE HIV-1 gp 41 enhancer peptide #1.  
XX  
KW Human immunodeficiency virus; HIV; gp 41; envelope protein; enhancer;  
KW antiviral; anti-HIV; virucide; hepatotropic; antiinflammatory;  
KW hybrid polypeptide; coiled-coil peptide interaction;  
KW fusion-related disorder; bacterial infection; viral infection.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO200103723-A1.  
XX  
PD 18-JAN-2001.  
XX  
PF 10-JUL-2000; 2000WO-US18772.  
XX  
PR 09-JUL-1999; 99US-0350641.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI; 2001-147136/15.  
XX  
DR New hybrid polypeptide, useful for preventing, treating and diagnosing  
PT e.g. viral infections, comprises an enhancer peptide linked to a core  
PT polypeptide -  
XX  
PS Disclosure; Fig 2A; 151pp; English.  
XX  
CC The present sequence is an enhancer peptide which may be linked to  
CC a core polypeptide to form a novel hybrid polypeptide. The hybrid  
CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
CC those exhibited by the core polypeptide when introduced into a living  
CC system. It is used to increase the in vitro or ex vivo half-life of  
CC the core polypeptide. The hybrid and core polypeptides can be used for  
CC modulating fusogenic events and intracellular processes involving  
CC coiled-coil peptide interactions. Other uses include preventing,  
CC treating and/or diagnosing disorders involving fusion events (e.g.  
CC modulation of neurotransmitter exchange and sperm-egg fusion),  
CC intracellular processes involving coiled-coil peptides (e.g. bacterial  
CC infections) and viral infections that involve cell-cell and/or  
CC virus-cell fusion (e.g. viral infections caused by human  
CC immunodeficiency virus, respiratory syncytial virus, Epstein-Barr  
CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).  
CC The enhancer peptide sequence increases the half-life and reduces the  
CC clearance rate of therapeutic peptides, which increases their efficacy  
CC and minimises the incidence and severity of adverse side effects.  
CC In addition, this increases the sensitivity of the diagnostic procedure  
CC in which they are used.  
XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3

```

Db          5 DKE 7
|||
RESULT 61
AAB55779
ID AAB55779 standard; Peptide; 8 AA.
XX AC
XX AAB55779;
XX DT 07-MAR-2001 (first entry)
XX DE
XX KW PDZ motif sequence #10.
XX KW Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
XX KW allergy; asthma; multiple sclerosis; cancer; infection.
XX OS Synthetic.
XX PN WO200069896-A2.
XX XX
XX XX 23-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US13161.
XX PR 14-MAY-1999; 99US-0134114.
XX PR 14-MAY-1999; 99US-0134117.
XX PR 14-MAY-1999; 99US-0134118.
XX PR 21-OCT-1999; 99US-0160860.
XX PR 29-OCT-1999; 99US-0162498.
XX PR 13-DEC-1999; 99US-0170453.
XX PR 14-JAN-2000; 2000US-0176195.
XX PR 14-FEB-2000; 2000US-0182296.
XX PR 11-APR-2000; 2000US-0196460.
XX PR 11-APR-2000; 2000US-0196527.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS;
XX WPI; 2001-080245/09.
XX DR
XX PT Modulating a biological function of an endothelial cell or
XX PT hematopoietic cell, useful for treating autoimmune diseases and
XX PT infectious diseases, by administering an antagonist that inhibits
XX PT binding between a PDZ protein and a PL protein -
XX PS Disclosure; Page 87-94; 141pp; English.
XX CC The present invention relates to a new method for modulating a
XX CC biological function of an endothelial cell or hematopoietic cell. The
XX CC method involves introducing into a cell, an antagonist that inhibits
XX CC binding between a PDZ protein and a PL protein. The inhibitor is used
XX CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
XX CC disease. It may also be used to prevent transplantation rejection of
XX CC a solid organ transplant. The method may also be used in the treatment
XX CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
XX CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
XX CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
XX CC graft rejection, transplantation rejection), atherosclerosis, cancers,
XX CC infectious diseases, ischemia, vasculitis and Crohn's disease.
XX SQ Sequence 8 AA;
Query Match 100.0%; Score 3; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DKE 3
|||
Db          3 DKE 5
|||
RESULT 62
AAB57611
ID AAB57611 standard; Peptide; 8 AA.
XX AC
XX AAB57611;
XX DT 12-MAR-2001 (first entry)
XX DE
XX KW Neurexin C-terminal core sequence #5.
XX KW Endothelial cell; hematopoietic cell; PDZ domain protein;
XX KW PL domain protein; leukocyte activation; T cell surface receptor;
XX KW synapse formation; transmembrane neurotransmitter receptor;
XX KW autoimmune disease; transplantation rejection; inflammation; allergy;
XX KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
XX KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
XX KW ischaemia; vasculitis; Crohn's disease.
XX OS Homo sapiens.
XX PN WO200069897-A2.
XX XX
XX XX 23-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US13166.
XX PR 14-MAY-1999; 99US-0134114.
XX PR 14-MAY-1999; 99US-0134117.
XX PR 14-MAY-1999; 99US-0134118.
XX PR 21-OCT-1999; 99US-0160860.
XX PR 29-OCT-1999; 99US-0162498.
XX PR 13-DEC-1999; 99US-0170453.
XX PR 14-JAN-2000; 2000US-0176195.
XX PR 14-FEB-2000; 2000US-0182296.
XX PR 11-APR-2000; 2000US-0196460.
XX PR 11-APR-2000; 2000US-0196527.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS;
XX WPI; 2001-025003/03.
XX DR
XX PT New inhibitors of binding of a PDZ protein and PL protein for
XX PT inhibiting T cell-mediated response by hematopoietic cells, or for
XX PT treating diseases characterized by inflammatory and humoral immune
XX PT responses, e.g. inflammation, cancer -
XX PS Disclosure; Page 93; 139pp; English.
XX CC The present invention relates to a method for modulating a biological
XX CC function of an endothelial cell or hematopoietic cell, comprises
XX CC introducing into a cell an antagonist that inhibits binding between a
XX CC PDZ domain protein and a PL domain protein to result in inhibition of
XX CC leukocyte activation. The present sequence is a core sequence of a PL
XX CC domain protein (a T cell surface receptor). PDZ domains of proteins are
XX CC named after three prototypical proteins: PSD95, Drosophila large disc
XX CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
XX CC in synapse formation by organising transmembrane neurotransmitter
XX CC receptors through intracellular interactions. The inhibitors identified
XX CC by the present invention can be used to treat a disease mediated by
XX CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
XX CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
XX CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
XX CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
XX CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
XX CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
XX CC viral infection), ischaemia, vasculitis and Crohn's disease. The
XX CC inhibitors can also be used to prevent transplantation rejection of a
XX CC solid organ transplant.
XX SQ Sequence 8 AA;

```

Query Match 100.0%; Score 3; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 DKE 3  
|||  
Db 3 DKE 5

RESULT 63  
AAB58021  
ID AAB58021 standard; Peptide; 8 AA.  
XX  
AC AAB58021;  
XX  
DT 12-MAR-2001 (first entry)  
XX  
DE Neurexin C-terminal core sequence #5.  
XX  
KW Endothelial cell; haematopoietic cell; PDZ domain protein;  
KW PL domain protein; leukocyte activation; T cell surface receptor;  
KW synapse formation; transmembrane neurotransmitter receptor;  
KW autoimmune disease; transplantation rejection; inflammation; allergy;  
KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;  
KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
KW ischaemia; vasculitis; Crohn's disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200069898-A2.  
XX  
PD 23-NOV-2000.  
XX  
PF 12-MAY-2000; 2000WO-US13205.  
XX  
PR 14-MAY-1999; 99US-0134114.  
PR 14-MAY-1999; 99US-0134117.  
PR 14-MAY-1999; 99US-0134118.  
PR 21-OCT-1999; 99US-0160860.  
PR 29-OCT-1999; 99US-0162498.  
PR 13-DEC-1999; 99US-0170453.  
PR 14-JAN-2000; 2000US-0176195.  
PR 14-FEB-2000; 2000US-0182296.  
PR 11-APR-2000; 2000US-0196460.  
PR 11-APR-2000; 2000US-0196527.  
XX  
PA (ARBO-) ARBOR VITA CORP.  
XX  
PI Lu PS;  
XX  
XX WPI; 2001-061214/07.  
XX  
PT Modulating a biological function of a hematopoietic cell for treating  
PT an allergic response, or diseases mediated by immune-system cells,  
PT comprises introducing into the cell a PDZ-PL interaction enhancer or  
PT inhibitor -  
XX  
XX Disclosure; Page 95; 143pp; English.  
XX  
CC The present invention relates to a method for modulating a biological  
CC function of an endothelial cell or haematopoietic cell, comprises  
CC introducing into a cell an antagonist that inhibits binding between a  
CC PDZ domain protein and a PL domain protein to result in inhibition of  
CC leukocyte activation. The present sequence is a core sequence of a PL  
CC domain protein (a T cell surface receptor). PDZ domains of proteins are  
CC named after three prototypal proteins: PSD95, Drosophila large disc  
CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved  
CC in synapse formation by organising transmembrane neurotransmitter  
CC receptors through intracellular interactions. The inhibitors identified  
CC by the present invention can be used to treat a disease mediated by  
CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy  
CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,

CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic  
CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple  
CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,  
CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.  
CC viral infection), ischaemia, vasculitis and Crohn's disease. The  
CC inhibitors can also be used to prevent transplantation rejection of a  
CC solid organ transplant.  
XX  
SQ Sequence 8 AA;  
Query Match 100.0%; Score 3; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 DKE 3  
|||  
Db 3 DKE 5

RESULT 64  
ABG92308  
ID ABG92308 standard; Peptide; 8 AA.  
XX  
AC ABG92308;  
XX  
DT 29-NOV-2002 (first entry)  
XX  
DE OB-cadherin CAR peptide #104.  
XX  
KW Cancer metastasis; osteoblast cadherin; OB-cadherin CAR; cytostatic;  
KW protein therapy.  
XX  
OS Synthetic.  
XX  
PN US6433149-B1.  
XX  
PD 13-AUG-2002.  
XX  
PF 05-MAY-1999; 99US-0305927.  
XX  
PR 05-MAY-1998; 98US-0073040.  
PR 06-NOV-1998; 98US-0187859.  
PR 20-JAN-1999; 99US-0234395.  
PR 08-MAR-1999; 99US-0264516.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuk OW, Symonds JM, Byers S, Gour BJ;  
XX  
XX WPI; 2002-681212/73.  
XX  
PT Inhibiting cancer metastasis, and the use of osteoblast (OB)-cadherin  
PT peptides, and antibodies that bind them, to inhibit adhesion and  
PT metastasis of circulating cancer cells -  
XX  
PS Disclosure; Column 10; 82pp; English.  
XX  
XX The present invention relates to new methods for inhibiting cancer  
XX metastasis, and the use of osteoblast (OB)-cadherin peptides, and  
XX antibodies that bind them, to inhibit adhesion and metastasis of  
XX circulating cancer cells. The methods of the invention are used to  
XX inhibit cancer metastasis. The present amino acid sequence represents  
XX an OB-cadherin CAR peptide, as described in the invention.  
XX  
SQ Sequence 8 AA;  
Query Match 100.0%; Score 3; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 DKE 3  
|||  
Db 6 DKE 8

RESULT 65  
 ABJ05277  
 ID ABJ05277 standard; Peptide; 8 AA.  
 AC ABJ05277;  
 XX  
 DT 07-NOV-2002 (first entry)  
 XX  
 DE T-cell surface receptor C-terminal core peptide SEQ ID No 272.  
 XX  
 KW Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;  
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;  
 KW inflammatory; humoral immune response; inflammation; C-terminal core;  
 KW T-cell surface receptor.  
 XX  
 OS Unidentified.  
 OS  
 XX  
 PN WO200231512-A2.  
 XX  
 PD 18-APR-2002.  
 XX  
 XX 11-OCT-2001; 2001WO-US32150.  
 XX  
 PR 13-OCT-2000; 2000US-0688017.  
 XX  
 XX (ARBO-) ARBOR VITA CORP.  
 PA  
 XX Rabinowitz JD, Lu PS, Schweizer J;  
 PI WPI; 2002-416878/44.  
 DR  
 XX Assays for determining the affinity of binding between a PDZ domain and  
 PT a ligand, and determining the Ki of an inhibitor of the binding,  
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ  
 PT domain -  
 XX  
 PS Disclosure; Page 117; 164pp; English.  
 XX  
 CC The invention relates to methods and reagents for determining the  
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The  
 CC invention also relates to methods and reagents for determining the Ki of  
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an  
 CC agent that enhances binding of a PDZ domain and a ligand, and determining  
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by  
 CC determining the ligand bound with an immobilised polypeptide comprising a  
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,  
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a  
 CC disease characterised by leukocyte activation, e.g., an autoimmune  
 CC disease that is characterised by inflammatory or humoral immune response,  
 CC and for reducing inflammation in a subject. This sequence represents a T-  
 CC cell surface receptor C-terminal core peptide relating to the PDZ  
 CC containing proteins of the invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 3; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DKE 3  
 |||  
 Db 3 DKE 5  
 |||  
 RESULT 66  
 ABP63505  
 ID ABP63505 standard; Peptide; 8 AA.  
 XX  
 AC ABP63505;  
 XX  
 DT 28-OCT-2002 (first entry)

PDZ motif (PL) peptide SEQ ID NO:232.  
 Molecular interaction; haematopoietic cell; immune response; T cell;  
 PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;  
 Drosophila large disc protein; zonula Occludin 1 protein; PL protein;  
 immunosuppressive; antiinflammatory; anti-allergic; antiatherosclerotic;  
 KW antitumor; antipsoriatic; dermatological; antiasthmatic; cytostatic;  
 KW antimicrobial; vasotropic; inflammatory immune response; inflammation;  
 KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;  
 KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;  
 KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;  
 KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;  
 KW angiogenesis-dependent disorder; infectious disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 PN WO200242422-A2.  
 XX  
 PD 30-MAY-2002.  
 XX  
 XX 09-NOV-2001; 2001WO-US44138.  
 XX  
 XX 11-NOV-2000; 2000US-0710059.  
 PR 24-NOV-2000; 2000US-0721915.  
 PR 24-NOV-2000; 2000US-0722069.  
 PR 28-NOV-2000; 2000US-0724553.  
 XX  
 XX (ARBO-) ARBOR VITA CORP.  
 PA  
 XX Lu P, Rabinowitz JD, Schweizer J;  
 PI WPI; 2002-608221/65.  
 DR  
 XX Modulating the biological function of an endothelial cell or  
 PT haematopoietic cell e.g., a T-cell or B-cell comprises introducing into  
 PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ  
 PT ligand protein in the cell -  
 XX  
 PS Disclosure; Page 135; 207pp; English.  
 XX  
 CC The present invention describes a method (M1) for modulating a biological  
 CC function of an endothelial cell or haematopoietic cell. M1 comprises  
 CC introducing into the cell, an agent that inhibits binding of a PDZ  
 CC (PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein)  
 CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the  
 CC biological function. Also described is a method (M2) for determining  
 CC whether a test compound is an inhibitor of binding between a PDZ protein  
 CC and a PL protein. M1 is used for modulating a biological function of an  
 CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an  
 CC inflammatory or humoral immune response, or an autoimmune disease. An  
 CC inhibitor (I) is useful for treating a disease characterised by leukocyte  
 CC activation, where the disease is characterised by an inflammatory or  
 CC humoral immune response, e.g., an autoimmune disease. The compounds  
 CC e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating  
 CC symptoms of) a variety of diseases and conditions characterised by  
 CC inflammatory and humoral immune responses e.g., inflammation, allergy,  
 CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,  
 CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic  
 CC diseases such as asthma, allergic rhinitis, transplantation rejection  
 CC (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,  
 CC autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,  
 CC angiogenesis-dependent disorders, infectious diseases and ischaemia.  
 CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 3; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXE 3  
Db 3 DXE 5

## RESULT 67

ABR48409  
ID ABR48409 standard; Peptide; 8 AA.

XX AC  
XX ABR48409;

DT 12-JUN-2003 (first entry)

DE Peptide SEQ ID NO:161.

XX Differentiation; proliferation; regeneration; plasticity; survival;  
KW immunoglobulin; Ig; fibronectin III; neural cell adhesion molecule;  
KW Fn3; NCAM; fibroblast growth factor receptor; FGF receptor; ATP; Li;  
KW adenosine triphosphate; vulnary; neurotropic; neuroprotective; cardiant;  
KW antiparkinsonian; anticonvulsant; antidiabetic; neuroleptic; cytosstatic;  
KW nephrotropic; central nervous system disorder; post-ischaemic damage;  
KW peripheral nervous system disorder; nerve damage; multiple sclerosis;  
KW diabetic nerve degeneration; Alzheimer's disease; Parkinson's disease;  
KW Huntington's disease; muscle disease; diabetes; cancer.

OS Homo sapiens.

XX WO2003016351-A2.

XX 27-FEB-2003.

XX 19-AUG-2002; 2002WO-DK00541.

XX 17-AUG-2001; 2001DK-0001228.

PR 02-MAY-2002; 2002DK-0000667.

XX (ENKA-) ENKAM PHARM AS.

XX Kiselyov VV, Skladchikova G, Berezin V, Bock E;

DR WPI; 2003-342416/32.

PT New fragments of neural adhesion molecule, useful for treating e.g.  
PT disorders of the central or peripheral nervous systems or heart muscle

PS Claim 17; Page 50; 108pp; English.

XX The present invention describes a compound (I) comprising at least one of  
CC the 3rd, 4th, and/or 5th immunoglobulin (Ig 3-5) modules and/or the 1st  
CC or 2nd fibronectin III modules (Fn3.1 or 3.2) of neural cell adhesion  
CC molecule (NCAM), or its fragments or variants, able to interact with a  
CC fibroblast growth factor (FGF) receptor, and/or adenosine triphosphate  
CC (ATP) and/or Li (a neural cell adhesion molecule). (I) can have cardiant,  
CC neurotropic, neuroprotective, antiparkinsonian, anticonvulsant, cytosstatic,  
CC antidiabetic, neuroleptic and nephrotropic activities. (I) stimulates  
CC signalling through the FGF receptor, and so modulates the proliferation,  
CC differentiation, regeneration, neural plasticity and/or survival of cells  
CC that express the FGF receptor. (I), optionally used in combination with a  
CC proshesis (nerve guide) can be used for treating diseases of the central  
CC and peripheral nervous systems, e.g. nerve damage, post-ischaemic damage,  
CC multiple sclerosis, diabetic nerve degeneration, Alzheimer's, Parkinson's  
CC and Huntington's diseases, treating diseases of muscles, e.g. impaired  
CC neuro-muscular connections, diabetes types I and II, degeneration of  
CC kidney or pancreas, preventing death of heart muscle cells, e.g. after  
CC acute myocardial infarct, and for revascularisation, promotion of wound  
CC healing, inhibition of angiogenesis, treatment of cancers (where these  
CC express NCAM ligands), to stimulate memory and learning and to modulate  
CC the proliferation, differentiation, regeneration, neural plasticity  
CC and/or survival of cells. (I) can also be used to identify motifs in  
CC peptide ligands expected to bind to the fibroblast growth factor receptor  
CC and/or ATP. ABR48249 to ABR48452 represent peptides which can be used in  
CC a compound from the present invention.

CC N.B. SEQ ID NO:91 to 116 and 118 to 203, 205 and 206 mentioned in the  
CC claims correspond with SEQ ID NO:90 to 203 respectively given in the  
CC Sequence Listing.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 24; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.2e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DXE 3

Db 3 DXE 5

## RESULT 68

ABR48410

ID ABR48410 standard; Peptide; 8 AA.

XX AC

XX ABR48410;

DT 12-JUN-2003 (first entry)

XX Peptide SEQ ID NO:162.

XX Differentiation; proliferation; regeneration; plasticity; survival;  
KW immunoglobulin; Ig; fibronectin III; neural cell adhesion molecule;  
KW Fn3; NCAM; fibroblast growth factor receptor; FGF receptor; ATP; Li;  
KW adenosine triphosphate; vulnary; neurotropic; neuroprotective; cardiant;  
KW antiparkinsonian; anticonvulsant; antidiabetic; neuroleptic; cytosstatic;  
KW nephrotropic; central nervous system disorder; post-ischaemic damage;  
KW peripheral nervous system disorder; nerve damage; multiple sclerosis;  
KW diabetic nerve degeneration; Alzheimer's disease; Parkinson's disease;  
KW Huntington's disease; muscle disease; diabetes; cancer.

OS Mus sp.

XX WO2003016351-A2.

XX 27-FEB-2003.

XX 19-AUG-2002; 2002WO-DK00541.

XX 17-AUG-2001; 2001DK-0001228.

PR 02-MAY-2002; 2002DK-0000667.

XX (ENKA-) ENKAM PHARM AS.

XX Kiselyov VV, Skladchikova G, Berezin V, Bock E;

DR WPI; 2003-342416/32.

PT New fragments of neural adhesion molecule, useful for treating e.g.  
PT disorders of the central or peripheral nervous systems or heart muscle

PS Claim 17; Page 50; 108pp; English.

XX The present invention describes a compound (I) comprising at least one of  
CC the 3rd, 4th, and/or 5th immunoglobulin (Ig 3-5) modules and/or the 1st  
CC or 2nd fibronectin III modules (Fn3.1 or 3.2) of neural cell adhesion  
CC molecule (NCAM), or its fragments or variants, able to interact with a  
CC fibroblast growth factor (FGF) receptor, and/or adenosine triphosphate  
CC (ATP) and/or Li (a neural cell adhesion molecule). (I) can have cardiant,  
CC neurotropic, neuroprotective, antiparkinsonian, anticonvulsant, cytosstatic,  
CC antidiabetic, neuroleptic and nephrotropic activities. (I) stimulates  
CC signalling through the FGF receptor, and so modulates the proliferation,  
CC differentiation, regeneration, neural plasticity and/or survival of cells  
CC that express the FGF receptor. (I), optionally used in combination with a  
CC proshesis (nerve guide) can be used for treating diseases of the central  
CC and peripheral nervous systems, e.g. nerve damage, post-ischaemic damage,  
CC multiple sclerosis, diabetic nerve degeneration, Alzheimer's, Parkinson's  
CC and Huntington's diseases, treating diseases of muscles, e.g. impaired

CC neuro-muscular connections, diabetes types I and II, degeneration of  
 CC kidney or pancreas, preventing death of heart muscle cells, e.g. after  
 CC acute myocardial infarct, and for revascularisation, promotion of wound  
 CC healing, inhibition of angiogenesis, treatment of cancers (where these  
 CC express NCAM ligands), to stimulate memory and learning and to modulate  
 CC the proliferation, differentiation, regeneration, neural plasticity  
 CC and/or survival of cells. (I) can also be used to identify motifs in  
 CC peptide ligands expected to bind to the fibroblast growth factor receptor  
 CC and/or ATP. ABR48249 to ABR48452 represent peptides which can be used in  
 CC a compound from the present invention.  
 CC N.B. SEQ ID NO:91 to 116 and 118 to 203, 205 and 206 mentioned in the  
 CC claims correspond with SEQ ID NO:90 to 203 respectively given in the  
 CC Sequence Listing.

XX SQ Sequence 8 AA;  
 Query Match 100.0%; Score 3; DB 24; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 Db 3 DKE 5

RESULT 69  
 ABU60031  
 ID ABU60031 standard; Peptide; 8 AA.

AC ABU60031;

XX 24-APR-2003 (first entry)

XX OB-cadherin cell adhesion recognition cyclic sequence #62.

XX Metastasis; cancer; binding agent; cell adhesion recognition; CAR;  
 KW OB-cadherin; N-cadherin; prostate cancer; ovarian cancer; breast cancer;  
 KW leukaemia; cyclic.

XX Synthetic.

XX US2002146687-A1.

XX 10-OCT-2002.

XX 05-MAY-1999; 99US-0305928.

XX 05-MAY-1998; 98US-0073040.

PR 06-NOV-1998; 98US-0187859.

PR 20-JAN-1999; 99US-0234395.

XX (BLAS/) BLASCHUK O W.

PA (SYMO/) SYMONDS J M.

PA (BYER/) BYERS S.

PA (GOUR/) GOUR B J.

XX Blaschuk OW, Symonds JM, Byers S, Gour BJ;  
 PI WPI; 2003-246575/25.

DR Diagnosing or evaluating metastatic potential of cancer in patient by

XX contacting biological sample obtained from patient with specified  
 PT binding agent or oligonucleotide, and detecting polypeptide that binds  
 PT to the binding agent -

XX Disclosure; Page 7; 94pp; English.

XX The invention discloses a method for diagnosing or evaluating metastatic  
 CC potential of cancer in a patient. The method comprises contacting a  
 CC biological sample obtained from the patient with a binding agent,  
 CC preferentially antibodies or cell adhesion recognition (CAR) sequences,  
 CC that specifically bind to OB-cadherin or N-cadherin or an oligonucleotide  
 CC that hybridises to a polynucleotide encoding OB-cadherin or N-cadherin

CC and then detecting the amount of polypeptide that binds to the binding  
 CC agent. The inventive method is useful for diagnosing or evaluating  
 CC metastatic potential of cancer, such as prostate, ovarian or breast  
 CC cancer, as well as leukaemia in a patient. It can also be employed for  
 CC monitoring the progression of cancer in a patient. The inventive method  
 CC provides accurate diagnosis or evaluation of metastatic potential of  
 CC cancer in a patient in a simple and economical manner. The sequences  
 CC presented in ABUS59970-ABU60210 are the OB-cadherin cyclic CAR sequences.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 3; DB 24; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 Db 6 DKE 8

RESULT 70

ABUS5840

ID ABUS5840 standard; Peptide; 8 AA.

XX AC ABUS5840;

XX 21-MAR-2003 (first entry)

XX OB-cadherin cell adhesion recognition sequence peptide analogue #84.

XX OB-cadherin; cell adhesion recognition; CAR; cytostatic; vulnary;  
 KW OB-cadherin mediated cell adhesion; cyclisation; central nervous system;  
 KW cancer; metastasis; tumour; blood vessel regression; wound healing;  
 KW vasopermeability; cell adhesion modulation; cyclic.

XX Unidentified.

XX US6472367-B1.

XX 29-OCT-2002.

XX 05-MAY-1998; 98US-0073040.

XX 05-MAY-1998; 98US-0073040.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Symonds JM, Gour BJ;  
 PI WPI; 2003-165425/16.

XX Novel cell adhesion modulating agent useful for e.g. modulating cell

PT adhesion of OB-cadherin-expressing cells and enhancing the delivery of  
 PT a drug to a tumour, comprises a native OB-cadherin cell adhesion  
 PT recognition sequence -

XX Disclosure; Column 3; 42pp; English.

XX The invention relates to a cell adhesion modulating agent comprising a  
 CC peptide four to nine amino acids in length that detectably inhibits  
 CC OB-cadherin mediated cell adhesion, consisting of a native OB-cadherin  
 CC cell adhesion recognition (CAR) sequence that comprises the sequence DDK  
 CC and optionally a residue on one or both sides of the CAR sequence to  
 CC facilitate cyclisation. The modulating agent is useful for modulating  
 CC cell adhesion of OB-cadherin-expressing cells and for enhancing the  
 CC delivery of a drug to a tumour or to the central nervous system in a  
 CC mammal. The agent is also useful for treating cancer and/or inhibiting  
 CC invasion and metastasis of a cancer. The agent is further useful for  
 CC stimulating blood vessel regression, for enhancing wound healing in a  
 CC mammal, for increasing adhesion of foreign tissue implanted within a  
 CC mammal, for increasing vasopermeability in a mammal, for disrupting cell  
 CC adhesion mediated by multiple adhesion molecules, to facilitate cell  
 CC identification, sorting in vitro or imaging in vivo and for permitting

CC the selection of cells expressing OB-cadherin. This sequence represents  
 CC an OB-cadherin CAR sequence cyclic peptide analogue, used as a cell  
 CC adhesion modulating agent.

XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 3; DB 24; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DXE 3  
 DB 6 DXE 8

RESULT 71  
 AAW21332  
 ID AAW21332 standard; peptide; 9 AA.

XX AC AAW21332;  
 XX 29-JUL-1997 (first entry)  
 DT  
 XX Glucagon precursor derived signal oligopeptide #37.

XX Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;  
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;  
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;  
 KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;  
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;  
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
 KW Treponema pallidum membrane protein; TWPA; islet amyloid polypeptide;  
 KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;  
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX Homo sapiens.  
 XX WO9519568-A1.

XX 20-JUL-1995.  
 XX 12-JAN-1995; 95WO-US00575.  
 XX 14-JAN-1994; 94US-0182248.

XX (RATH/) RATH M.

XX Rath M;

XX WPI; 1995-263953/34.

XX Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
 PT regions of max. hydrophilicity, used in modulating communication  
 PT between protein(s)

XX Claim 5; Page 44; 88pp; English.

XX The sequences given in AAW21301-560 represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are localised on the surface  
 CC of the protein and are represented by the hydrophilicity maxima of  
 CC the protein. These peptides are enriched in charged amino acids  
 CC arranged with neutral spacer amino acids. The specific signal  
 CC character of these oligopeptides is determined by a characteristic  
 CC combination of conformation and charge within the signal sequence.  
 CC These oligopeptides may be used as vaccines in the treatment of  
 CC human disease, as competitive inhibitors to prevent or reduce the  
 CC metabolic action or interaction of a selected protein by blocking  
 CC its specific signal sequences, or as therapeutic agents to function  
 CC as feedback regulators to reduce synthesis rate of a selected protein.  
 CC These peptides may be modified by omitting one or more amino acids at  
 CC the N- and/or C-terminal, by substituting one or more amino acids

CC without consideration of charge and polarity, by substituting one or  
 CC more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these.

XX Sequence 9 AA;

Query Match 100.0%; Score 3; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DXE 3  
 DB 3 DXE 5

RESULT 72  
 AAR74191  
 ID AAR74191 standard; Peptide; 9 AA.

XX AC AAR74191;  
 XX 24-DEC-1995 (first entry)  
 DT  
 XX Netrin domain V peptide p75(272-280).

XX Neutral axon out-growth modulator; epidermal growth factor; EGF;  
 KW netrin-1; netrin-2; p78; p75; neurodegenerative disease.

XX Gallus sp.

XX WO9513367-A1.

XX 18-MAY-1995.

XX 08-NOV-1994; 94WO-US12913.

XX 12-NOV-1993; 93US-0152019.

XX (REGC ) UNIV CALIFORNIA.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Dodd J, Jessell T, Kennedy T, Placzek M, Serafini T;  
 XX Tessier-Lavigne M;

XX WPI; 1995-194086/25.

XX Neural axon out-growth modulators derived from EGF-like repeats of  
 PT netrin 1 or netrin 2 - comprise peptide(s) capable of selectively  
 PT increasing spinal axon out-growth or directing axon orientation

XX Disclosure; Page 4; 58pp; English.

XX The peptides given in AAR74189-200 and AAR76042-58 have axon outgrowth  
 CC and/or orienting activity and are based on domain V, domain VI  
 CC or the C-terminal domains of chick p78 and p75 (AAR74186-87).

XX Sequence 9 AA;

Query Match 100.0%; Score 3; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DXE 3  
 DB 3 DXE 5

RESULT 73  
 AAY55530  
 ID AAY55530 standard; peptide; 9 AA.

XX AAY55530;

XX

```

DT 17-JAN-2000 (first entry)
XX
DE HLA binding plu-1 peptide.
XX
KW Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;
KW breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;
KW therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9949034-A1.
PN
XX
XX 30-SEP-1999.
PD
XX
XX 19-MAR-1999; 99WO-GB00866.
PF
XX
XX 20-MAR-1998; 98GB-0005877.
PR
XX
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX
XX Taylor-papadimitriou J;
PI
XX
XX WPI; 1999-591090/50.
DR
XX
XX New nucleic acid encoding the cancer-associated polypeptide plu-1, for
PT diagnosis, treatment and prevention of cancer, especially of breast and
PT ovary.
XX
XX Example 2; Fig 12; 173pp; English.
PS
XX
XX The invention relates to a human cancer-associated polypeptide plu-1.
CC The plu-1 polypeptide can be recombinantly expressed by standard
CC recombinant methodology. Detection of the plu-1 nucleic acid or the
CC polypeptide is used for the following: (i) diagnosis (including imaging)
CC and prognosis of, and determination of susceptibility to, cancer,
CC specifically ovarian or breast cancer; and (ii) treating cancer (by
CC inducing an immune response against cancer cells, e.g. as a vaccine, or
CC by antisense inhibition). Antigens derived from the polypeptide are used
CC to generate activated cytotoxic T lymphocytes, or dendritic cells, for
CC subsequent return to the patient for treatment of cancer. The polypeptide
CC may also be used to identify inhibitors of plu-1 activity. Fragments of
CC the polypeptide, and antibodies raised against plu-1, are useful as assay
CC and imaging agents, also therapeutically (to induce an anti-idiotype
CC response or where conjugated to cytotoxic agents). The plu-1 antigen is
CC expressed more commonly in breast tumors than some known tumor antigens.
CC Sequences AAY5320-629 represent predicted peptides from the plu-1
CC polypeptide which may bind to the human class I alleles B27, A2, A3 and
CC A11.
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 3; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3
Db 6 DKE 8

RESULT 74
AAY25228
ID AAY25228 standard; peptide; 9 AA.
XX
XX AAY25228;
AC
XX
XX 03-SEP-1999 (first entry)
DT
XX HIV gag protein derived peptide fragment #15.
DE
XX Heat shock protein; HSP; complex; denatured protein matrix; antigen;
XX vaccine; allergic disease; treatment; susceptibility; Th2; skin rash;
KW

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KW allergic reaction; asthma; gag protein.
XX
OS Human immunodeficiency virus.
XX
XX WO9929182-A1.
PN
XX
XX 17-JUN-1999.
PD
XX
XX 04-DEC-1998; 98WO-US25734.
PF
XX
XX 05-DEC-1997; 97US-0986234.
PR
XX
XX 05-DEC-1997; 97US-0985548.
PR
XX
XX (UYNE-) UNIV NEW MEXICO STATE.
PA
XX
XX Moseley PL, Wallen ES;
PI
XX
XX WPI; 1999-394912/33.
DR
XX
XX Synthesizing heat shock protein complexes using a denatured protein
PT matrix
PT
XX
XX Example 1; Fig 1C; 33pp; English.
PS
XX
XX This invention describes a novel method for synthesizing heat shock
CC protein (HSP) complexes comprising adding a heat shock protein to a
CC denatured protein matrix for binding, and adding a complexing solution
CC comprising a peptide to elute a heat shock protein-peptide complex. A
CC HSP-antigen complex is useful as a vaccine for treating an allergic
CC disease (in a mammal, preferably a human) to reduce susceptibility of
CC the Th2 response, the complex comprising a HSP-antigenic peptide complex.
CC The complex is administered to prevent a mammal from having an allergic
CC reaction to an allergic disease, or administered to a mammal having an
CC allergic disease, to reduce the allergic reactions. Allergic diseases
CC include asthma and skin rashes. Prior art methods or preventing/treating
CC allergic diseases include antihistamines which treat only the symptoms,
CC corticosteroids which have severe side effects and desensitization
CC therapy which has limited uses. The new method also allows more
CC flexibility of use of peptide-based vaccines, as prior art HSP-based
CC vaccines require isolation from a portion of the tumour itself. This
CC sequence represents a peptide fragment derived from the HIV gag protein
CC which is used in the method of the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 3; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3
Db 3 DKE 5

RESULT 75
AAB22053
ID AAB22053 standard; peptide; 9 AA.
XX
XX AAB22053;
AC
XX
XX 08-JAN-2001 (first entry)
DT
XX Fyn protein N-myristoylation/palmitoylation site.
DE
XX Fyn protein; N-myristoylation site; enzyme activity; palmitoylation;
XX post-translational modification.
KW
XX Unidentified.
XX
XX WO200050630-A2.
PN
XX
XX 31-AUG-2000.
PD
XX

```



PF 25-FEB-2000; 2000WO-GB00663.  
XX  
PR 25-FEB-1999; 99GB-0004392.  
PR 25-FEB-1999; 99GB-0004393.  
PR 25-FEB-1999; 99GB-0004395.  
PR 25-FEB-1999; 99GB-0004398.  
PR 25-FEB-1999; 99GB-0004401.  
PR 25-FEB-1999; 99GB-0004407.  
PR 13-JAN-2000; 2000GB-0000771.  
XX  
XX (FLUO-) FLUORESCENCE LTD.  
XX  
PI Colyer J, Craig RK;  
XX  
XX WPI; 2000-572100/53.  
XX  
PT Measuring different enzyme activities simultaneously by contacting with  
PT a binding domain and a binding partner having a site  
PT post-translationally modifiable by the enzyme and measuring interaction  
PT between them -  
XX  
PS Disclosure; Page 37; 78pp; English.  
XX  
XX The present sequence is the N-myristoylation/palmitoylation site from Fyn  
CC protein. This site may be used in the method of the present invention, in  
CC which, the activity of two enzymes may be measured simultaneously via  
CC contacting the enzymes separately with a binding domain and a binding  
CC partner. The binding domain and binding partner comprise a site subject  
CC to post-translational modification by the enzyme under investigation e.g.  
CC an enzyme involved in N-myristoylation. Modification of the site by the  
CC enzyme affects the interaction between the binding domain and the binding  
CC partner and so this interaction may be measured in order to measure the  
CC enzyme activity. The present sequence may be used as a binding domain or  
CC partner in the method of the present invention.  
XX  
SQ Sequence 9 AA;  
  
Query Match 100.0%; Score 3; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DKE 3  
Db 7 DKE 9  
|||  
|||  
  
Search completed: November 25, 2003, 18:15:54  
Job time : 10.7181 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 7.22872 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-11

Perfect score: 3  
Sequence: 1 DXE 3

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	100.0	8	4	Q9H4D3
2	3	100.0	14	4	O15222
3	3	100.0	15	11	Q62531
4	3	100.0	16	6	Q9TRA2
5	3	100.0	17	11	Q9QVS6
6	3	100.0	17	11	Q9QVS8
7	3	100.0	18	4	Q9NQC0
8	3	100.0	19	1	O50844
9	3	100.0	19	13	Q9PRG2
10	3	100.0	19	13	Q9PS73
11	2	66.7	8	2	Q9R7T2
12	2	66.7	8	4	Q9P0K3
13	2	66.7	8	5	Q9N6M5
14	2	66.7	8	6	Q9BFA7
15	2	66.7	8	6	O18854
16	2	66.7	8	6	Q95M23

17	2	66.7	8	13	Q8AWW0
18	2	66.7	8	13	Q8AWV9
19	2	66.7	8	13	Q8AWV8
20	2	66.7	8	13	Q8AWV7
21	2	66.7	9	2	P70740
22	2	66.7	9	2	Q51349
23	2	66.7	9	2	Q937J8
24	2	66.7	9	2	Q937H9
25	2	66.7	9	2	Q93E20
26	2	66.7	9	4	Q9BQT4
27	2	66.7	9	5	P82208
28	2	66.7	9	7	O78225
29	2	66.7	9	7	O78226
30	2	66.7	9	12	Q84333
31	2	66.7	9	12	Q9ILX6
32	2	66.7	9	13	Q8JJ12
33	2	66.7	9	13	Q8JJ18
34	2	66.7	9	13	Q8JJ14
35	2	66.7	9	13	Q8JJ10
36	2	66.7	9	13	Q8JJ16
37	2	66.7	10	1	Q9UWM5
38	2	66.7	10	1	Q50843
39	2	66.7	10	2	Q9F9H5
40	2	66.7	10	2	Q9RSN4
41	2	66.7	10	2	Q9RSN6
42	2	66.7	10	2	Q8RSU1
43	2	66.7	10	2	Q51812
44	2	66.7	10	2	Q8RIT1
45	2	66.7	10	2	P83067
46	2	66.7	10	2	P83160
47	2	66.7	10	3	Q9UVW2
48	2	66.7	10	4	Q96QT9
49	2	66.7	10	4	Q9NP06
50	2	66.7	10	4	Q8WXB5
51	2	66.7	10	4	Q9NP07
52	2	66.7	10	8	P82136
53	2	66.7	10	11	O70580
54	2	66.7	11	2	Q47606
55	2	66.7	11	2	Q9EUZ3
56	2	66.7	11	2	Q47345
57	2	66.7	11	3	Q9UR95
58	2	66.7	11	4	Q9H4H5
59	2	66.7	11	5	Q9UAR8
60	2	66.7	11	6	Q9TRW5
61	2	66.7	11	6	P83128
62	2	66.7	11	12	Q84189
63	2	66.7	11	16	Q9K7A4
64	2	66.7	12	2	Q9R5F7
65	2	66.7	12	2	Q93A08
66	2	66.7	12	2	Q9R5F5
67	2	66.7	12	2	O8VLX8
68	2	66.7	12	2	Q9L4M9
69	2	66.7	12	2	P97134
70	2	66.7	12	2	Q9R3B3
71	2	66.7	12	4	Q9UMR0
72	2	66.7	12	4	Q96PK0
73	2	66.7	12	4	Q9UMZ8
74	2	66.7	12	5	Q9TWV4
75	2	66.7	12	6	Q9TQW3
76	2	66.7	12	6	Q9XS31
77	2	66.7	12	8	Q8MES0
78	2	66.7	12	8	Q9XNR6
79	2	66.7	12	11	Q9QZD0
80	2	66.7	12	12	Q89243
81	2	66.7	12	13	Q8JHC1
82	2	66.7	12	13	Q8JHC2
83	2	66.7	12	13	Q8AUP8
84	2	66.7	12	13	Q8AUP7
85	2	66.7	12	15	Q98YN6
86	2	66.7	12	15	O12036
87	2	66.7	12	15	Q9ICE5
88	2	66.7	12	16	O25179
89	2	66.7	13	2	Q55094

Q8AWW0	coscoroba c
Q8AWV9	anser caeru
Q8AWV8	cygnus colu
Q8AWV7	anas platyr
P70740	alcaligenes
Q51349	pseudomonas
Q937J8	escherichia
Q937H9	enterobacte
Q93E20	streptococc
Q9BQT4	homo sapien
P82208	bombyx mori
O78225	mus musculu
O78226	mus musculu
Q84333	simian viru
Q9ILX6	macaca neme
Q8JJ12	carassius a
Q8JJ18	danio aequi
Q8JJ14	danio frank
Q8JJ10	notropis ch
Q8JJ16	danio albol
Q9UWM5	sulfolobus
O50843	methanococc
Q9F9H5	helicobacte
Q9RSN4	clostridium
Q9RSN6	clostridium
Q8RSU1	helicobacte
Q51812	escherichia
Q8RIT1	anaplasm p
P83067	bacillus ce
P83160	anabaena sp
Q9UVW2	schizophyll
Q96QT9	homo sapien
Q9NP06	homo sapien
Q8WXB5	homo sapien
Q9NP07	homo sapien
P82136	spinacia ol
O70580	mus musculu
Q47606	escherichia
Q9EUZ3	escherichia
Q47345	escherichia
Q9UR95	pichia angu
Q9H4H5	homo sapien
Q9UAR8	aedes aegyp
Q9TRW5	bos taurus
P83128	bos indicus
Q84189	subacure sc
Q9K7A4	bacillus ha
Q9R5F7	helicobacte
Q93A08	thiobacillu
Q9R5F5	helicobacte
Q8VLX8	thermus the
Q9L4M9	streptococc
P97134	rhizobium l
Q9R3B3	helicobacte
Q9UMR0	homo sapien
Q96PK0	homo sapien
Q9UMZ8	homo sapien
Q9TWV4	lymaea eta
Q9TQW3	bos taurus
Q9XS31	sus scrofa
Q8MES0	anoda crist
Q9XNR6	pylailia l
Q9QZD0	mus musculu
Q89243	woodchuck h
Q8JHC1	cyprinus ca
Q8JHC2	carassius a
Q8AUP8	salmo trutt
Q8AUP7	salmo salar
Q98YN6	human immun
O12036	caprine art
Q9ICE5	human immun
O25179	helicobacte
Q55094	synechocyst

90 Q9R89 2 66.7 13 2 Q9R89 09r89 streptococ  
91 Q9RSN5 2 66.7 13 2 Q9RSN5 09rsn5 clostridium  
92 Q4793 2 66.7 13 2 Q4793 04793 escherichia  
93 Q8G312 2 66.7 13 2 Q8G312 08g312 photobacter  
94 Q9UM46 2 66.7 13 4 Q9UM46 09um46 homo sapien  
95 Q9H4C1 2 66.7 13 4 Q9H4C1 09h4c1 homo sapien  
96 Q8WY56 2 66.7 13 4 Q8WY56 08wy56 homo sapien  
97 Q8I2R0 2 66.7 13 4 Q8I2R0 08i2r0 homo sapien  
98 Q9W5Q6 2 66.7 13 5 Q9W5Q6 09w5q6 drosophila  
99 Q8I2E2 2 66.7 13 5 Q8I2E2 08i2e2 plasmodium  
100 Q9TQ84 2 66.7 13 6 Q9TQ84 09tq84 equus caball

## ALIGNMENTS

RESULT 1  
Q9H4D3 ID Q9H4D3 PRELIMINARY; PRT; 8 AA.  
AC Q9H4D3  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE LIM domain only 1 protein (Fragment).  
GN LMO1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TSSUE=Blood;  
RA Brueckmann T., Winterspacht A., Hankeln T., Schmidt E.R., Zabel B.U.;  
RT "Human PAC clone RCP1704K03781 (pD7 781K3), sequenced in DHGP project  
RT (Comparative Sequencing of a 1 Mb Region in Man (Chromosome 11p15) and  
RL Mouse (Chromosome 7)).";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ277661; CAC14573.1; -.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 980 MW; F3AB133AA732C696 CRC64;

Query Match 100.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
|||  
DB 5 DXE 7

RESULT 2  
O15222 ID O15222 PRELIMINARY; PRT; 14 AA.  
AC O15222  
DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE HOXC9 protein (Fragment).  
GN HOXC9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98019011; PubMed=9357979;  
RA Flaggiello D., Gibaud A., Dutrillaux B., Poupon M.F., Malfoy B.;  
RT "Distinct patterns of all-trans retinoic acid dependent expression of  
RT the HOXC9 and HOXC10 homeogenes in human embryonal and small-cell lung  
RT ,carcinoma cell lines";  
RL FEBS Lett. 415:263-267(1997).  
DR EMBL: X99682; CAA67998.1; -.  
DR TRANSFAC; T0327; -.

FT NON TER 1  
SQ SEQUENCE 14 AA; 1725 MW; 6C5D7272C5499A3B CRC64;  
Query Match 100.0%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
|||  
DB 10 DXE 12

RESULT 3  
Q62531 ID Q62531 PRELIMINARY; PRT; 15 AA.  
AC Q62531  
DT 01-JUN-1998 (TReMBLrel. 06, Created)  
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
DE Placental calcium-binding protein (18A2) (PEL98) (MTS1 protein)  
DE (Metastatic cell protein) (Fragment).  
GN MTS1.  
OS Mus spretus (Western wild mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10096;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRET/EI;  
RX MEDLINE=94319082; PubMed=8043949;  
RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,  
RA Nadeau J.H.;  
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";  
RL Mamm. Genome 5:349-355(1994).  
CC -I- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, AND MORE  
CC SPECIFICALLY TO S-100/CABP LIKE PROTEINS.  
DR EMBL: U05696; AAA61936.1; -.  
KW Calcium-binding; Placenta.  
FT NON TER 1  
SQ SEQUENCE 15 AA; 1824 MW; 31EBEA50E3987741 CRC64;

Query Match 100.0%; Score 3; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXE 3  
|||  
DB 9 DXE 11

RESULT 4  
Q9TRA2 ID Q9TRA2 PRELIMINARY; PRT; 16 AA.  
AC Q9TRA2  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE Tropomyosin (fragment).  
GN Tropomyosin.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95029805; PubMed=7943254;  
RA Rao U.J., Denslow N.D., Block E.R.;  
RT "Hypoxia induces the synthesis of tropomyosin in cultured porcine  
RT pulmonary artery endothelial cells";  
RL Am. J. Physiol. 267:L271-L281(1994).  
SQ SEQUENCE 16 AA; 1950 MW; E042C558DE4A778D CRC64;  
Query Match 100.0%; Score 3; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 14 DKE 16

## RESULT 5

ID Q9QV56 PRELIMINARY; PRT; 17 AA.  
AC Q9QV56;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Lactate dehydrogenase-A (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95201434; PubMed=7534515;  
RA Sandulache R., Pretsch W., Chatterjee B., Gimbel W., Graw J.,  
RA Favor J.;  
RT "Molecular analysis of four lactate dehydrogenase-A mutants in the  
RT mouse.";  
RL Mamm. Genome 5:777-780(1994).  
SQ SEQUENCE 17 AA; 1988 MW; E941E0A122477605 CRC64;

Query Match 100.0%; Score 3; DB 11; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 11 DKE 13

## RESULT 6

ID Q9QV58 PRELIMINARY; PRT; 17 AA.  
AC Q9QV58;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Lactate dehydrogenase-A (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95201434; PubMed=7534515;  
RA Sandulache R., Pretsch W., Chatterjee B., Gimbel W., Graw J.,  
RA Favor J.;  
RT "Molecular analysis of four lactate dehydrogenase-A mutants in the  
RT mouse.";  
RL Mamm. Genome 5:777-780(1994).  
SQ SEQUENCE 17 AA; 1888 MW; E941E0A3F0CD7605 CRC64;

Query Match 100.0%; Score 3; DB 11; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 11 DKE 13

## RESULT 7

ID Q9NQGO PRELIMINARY; PRT; 18 AA.  
AC Q9NQGO;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE DJ1168M15.1 (Similar to ubiquitin) (Fragment).  
GN DJ1168M15.1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lovell J.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL118499; CAC00663.1; -.  
DR HSSP; P02248; 1UBI.  
DR Gene; HGNC:16103; C20orf109.  
DR InterPro; IPR000626; Ubiquitin.  
DR Pfam; PF00240; ubiquitin; 1.  
FT NON\_TER 1  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2057 MW; 35D2F50DBD032F49 CRC64;

Query Match 100.0%; Score 3; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 16 DKE 18

## RESULT 8

ID Q50844 PRELIMINARY; PRT; 19 AA.  
AC Q50844;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)  
DE RNA polymerase gene 5' flanking region with AT-rich DNA sequence  
DE (Fragment).  
OS Methanococcus voltae.  
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
OC Methanococcaceae; Methanococcus.  
OX NCBI\_TaxID=2188;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85230552; PubMed=4006907;  
RA Bollschweiler C., Kuehn R., Klein A.;  
RT "Non-repetitive AT-rich sequences are found in intergenic regions of  
RT Methanococcus voltae DNA.";  
RL EMBO J. 4:805-809(1985).  
DR EMBL; X02516; CAA26350.1; -.  
FT NON\_TER 1  
FT NON\_TER 18  
SQ SEQUENCE 19 AA; 2268 MW; 22A17D3A28540A57 CRC64;

Query Match 100.0%; Score 3; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DKE 3  
|||  
Db 11 DKE 13

## RESULT 9

ID Q9PRG2 PRELIMINARY; PRT; 19 AA.  
AC Q9PRG2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE 21 kDa high mobility group protein homolog (Fragment).  
OS Salmo salar (Atlantic salmon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
OX NCBI\_TaxID=8030;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93383548; PubMed=8372558;  
RA von der Decken A., Waters S.;  
RT "Modulation of hepatic chromatin structure in response to 17-beta  
RT estradiol induced activation of the vitellogenin gene regions in  
RT Atlantic salmon, *Salmo salar*.";  
RL Acta Biochim. Pol. 40:23-28(1993).  
RN [2]  
RP SEQUENCE.  
RX MEDLINE=93113266; PubMed=1472904;  
RA Waters S., Khamis M., von der Decken A.;  
RT "Purification of the Atlantic salmon hepatic 21 kDa protein and  
RT classification as a high mobility group chromatin protein.";  
RL Cell. Mol. Biol. 38:783-789(1992).  
SQ SEQUENCE 19 AA; 2222 MW; D5A3F6A69239C41E CRC64;

Query Match 100.0%; Score 3; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKE 3  
|||  
DB 11 DKE 13

RESULT 10  
ID Q9PS73 PRELIMINARY; PRT; 19 AA.  
AC Q9PS73;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE P0-MAIN glycoprotein in PNS myelin (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92126243; PubMed=1722981;  
RA Schliess F., Stoffel W.;  
RT "Evolution of the myelin integral membrane proteins of the central  
RT nervous system";  
RL Biol. Chem. Hoppe-Seyler 372:865-874(1991).  
FT NON\_TER 1  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2069 MW; A0D5651D4C4B769B CRC64;

Query Match 100.0%; Score 3; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DKE 3  
|||  
DB 6 DKE 8

RESULT 11  
ID Q9R7T2 PRELIMINARY; PRT; 8 AA.  
AC Q9R7T2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hypothetical 1.0 kDa protein (Fragment).  
GN YOFG.  
OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97061202; PubMed=8905232;  
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mirobuchi K.,  
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
RA Sappei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
RA Yano M., Horiuchi T.;  
RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding  
RT to the 12.7-28.0 min Region on the Linkage Map.";  
RL DNA Res. 3:137-155(1996).  
DR EMBL; D90705; BAA35310.1;  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 66.7%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KE 3  
||  
DB 7 KE 8

RESULT 12  
ID Q9P0K3 PRELIMINARY; PRT; 8 AA.  
AC Q9P0K3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE CGMP-specific phosphodiesterase PDE5A2 (Fragment).  
GN PDE5A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20145478; PubMed=10679249;  
RA Lin C.S., Lau A., Tu R., Lue T.F.;  
RT "Identification of three alternative first exons and an intronic  
RT promoter of human PDE5A gene.";  
RL Biochem. Biophys. Res. Commun. 268:596-602(2000).  
DR EMBL; AF155195; AAF40302.1;  
FT NON\_TER 8  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 908 MW; E8A33AA879D76726 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DK 2  
||  
DB 6 DK 7

RESULT 13  
ID Q9N6M5 PRELIMINARY; PRT; 8 AA.  
AC Q9N6M5;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Dihydrofolate reductase thymidylate synthase (Fragment).  
GN FOL1.  
OS Toxoplasma gondii.

```

OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH, COUGAR TC751G134, SEA OTTER TC828G1, and BEVERLEY;
RA Lehmann T., Blackston C.R., Farmlay S.F., Remington J.S., Dubey J.P.;
RT "Strain Typing of Toxoplasma gondii: Comparison of Antigen-Coding and
RT Housekeeping Genes.";
RL J. Parasitol. 0:0-0(2000).
DR EMBL; AF249695; AAF79153.1; -.
DR EMBL; AF249692; AAF79150.1; -.
DR EMBL; AF249693; AAF79151.1; -.
DR EMBL; AF249694; AAF79152.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1035 MW; 33CAAA05B133044 CRC64;

Query Match 66.7%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 3 KE 4

RESULT 14
Q9BFA7 PRELIMINARY; PRT; 8 AA.
AC Q9BFA7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE cAMP responsive element moderator (Fragment).
OS CREM.
GN Macrosclides proboscideus (Short-eared elephant shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Macroscelidea; Macroscelididae; Macroscelides.
OX NCBI_TaxID=29082;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011636; AAG47551.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 940 MW; DF1DD33AB5AB572A CRC64;

Query Match 66.7%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 5 DK 6

RESULT 15
O18854 PRELIMINARY; PRT; 8 AA.
AC O18854;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CD19 antigen (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]

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RP SEQUENCE FROM N.A.
RA Liu P.-C., Shibuya H., Katz M.L., Johnson G.S.;
RT "A BsmFI PCR/RFLP in the canine CD19 antigen gene.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF024717; AAB81967.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 832 MW; 6735A1ADDB1325A7 CRC64;

Query Match 66.7%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 3 KE 4

RESULT 16
Q95M23 PRELIMINARY; PRT; 8 AA.
AC Q95M23;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Na+/K+ ATPase alpha subunit (EC 3.6.1.37) (Fragment).
GN ATP1A1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pietrain;
RA Blazkova P., Stratil A., Peelman L.J., Van Poucke M., Reiner G.,
RA Geldermann H., Kopecky M.;
RT "RH mapping of the porcine ATP1A1, ATP1B1, V-ATPase, IVL genes and
RT linkage assignments of ATP1A1 and IVL to chromosome 4.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344138; CAC51422.1; -.
KW Hydrolase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 1117 MW; 604B41AB133B02D3 CRC64;

Query Match 66.7%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 4 KE 5

RESULT 17
Q8AWW0 PRELIMINARY; PRT; 8 AA.
AC Q8AWW0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LDH-B (Fragment).
OS LDH-B.
OC Coscoroba coscoroba (Coscoroba swan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Coscoroba.
OX NCBI_TaxID=8863;
RN [1]
RP SEQUENCE FROM N.A.
RA Cotter J.-P., StJohn J., Quinn T.W.;
RT "Isolation of a precisely delineated, Recently Transposed Chicken
RT Repeat 1 (CR1) Retrotransposon Within an Intron of the Coscoroba
RT coscoroba.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY123324; AAM96898.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 66.7%; Score 2; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
Db 7 DK 8

RESULT 18
Q8AWV9 PRELIMINARY; PRT; 8 AA.
ID Q8AWV9
AC Q8AWV9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LDH-B (Fragment).
GN LDH-B.
OS Anser caerulescens caerulescens (snow goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=70340;
RN [1]
RP SEQUENCE FROM N.A.
RA Cotter J.-P., StJohn J., Quinn T.W.;
RT "Isolation of a Precisely Delineated, Recently Transposed Chicken
RT Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba
RT coscoroba.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123325; AAM96899.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 66.7%; Score 2; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
Db 7 DK 8

RESULT 19
Q8AWV8 PRELIMINARY; PRT; 8 AA.
ID Q8AWV8
AC Q8AWV8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LDH-B (Fragment).
GN LDH-B.
OS Cygnus columbianus (tundra swan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cygnus.
OX NCBI_TaxID=110926;
RN [1]
RP SEQUENCE FROM N.A.
RA Cotter J.-P., StJohn J., Quinn T.W.;
RT "Isolation of a Precisely Delineated, Recently Transposed Chicken
RT Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba
RT coscoroba.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123326; AAM96900.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 66.7%; Score 2; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
Db 7 DK 8

RESULT 20
Q8AWV7 PRELIMINARY; PRT; 8 AA.
ID Q8AWV7
AC Q8AWV7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LDH-B (Fragment).
GN LDH-B.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Cotter J.-P., StJohn J., Quinn T.W.;
RT "Isolation of a Precisely Delineated, Recently Transposed Chicken
RT Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba
RT coscoroba.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123327; AAM96901.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 66.7%; Score 2; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
Db 7 DK 8

RESULT 21
P70740 PRELIMINARY; PRT; 9 AA.
ID P70740
AC P70740;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HoxA protein (Fragment).
GN HoxA.
OS Alcaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H16;
RX MEDLINE=94292469; PubMed=8021224;
RA Lenz O., Schwartz E., Dervede J., Eitinger M., Friedrich B.;
RT "The Alcaligenes eutrophus H16 hoxA gene participates in hydrogenase
RT regulation.";
RL J. Bacteriol. 176:4385-4393(1994).
DR EMBL; X74670; CAA52736.1; -.
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 992 MW; 970BD1ADC6D33AB5 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
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Db          ||
3 DK 4

RESULT 22
Q51349      PRELIMINARY;      PRT;      9 AA.
ID Q51349
AC Q51349;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cn1A1 leader peptide.
OS Pseudomonas aeruginosa.
OG Plasmid R1033, and Plasmid RPL11.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=R1033; TRANSPON=IS6100delta;
RX MEDLINE=92052679; PubMed=1658833;
RA Stokes H.W., Hall R.M.;
RT "Sequence analysis of the inducible chloramphenicol resistance
RT determinant in the Tn1696 integron suggests regulation by
RT translational attenuation.";
RL Plasmid 26:10-19(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC PLASMID=R1033; TRANSPON=IS6100delta;
RX MEDLINE=91294195; PubMed=1648560;
RA Bessonnette L., Champetier S., Buissou J.P., Roy P.H.;
RT "Characterization of the nonenzymatic chloramphenicol resistance
RT (cmlA) gene of the In4 integron of Tn1696: similarity of the product
RT to transmembrane transport proteins.";
RL J. Bacteriol. 173:4493-4502(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMID=RPL11; TRANSPON=Tn1403;
RA Partridge S.R., Rechia G.D., Stokes H.W., Hall R.M.;
RT "A family of class 1 integrons related to In4 from Tn1696.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12338; AAB60003.1; -.
DR EMBL; AFJ13472; AAK50390.1; -.
KW Plasmid.
SQ SEQUENCE 9 AA; 981 MW; 9303ADD44325A1B5 CRC64;

Query Match      66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DK 2
      ||
Db      8 DK 9

RESULT 23
Q937J8      PRELIMINARY;      PRT;      9 AA.
ID Q937J8
AC Q937J8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative transposition protein TniQ (Fragment).
OS TniQ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH210; TRANSPON=Tn5057;
RX MEDLINE=21604134; PubMed=11763242;
RA Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.,

Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
Yurieva O.V., Nikiforov V.G.;
RA "Mercury resistance transposons of Gram-negative environmental
RT bacteria and their classification.";
RL Res. Microbiol. 152:811-822(2001).
DR EMBL; AJ302765; CAC82977.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1023 MW; 1B963AB5B7287AA4 CRC64;

Query Match      66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DK 2
      ||
Db      7 DK 8

RESULT 24
Q937H9      PRELIMINARY;      PRT;      9 AA.
ID Q937H9
AC Q937H9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative TniQ protein (Fragment).
OS TniQ.
OS Enterobacter sp. CH2-4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=143777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH2-4; TRANSPON=Tn5057v1;
RX MEDLINE=21604134; PubMed=11763242;
RA Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.,
RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental
RT bacteria and their classification.";
RL Res. Microbiol. 152:811-822(2001).
DR EMBL; AJ291727; CAC83017.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1023 MW; 1B963AB5B7287AA4 CRC64;

Query Match      66.7%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DK 2
      ||
Db      7 DK 8

RESULT 25
Q93EZ0      PRELIMINARY;      PRT;      9 AA.
ID Q93EZ0
AC Q93EZ0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ScpB (Fragment).
OS ScpB.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O50R;
RX MEDLINE=21424698; PubMed=11532154;
RA Franken C., Haase G., Brandt C., Weber-Heymann J., Martin S.,
RA Lammler C., Podbielski A., Lutticken R., Spellberg B.;

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RT "Horizontal gene transfer and host specificity of beta-haemolytic  
 RT streptococci: the role of a putative composite transposon containing  
 RT scpB and lmb.";  
 RL Mol. Microbiol. 41:925-935(2001).  
 DR EMBL; AF327852; AAL10713.1; -;  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1146 MW; 543721AB1326CA03 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 5 KE 6

RESULT 26  
 Q9BQT4 PRELIMINARY; PRT; 9 AA.  
 AC Q9BQT4;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CLIP-associating protein CLASP2 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Galjart N.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=21185938; PubMed=11290329;  
 RA Akhmanova A., Hoogenraad C.C., Drabek K., Stepanova T., Dortland B.,  
 RA Verkerk T., Vermeulen W., Burgering B.M., de Zeeuw C.I., Grosveld F.,  
 RA Galjar N.;  
 RT "CLASPs are CLIP-115 and -170 associating proteins involved in the  
 RT regional regulation of microtubule dynamics in motile fibroblasts.";  
 RL Cell 104:923-935(2001).  
 DR EMBL; AJ288058; CAC35157.1; -;  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1001 MW; C3ECB33AAAA8769D CRC64;

Query Match 66.7%; Score 2; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 6 DK 7

RESULT 27  
 P82208 PRELIMINARY; PRT; 9 AA.  
 AC P82208;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE Unknown protein from 2D-page (Fragment).  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE.  
 RP STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;

RX MEDLINE=21177481; PubMed=11280994;  
 RA Zhong B.X.;  
 RT "Protein database for several tissues derived from five instar of  
 RT silkworm.";  
 RL I Chuan Hsueh Pao 28:217-224(2001).  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1009 MW; 377C3ABB45B042D7 CRC64;

Query Match 66.7%; Score 2; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 7 DK 8

RESULT 28  
 O78225 PRELIMINARY; PRT; 9 AA.  
 AC O78225;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Lymphocyte antigen (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CRO435; TISSUE=Kidney;  
 RX MEDLINE=88084418; PubMed=3622165;  
 RA Golubic M., Budimir O., Schoepfer R., Kasahara M., Mayer W.E.,  
 RA Figueroa F., Klein J.;  
 RT "Nucleotide sequence analysis of class II genes borne by mouse t  
 RT chromosomes.";  
 RL Genet. Res. 50:137-146(1987).  
 DR EMBL; L38589; AAA57293.1; -;  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1143 MW; 9E681772C729C33A CRC64;

Query Match 66.7%; Score 2; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 2 DK 3

RESULT 29  
 O78226 PRELIMINARY; PRT; 9 AA.  
 AC O78226;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Lymphocyte antigen (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CRO437; TISSUE=Kidney;  
 RX MEDLINE=88084418; PubMed=3622165;  
 RA Golubic M., Budimir O., Schoepfer R., Kasahara M., Mayer W.E.,  
 RA Figueroa F., Klein J.;  
 RT "Nucleotide sequence analysis of class II genes borne by mouse t  
 RT chromosomes.";  
 RL Genet. Res. 50:137-146(1987).

DR EMBL; I28590; AAA57294.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1176 MW; 86CB1412C729C33A CRC64;

Query Match 66.7%; Score 2; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 DB 2 DK 3

RESULT 30  
 Q84333 PRELIMINARY; PRT; 9 AA.  
 AC Q84333;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE (Defective variant in 1449) with monkey alu-type insert (Fragment).  
 DE Simian virus 40 (SV40).  
 OS Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OC NCBI\_TaxID=10633;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81054804; PubMed=6254029;  
 RA Dhruva B.R., Shenk T., Subramanian K.N.;  
 RT "Integration in vivo into Simian virus 40 DNA of a sequence that resembles a certain family of genomic interspersed repeated sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:4514-4518(1980).  
 DR EMBL; K01001; AAA47875.1; -.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1133 MW; 802204044732C33A CRC64;

Query Match 66.7%; Score 2; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 DB 2 DK 3

RESULT 31  
 Q91LX6 PRELIMINARY; PRT; 9 AA.  
 AC Q91LX6;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE ORF 10-like protein (Fragment).  
 OS Macaca nemestrina rhadinovirus 2.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.  
 OC NCBI\_TaxID=123630;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mne442N;  
 RX MEDLINE=20240083; PubMed=10775636;  
 RA Schultz E.R., Rankin G.W. Jr., Blanc M.P., Raden B.W., Tsai C.C., Rose T.M.;  
 RT "Characterization of two divergent lineages of macaque rhadinoviruses related to Kaposi's sarcoma-associated herpesvirus."  
 RL J. Virol. 74:4919-4928(2000).  
 DR EMBL; AF204167; AAF81665.1; -.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1003 MW; 41EBD5B7233AB2C7 CRC64;

Query Match 66.7%; Score 2; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 DB 4 DK 5

RESULT 32  
 Q8JJ12 PRELIMINARY; PRT; 9 AA.  
 AC Q8JJ12;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Alpha globin (Fragment).  
 GN ALPHA GLOBIN.  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.  
 OC NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Vidal G.A., D'Surney S., Scheffler B.;  
 RT "Biomolecular and polygenetic comparison of the a globin and b globin flanking sequences of zebrafish and some of it Cyprinidae relatives."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF496558; AAM21654.1; -.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1009 MW; 971A3AB1AAB5B735 CRC64;

Query Match 66.7%; Score 2; DB 13; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 DB 7 DK 8

RESULT 33  
 Q8JJ18 PRELIMINARY; PRT; 9 AA.  
 AC Q8JJ18;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Alpha globin (Fragment).  
 GN ALPHA GLOBIN.  
 OS Danio aequipinnatus (Giant danio) (Brachydanio aequipinnatus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 OC NCBI\_TaxID=46778;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Vidal G.A., D'Surney S., Scheffler B.;  
 RT "Biomolecular and polygenetic comparison of the a globin and b globin flanking sequences of zebrafish and some of it Cyprinidae relatives."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF496555; AAM21648.1; -.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 976 MW; 9DEA3ABAEAB5B735 CRC64;

Query Match 66.7%; Score 2; DB 13; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 DB 7 DK 8

```
RESULT 34
Q8J14
ID Q8J14 PRELIMINARY; PRT; 9 AA.
AC Q8J14;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alpha globin (Fragment).
GN ALPHA GLOBIN.
OS Danio frankelii (Leopard danio) (Brachydanio rerio frankelii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=27702;
RN [1]
RP SEQUENCE FROM N.A.
RA Vidal G.A., D'Surney S., Scheffler B.;
RT "Biomolecular and phylogenetic comparison of the a globin and b globin
RT flanking sequences of zebrafish and some of it Cyprinidae relatives.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF496557; AAM21652.1; -
FT NON_TER 9
FT SEQUENCE 9 AA; 967 MW; 9DEA3AB1AAB5B735 CRC64;
SQ

Query Match 66.7%; Score 2; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
Db |||
7 DK 8

RESULT 35
Q8J10
ID Q8J10 PRELIMINARY; PRT; 9 AA.
AC Q8J10;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alpha globin (Fragment).
GN ALPHA GLOBIN.
OS Notropis chrysolaemus (Golden shiner).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Notropis.
OX NCBI_TaxID=42065;
RN [1]
RP SEQUENCE FROM N.A.
RA Vidal G.A., D'Surney S., Scheffler B.;
RT "Biomolecular and phylogenetic comparison of the a globin and b globin
RT flanking sequences of zebrafish and some of it Cyprinidae relatives.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF496559; AAM21656.1; -
FT NON_TER 9
FT SEQUENCE 9 AA; 967 MW; 9DEA3AB1AAB5B735 CRC64;
SQ

Query Match 66.7%; Score 2; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
Db |||
7 DK 8

RESULT 36
Q8J16
ID Q8J16 PRELIMINARY; PRT; 9 AA.
AC Q8J16;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
```

```
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alpha globin (Fragment).
GN ALPHA GLOBIN.
OS Danio albolineatus (pearl danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=27699;
RN [1]
RP SEQUENCE FROM N.A.
RA Vidal G.A., D'Surney S., Scheffler B.;
RT "Biomolecular and phylogenetic comparison of the a globin and b globin
RT flanking sequences of zebrafish and some of it Cyprinidae relatives.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF496556; AAM21650.1; -
FT NON_TER 9
FT SEQUENCE 9 AA; 967 MW; 9DEA3AB1AAB5B735 CRC64;
SQ

Query Match 66.7%; Score 2; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
Db |||
7 DK 8

RESULT 37
Q9UW5
ID Q9UW5 PRELIMINARY; PRT; 10 AA.
AC Q9UW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ribosomal protein L4 (Fragment).
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE.
RX MEDLINE=92042057; PubMed=1939187;
RA Casiano C., Traut R.R.;
RT "Protein topography of Sulfolobus solfataricus ribosomes by cross-
RT linking with 2-iminothiolane. Sso L12e, Sso L10e, and Sso L11e ate
RT neighbors.";
RL J. Biol. Chem. 266:21578-21583(1991).
FT NON_TER 10
FT SEQUENCE 10 AA; 1134 MW; C0336E35BAA33AAD CRC64;
SQ

Query Match 66.7%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
Db |||
4 DK 5

RESULT 38
Q50843
ID Q50843 PRELIMINARY; PRT; 10 AA.
AC Q50843;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE RNA polymerase gene 3' flanking region with AT-rich DNA sequence
DE (Fragment).
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=2188;
RN [1]
```

RP SEQUENCE FROM N.A.  
RX MEDLINE=85230552; PubMed=4006907;  
RA Bollschweiler C., Kuehn R., Klein A.;  
RT "Non-repetitive AT-rich sequences are found in intergenic regions of  
RT Methanococcus voltae DNA.";  
RL ENBO J. 4:805-809(1985).  
DR EMBL; X02517; CAA26353.1; -.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1149 MW; 27F22A2772CAA9C8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
DB 8 KE 9

RESULT 39  
Q9F9H5 PRELIMINARY; PRT; 10 AA.  
AC Q9F9H5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Glutamate racemase (Fragment).  
GN GLR.  
OS Helicobacter pylori (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=210;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=India75A;  
RX MEDLINE=20270152; PubMed=10809702;  
RA Kersulyte D., Mukhopadhyay A.K., Velapattino B., Su W.W., Pan Z.J.,  
RA Garcia C., Hernandez V., Valdez Y., Mistry R.S., Gilman R.H., Yuan Y.,  
RA Gao H., Alarcon T., Lopez-Brea M., Balakrish Nair G., Chowdhury A.,  
RA Datta S., Shirai M., Nakazawa T., Ally R., Segal I., Wong B.C.,  
RA Lam S.K., Olfat P.O., Boren T., Engstrand L., Torres O., Schneider R.,  
RA Thomas J.E., Czinn S., Berg D.E.;  
RT "Differences in genotypes of Helicobacter pylori from different human  
RT populations.";  
RL J. Bacteriol. 182:3210-3218(2000).  
DR EMBL; AF190663; AAG18486.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1273 MW; CAD126337B133DC6 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
DB 5 KE 6

RESULT 40  
Q9R5N4 PRELIMINARY; PRT; 10 AA.  
AC Q9R5N4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Neurotoxin type A HN+ 35 kDa subunit (Fragment).  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92143938; PubMed=1781887;

RA Somers E., DasGupta B.R.;  
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or  
RT without hemagglutinating activity: do they share common amino acid  
RT sequences and genes?";  
RL J. Protein Chem. 10:415-425(1991).  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1143 MW; CF3CB4A44735B456 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
DB 8 DK 9

RESULT 41  
Q9R5N6 PRELIMINARY; PRT; 10 AA.  
AC Q9R5N6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Neurotoxin type B HN+ 35 kDa SUBUNIT=BAND 3A (Fragment).  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92143938; PubMed=1781887;  
RA Somers E., DasGupta B.R.;  
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or  
RT without hemagglutinating activity: do they share common amino acid  
RT sequences and genes?";  
RL J. Protein Chem. 10:415-425(1991).  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1169 MW; 00CF7E3AA4472054 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
DB 7 DK 8

RESULT 42  
Q8RSU1 PRELIMINARY; PRT; 10 AA.  
AC Q8RSU1;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Urease alpha subunit (EC 3.5.1.5) (Fragment).  
GN UREA.  
OS Helicobacter pylori (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=210;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1061;  
RA van Vliet A.H.M., Poppelaars S.W., Davies B.J., Stoof J.,  
RA Bereswill S., Kist M., Penn C.W., Kuipers E.J., Kuipers J.G.;  
RT "NikR mediates nickel-responsive transcriptional induction of urease  
RT expression in Helicobacter pylori.";  
RL Infect. Immun. 0:0-0(2002).  
DR EMBL; AY078177; AAL77213.1; -.

KW Hydrolase. 10 10  
 FT NON TER 10 AA; 1202 MW; 57C29E2B132771A7 CRC64;  
 SQ SEQUENCE 10 AA; 1202 MW; 57C29E2B132771A7 CRC64;  
 Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DK 2  
 Db 9 DK 10  
 RESULT 43  
 Q51812 PRELIMINARY; PRT; 10 AA.  
 ID Q51812  
 AC Q51812;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE DNA helicase (Fragment).  
 GN TRAI.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Bacteriia; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=K-12;  
 RC MEDLINE=92009201; PubMed=1916281;  
 RA Cram D.S., Loh S.M., Cheah K.C., Skurray R.A.;  
 RT "Sequence and conservation of genes at the distal end of the transfer  
 region on plasmids F and R6-S.";  
 RL Gene 104:85-90(1991).  
 DR EMBL; M38047; AAA98090.1; -.  
 KW Helicase; Plasmid.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1088 MW; 59A3047731A33B13 CRC64;  
 Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KE 3  
 Db 3 KE 4  
 RESULT 44  
 Q8RT1 PRELIMINARY; PRT; 10 AA.  
 ID Q8RT1  
 AC Q8RT1;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Heat shock protein groES (Fragment).  
 GN GROES.  
 OS Anaplasma phagocytophilum (Ehrlichia phagocytophila).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
 OC Anaplasmataceae; Anaplasma.  
 OX NCBI\_TaxID=948;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RA von Loewenich F.D., Bogdan C.;  
 RT "A case of equine granulocytic ehrlichiosis provides further evidence  
 for the presence of the HGE agent in Germany.";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF482760; AAU88676.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1103 MW; 9792B43DD0505AB5 CRC64;  
 Query Match 66.7%; Score 2; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KE 3  
 Db 1 KE 2  
 RESULT 45  
 P83067 PRELIMINARY; PRT; 10 AA.  
 ID P83067  
 AC P83067;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE 82 kDa protein (Fragment).  
 OS Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1396;  
 [1]  
 RN SEQUENCE AND INDUCTION.  
 RC STRAIN=NCIMB 11796;  
 RA Browne N., Dowds B.C.A.;  
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
 CC -I- INDUCTION: BY SALT STRESS.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1200 MW; 72DBA14B1325AAEB CRC64;  
 Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KE 3  
 Db 6 KE 7  
 RESULT 46  
 P83160 PRELIMINARY; PRT; 10 AA.  
 ID P83160  
 AC P83160;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribulose biphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO  
 small subunit) (Fragment).  
 OS Anabaena sp. (strain 131).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
 OX NCBI\_TaxID=29412;  
 [1]  
 RN SEQUENCE.  
 RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;  
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.  
 CC -I- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-  
 RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC  
 CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF  
 THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH  
 REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME  
 ACTIVE SITE.  
 CC -I- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-  
 PHOSPHO-D-GLYCERATE.  
 CC -I- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-  
 PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.  
 CC -I- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.  
 CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -I- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.  
 KW Photosynthesis; Carbon dioxide fixation; Photorespiration; Lyase;  
 KW Oxidoreductase; Monooxygenase; Calvin cycle.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1322 MW; 8B4E2D0B13276731 CRC64;  
 Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

Db 6 KE 7

#### RESULT 47

Q9UW2 PRELIMINARY; PRT; 10 AA.  
AC Q9UW2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE Bap2(1).  
GN BAP2(1).  
OS Schizophyllum commune (Bracket fungus).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Agaricales; Schizophyllaceae; Schizophyllum.  
OX NCBI\_TaxID=5334;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=12-43;  
RA Siebert-Bartholmei C., Kothe E.;  
RT "Basidiomycete pheromone recognition studied in yeast."  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF102785; AAF03757.1; -.  
SQ SEQUENCE 10 AA; 1076 MW; D7D803AEB1E861B2 CRC64;

Query Match 66.7%; Score 2; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

Db 8 DK 9

#### RESULT 48

Q96QT9 PRELIMINARY; PRT; 10 AA.  
AC Q96QT9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE Protein tyrosine phosphatase 1B (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21326081; PubMed=11116810;  
RA Fukada T., Tonks N.K.;  
RT "The Reciprocal Role of Egr-1 and Sp Family Proteins in Regulation of the PTPIB Promoter in Response to the p210 Bcr-Abl Oncoprotein-tyrosine Kinase."  
RL J. Biol. Chem. 276:25512-25519 (2001).  
DR EMBL; AY029236; AAK31734.1; -.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1314 MW; AC08E219CB133B16 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

Db 5 KE 6

#### RESULT 49

Q9NP06 PRELIMINARY; PRT; 10 AA.  
AC Q9NP06;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE Cystic fibrosis transmembrane conductance regulator (Fragment).  
GN CFTR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92058253; PubMed=1719770;  
RA Schwarz M., Summers C., Heptinstall L., Newton C., Markham A.,  
Super M.;  
RT "A deletion mutation of the cystic fibrosis transmembrane conductance regulator (CFTR) locus: Delta 1507."  
RL Adv. Exp. Med. Biol. 290:393-398 (1991).  
DR EMBL; S64643; AAB20219.2; -.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1107 MW; 58CFCC79C0544B13 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

Db 3 KE 4

#### RESULT 50

Q8WXB5 PRELIMINARY; PRT; 10 AA.  
AC Q8WXB5;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DE EYA2B (Fragment).  
GN EYA2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Fee B.E., Doyle C.A., Cleveland J.L.;  
RT "A novel eyes absent protein is expressed in the human eye."  
RL Gene 0:0-0(2002).  
DR EMBL; AF455148; AAL57875.1; -.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1298 MW; 18021202C69B132B CRC64;

Query Match 66.7%; Score 2; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

Db 4 KE 5

#### RESULT 51

Q9NP07 PRELIMINARY; PRT; 10 AA.  
AC Q9NP07;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE Cystic fibrosis transmembrane conductance regulator (Fragment).  
GN CFTR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Fee B.E., Doyle C.A., Cleveland J.L.;  
RT "A novel eyes absent protein is expressed in the human eye."  
RL Gene 0:0-0(2002).  
DR EMBL; AF455148; AAL57875.1; -.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1298 MW; 18021202C69B132B CRC64;

#### RESULT 49

Q9NP06 PRELIMINARY; PRT; 10 AA.  
AC Q9NP06;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE Cystic fibrosis transmembrane conductance regulator (Fragment).  
GN CFTR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92058253; PubMed=1719770;  
RA Schwarz M., Summers C., Heptinstall L., Newton C., Markham A.,  
Super M.;  
RT "A deletion mutation of the cystic fibrosis transmembrane conductance regulator (CFTR) locus: Delta 1507."  
RL Adv. Exp. Med. Biol. 290:393-398 (1991).  
DR EMBL; S64643; AAB20219.2; -.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1107 MW; 58CFCC79C0544B13 CRC64;

GN CFTR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92058253; PubMed=1719770;  
 RA Schwarz M., Summers C., Hepinstall L., Newton C., Markham A.,  
 RA Super M.;  
 RT "A deletion mutation of the cystic fibrosis transmembrane conductance  
 RT regulator (CFTR) locus: Delta 1507.";  
 RL Adv. Exp. Med. Biol. 290:393-398(1991).  
 DR EMBL; S64640; AAB20220.2; -.  
 KW Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 10  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1073 MW; 58CFCC7050544B13 CRC64;  
 Query Match 66.7%; Score 2; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KE 3  
 Db ||  
 3 KE 4  
 RESULT 52  
 P82136  
 ID P82136 PRELIMINARY; PRT; 10 AA.  
 AC P82136;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Chloroplast 30S ribosomal protein S18 beta (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 ON NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. ALMARO; TISSUE=Leaf;  
 RX MEDLINE=20435797; PubMed=10874039;  
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;  
 RT "The plastid ribosomal proteins. Identification of all the proteins in  
 RT the small subunit of an organelle ribosome (chloroplast).";  
 RL J. Biol. Chem. 37:28455-28465(2000).  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC -1- MISCELLANEOUS: S18 ALPHA AND BETA FORMS DIFFER IN PL. S18 BETA  
 CC FORM IS THE LEAST BASIC FORM.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 KDA.  
 CC -1- SIMILARITY: BELONGS TO THE S18 FAMILY OF RIBOSOMAL PROTEINS.  
 CC InterPro; IPR001648; Ribosomal S18.  
 DR Pfam; PF01084; Ribosomal S18; PARTIAL.  
 DR PROSITE; PS00057; RIBOSOMAL S18; PARTIAL.  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 10  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1250 MW; 403B60D7740325B3 CRC64;  
 Query Match 66.7%; Score 2; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DK 2  
 Db ||  
 2 DK 3

RESULT 53

O70580  
 ID O70580 PRELIMINARY; PRT; 10 AA.  
 AC O70580;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Carbonic anhydrase III (Fragment).  
 GN CAR3 OR CAR5 OR CA3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sowden J., Smith H., Morrison K., Edwards Y.;  
 RT "Sequence comparisons and functional studies of the proximal promoter  
 RT of the carbonic anhydrase 3 (CA3) gene.";  
 RL Gene 214:157-165(1999).  
 DR EMBL; AJ006474; CAA07057.1; -.  
 DR MGD; MGI:88270; Car3.  
 DR MGD; MGI:1351477; Cars.  
 FT NON\_TER 10  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1105 MW; 56F7FE71ADC37B13 CRC64;  
 Query Match 66.7%; Score 2; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KE 3  
 Db ||  
 3 KE 4  
 RESULT 54  
 Q47606  
 ID Q47606 PRELIMINARY; PRT; 11 AA.  
 AC Q47606;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Rease protein (Fragment).  
 GN REASE.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 ON NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91139577; PubMed=1995588;  
 RA Tao T., Bourne J.C., Blumenthal R.M.;  
 RT "A family of regulatory genes associated with type II restriction-  
 RT modification systems.";  
 RL J. Bacteriol. 173:1367-1375(1991).  
 DR EMBL; M63622; AAA24562.1; -.  
 FT NON\_TER 11  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;  
 Query Match 66.7%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KE 3  
 Db ||  
 5 KE 6  
 RESULT 55  
 Q9EUZ3  
 ID Q9EUZ3 PRELIMINARY; PRT; 11 AA.  
 AC Q9EUZ3;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)



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DE Ribosome binding factor A (Fragment).
GN RBFA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IQ490;
RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
RT Mortensen K.K.;
RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
RT 10490.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ132862; CAC20133.1; -
FT NON TER 11
SQ SEQUENCE 11 AA; 1319 MW; 6B234CFE740879CB CRC64;

Query Match 66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 3 KE 4

RESULT 56
Q47345
ID Q47345 PRELIMINARY; PRT; 11 AA.
AC Q47345;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Leader peptide.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Faber F., van Giezen M., Van Gorcom R.F.M., Harder W.;
RT "Identification of two Escherichia coli K12 proteins which are induced
RT in response to pollutant stress.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 2-11 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=85134883; PubMed=6396419;
RA Hudson G.S., Davidson B.E.;
RT "Nucleotide sequence and transcription of the phenylalanine and
RT tyrosine operons of Escherichia coli K12.";
RL J. Mol. Biol. 180:1023-1051(1984).
DR EMBL; Z70523; CAA94435.1; -
SQ SEQUENCE 11 AA; 1402 MW; 87AB199204141775 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 9 DK 10

RESULT 57
Q9UR95
ID Q9UR95 PRELIMINARY; PRT; 11 AA.
AC Q9UR95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

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DE Heat shock protein 60 homolog (Fragment).
OS Pichia angusta (Yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE.
RX MEDLINE=93223840; PubMed=8096822;
RA Evers M.E., Huhse B., Titorenko V.I., Kunau W.H., Hartl F.U.,
RA Harder W., Veenhuis M.;
RT "Affinity purification of molecular chaperones of the yeast Hansenula
RT polymorpha using immobilized denatured alcohol oxidase.";
RL FEBS Lett. 321:32-36(1993).
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 66.7%; Score 2; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 3 KE 4

RESULT 58
Q9H4H5
ID Q9H4H5 PRELIMINARY; PRT; 11 AA.
AC Q9H4H5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE DJ661I20.2 (Novel helicase C-terminal domain and SNF2 N-terminal
DE domains containing protein) (Fragment).
GN DJ620E11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Skuce C.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031669; CAC17164.2; -
FT NON TER 1
FT NON TER 11
SQ SEQUENCE 11 AA; 1420 MW; 5EB2C32A3326D053 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 8 KE 9

RESULT 59
Q9UAR8
ID Q9UAR8 PRELIMINARY; PRT; 11 AA.
AC Q9UAR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sialokinin I preproprotein (Fragment).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rockefeller/Red; TISSUE=Salivary gland;
RX MEDLINE=20099025; PubMed=10620041;
RA Beerntsen B.T., Champagne D.E., Coleman J.L., Campos Y.A., James A.A.;

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RT "Characterization of the Sialokinin I gene encoding the salivary  
 RL vasodilator of the yellow fever mosquito, *Aedes aegypti*.";  
 RT Insect Mol. Biol. 8:459-467(1999).  
 DR EMBL; AF108100; AAD16884.1; -;  
 DR InterPro; IPR002040; Tachykinin.  
 DR POSITE; PS00267; TACHYKININ; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1203 MW; 8BAD77C6B59C33A CRC64;

Query Match 66.7%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 4 DK 5

## RESULT 60

O9TRW5 PRELIMINARY; PRT; 11 AA.  
 ID Q9TRW5  
 AC Q9TRW5; 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE 25 kDa protein P25, peptide F4 (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 ON NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.

RA MEDLINE=91372400; PubMed=1909972;  
 RX Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,  
 RA Shiratsuchi A., Uchida T., Inahori K.;  
 RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a  
 RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";  
 RL FEBS Lett. 289:37-43(1991).  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 66.7%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 1 KE 2

## RESULT 61

P83128 PRELIMINARY; PRT; 11 AA.  
 ID P83128  
 AC P83128; 2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Pregnancy-associated glycoprotein (Fragment).  
 OS Bos indicus (Zebu).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 ON NCBI\_TaxID=9915;  
 RN [1]

RP SEQUENCE, AND GLYCOSYLATION.

RC TISSUE=Placenta;  
 RA Sousa N.M., Remy B., El Amiri B., Figueiredo J.R., Beckers J.F.;  
 RT "Characterization of pregnancy-associated glycoproteins extracted from  
 RT zebu (*Bos indicus*) placentas removed at different gestational  
 RT periods.";  
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.

CC -!- PTM: GLYCOSYLATED.  
 KW Glycoprotein.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1234 MW; CE8EA47EA0586B5D CRC64;

Query Match 66.7%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 1 DK 2

## RESULT 62

Q84189 PRELIMINARY; PRT; 11 AA.  
 ID Q84189  
 AC Q84189; 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Matrix protein.  
 OS Subacute sclerosing panencephalitis virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
 ON NCBI\_TaxID=11230;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Niigata-1;  
 RX MEDLINE=89361379; PubMed=2769235;  
 RA Enami M., Sato T.A., Sugitara A.;  
 RT "Matrix protein of cell-associated subacute sclerosing panencephalitis  
 RT viruses.";  
 RL J. Gen. Virol. 70:2191-2196(1989).  
 DR EMBL; D00493; BAA00379.1; -;  
 SQ SEQUENCE 11 AA; 1293 MW; 1594E803A9CAA1E0 CRC64;

Query Match 66.7%; Score 2; DB 12; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 8 DK 9

## RESULT 63

Q9K7A4 PRELIMINARY; PRT; 11 AA.  
 ID Q9K7A4  
 AC Q9K7A4; 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein BH3464.  
 GN BH3464.  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 ON NCBI\_TaxID=86665;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C-125 / JCM 9153;  
 RX MEDLINE=20512582; PubMed=11058132;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
 RA Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus*  
 RT halodurans and genomic sequence comparison with *Bacillus subtilis*.";  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 DR EMBL; AP001518; BAB07183.1; -;  
 SQ Hypothetical protein; Complete proteome.  
 KW SEQUENCE 11 AA; 1219 MW; 5F7D235CB7272B13 CRC64;

Query Match 66.7%; Score 2; DB 16; Length 11;

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j)
Best Local Similarity 100.0%; Pred. No. 2.8e+04; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 KE 3
DB 4 KE 5

RESULT 64
Q9R5F7
ID Q9R5F7 PRELIMINARY; PRT; 12 AA.
AC Q9R5F7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Urease small subunit (Fragment).
OS Helicobacter pylori.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE.
RX MEDLINE=93084378; PubMed=1452359;
RA Turbett G.R., Hoj P.B., Horne R., Mee B.J.;
RT "Purification and characterization of the urease enzymes of
RT Helicobacter species from humans and animals.";
RL Infect. Immun. 60:5259-5266(1992).
SQ SEQUENCE 12 AA; 1447 MW; 26CD07C29E2B1327 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 6 KE 7

RESULT 67
Q9VLX8
ID Q9VLX8 PRELIMINARY; PRT; 12 AA.
AC Q9VLX8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Lysyl-tRNA synthetase (fragment).
GN LYSS.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT8;
RA Spada S., Pembroke J.T., Wall J.G.;
RT "Cloning and characterisation of the cztB metal cation efflux protein
RT from T. thermophilus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ307316; CAC83721.1; -.
KW Aminoacyl-tRNA synthetase.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1327 MW; 5D2A33E27ECDB13 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 5 KE 6

RESULT 68
Q9L4M9
ID Q9L4M9 PRELIMINARY; PRT; 12 AA.
AC Q9L4M9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Guanosine bipyrophosphate synthetase, putative (fragment).
GN REL.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

Best Local Similarity 100.0%; Pred. No. 2.8e+04; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 KE 3
DB 4 KE 5

RESULT 65
Q93A08
ID Q93A08 PRELIMINARY; PRT; 12 AA.
AC Q93A08;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ResB protein (fragment).
GN RESB.
OS Thiobacillus ferrooxidans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC33020;
RA Levican G., Bruscella P., Guacanano M., Inostroza C., Jedlicki E.,
RA Bonnefoy V., Holmes D.S.;
RT "Characterization of the pet and res operons of Acidithiobacillus
RT ferrooxidans.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ413194; CAC88360.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1405 MW; 886AB7DF1E13240A CRC64;

Query Match 66.7%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+04; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 KE 3
DB 7 KE 8

RESULT 66
Q9R5F5
ID Q9R5F5 PRELIMINARY; PRT; 12 AA.
AC Q9R5F5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Urease small subunit (fragment).
OS Helicobacter felis.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=214;
RN [1]
RP SEQUENCE.
RX MEDLINE=93084378; PubMed=1452359;
RA Turbett G.R., Hoj P.B., Horne R., Mee B.J.;
RT "Purification and characterization of the urease enzymes of
RT Helicobacter species from humans and animals.";
RL Infect. Immun. 60:5259-5266(1992).
SQ SEQUENCE 12 AA; 1429 MW; 26CD1E129E2B1327 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 6 KE 7

```

OC Streptococcus.  
OX NCBI\_TaxID=119602;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20123454; PubMed=10660058;  
RC STRAIN=H46A;  
RA Geyer A., Schmidt K.H.;  
RT "Genetic organisation of the M protein region in human isolates of  
RT group C and G streptococci: two types of multigene regulator-Like  
RT (mgrC) regions.";  
RL Mol. Gen. Genet. 262:965-974 (2000).  
DR EMBL; AJ133440; CAB70616.1; -.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1334 MW; 0A82EC4258A72440 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
DB 3 KE 4

RESULT 69  
P97134 PRELIMINARY; PRT; 12 AA.  
ID P97134;  
AC P97134;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Fixod (Fragment).  
GN Fixod.  
OS Rhizobium leguminosarum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=384;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=VF39;  
RC MEDLINE=97348582; PubMed=9204566;  
RA Schluter A., Patschkowski T., Quandt J., Selinger L.B., Weidner S.,  
RA Kramer M., Zhou L., Hynes M., Priefer U.;  
RT "Functional and regulatory analysis of the two copies of the fixNOQP  
RT operon of Rhizobium leguminosarum strain VF39.";  
RL Mol. Plant Microbe Interact. 10:605-616 (1997).  
DR EMBL; Z80339; CAB02449.1; -.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1398 MW; 5D7CAFC18E833AA7 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
DB 6 DK 7

RESULT 70  
Q9R3B3 PRELIMINARY; PRT; 12 AA.  
ID Q9R3B3;  
AC Q9R3B3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Urease large subunit (Fragment).  
OS Helicobacter felis; and  
OS Helicobacter pylori (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=214, 210;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=93084378; PubMed=1452359;  
RA Turbett G.R., Hoj P.B., Horne R., Mee B.J.;  
RT "Purification and characterization of the urease enzymes of  
RT Helicobacter species from humans and animals.";  
RL Infect. Immun. 60:5259-5266 (1992).  
SQ SEQUENCE 12 AA; 1500 MW; 93F05D2362132415 CRC64;

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
DB 7 KE 8

RESULT 71  
Q9UMR0 PRELIMINARY; PRT; 12 AA.  
ID Q9UMR0;  
AC Q9UMR0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).  
GN FBP2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20237676; PubMed=10773464;  
RA Tillmann H., Stein S., Liehr T., Eschrich K.;  
RT "Structure and chromosomal localization of the human and mouse muscle  
RT fructose-1,6-bisphosphatase genes.";  
RL Gene 247:241-253 (2000).  
DR EMBL; AJ238483; CAB53359.1; -.  
KW Hydrolyase.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1382 MW; 4CEB259E57386403 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
DB 3 KE 4

RESULT 72  
Q96PK0 PRELIMINARY; PRT; 12 AA.  
ID Q96PK0;  
AC Q96PK0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE COPG2 (Fragment).  
GN COPG2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bonora E., Bacchelli E., Levy E.R., Biasi F., Marlow A., Monasco A.P.,  
RA Maestrini E.;  
RT "Mutation screening and imprinting analysis of four candidate genes  
RT for autism in the 7q32 region.";  
RL Mol. Psychiatry 0:0-0 (2001).  
DR EMBL; AF324497; AAL1778.1; -.

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FT NON TER 12 12
SQ SEQUENCE 12 AA; 1498 MW; C344E6689A333AA9 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 6 DK 7

RESULT 73
Q9UMZ8
ID Q9UMZ8 PRELIMINARY; PRT; 12 AA.
AC Q9UMZ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Coagulation factor VIII (Fragment).
GN F8C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Vidal F., Farsac E., Gallardo D.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF168366; AAD50437.1; -
FT NON TER 1 1
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1453 MW; 2CCABC3DB252D6C7 CRC64;

Query Match 66.7%; Score 2; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 11 KE 12

RESULT 74
Q9TWV4
ID Q9TWV4 PRELIMINARY; PRT; 12 AA.
AC Q9TWV4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Light yellow cell peptide (Fragment).
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaeae.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RX MEDLINE=93095719; PubMed=1334202;
RA Hoek R.M., Li K.W., van Minnen J., Geraerts W.P.;
RT "Chemical characterization of a novel peptide from the neuroendocrine
RT light yellow cells of Lymnaea stagnalis.";
RL Brain Res. Mol. Brain Res. 16:71-74(1992).
FT NON TER 1 1
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1385 MW; 44255417732045B3 CRC64;

Query Match 66.7%; Score 2; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 4 DK 5
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RESULT 75
Q9TQW3
ID Q9TQW3 PRELIMINARY; PRT; 12 AA.
AC Q9TQW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Growth-related protein 3 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20028318; PubMed=10556424;
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Cytokine Genes."
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140647; AAF07861.1; -
DR EMBL; AF140644; AAF07858.1; -
DR EMBL; AF140645; AAF07859.1; -
DR EMBL; AF140646; AAF07860.1; -
FT NON TER 1 1
SQ SEQUENCE 12 AA; 1430 MW; 4BA2P7EF2AA05053 CRC64;

Query Match 66.7%; Score 2; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 8 DK 9

Search completed: November 25, 2003, 18:25:32
Job time : 9.27872 sec
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# OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 1.45213 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-11

Perfect score: 3

Sequence: 1 DKE 3

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	100.0	10	1 SYK_CAMUP	Q46464 campylobact
2	3	100.0	20	1 SAMP_PLEPL	P20677 pleuronecte
3	2	66.7	6	1 ASP2_LACSN	P82655 lactobacill
4	2	66.7	7	1 WWA3_ACHFV	P35921 achatina fu
5	2	66.7	8	1 FAR2_MACRS	P83275 macrobrachi
6	2	66.7	9	1 COXE_THUOB	P80975 thunnus obe
7	2	66.7	9	1 FAR3_MACRS	P83276 macrobrachi
8	2	66.7	10	1 FIBB_CERSI	P14537 ceratotheri
9	2	66.7	10	1 ODP2_BOVIN	P11180 bos taurus
10	2	66.7	10	1 TKN1_SCYCA	P08608 scyllorhinu
11	2	66.7	10	1 TKS1_AEDAE	P42634 aedes aegyp
12	2	66.7	10	1 TKS2_AEDAE	P42635 aedes aegyp
13	2	66.7	11	1 MLG_THETS	P41989 theromyzon
14	2	66.7	12	1 FORD_METTM	P80903 methanobact
15	2	66.7	12	1 RS19_CLYEP	Q46490 clover yell
16	2	66.7	12	1 RS19_ELYEP	Q47881 elm yellows
17	2	66.7	12	1 RS19_TORBP	Q56251 tomato big
18	2	66.7	12	1 SOIS_BACSU	P80883 bacillus su
19	2	66.7	13	1 CRIC_BOVIN	P28489 bos taurus
20	2	66.7	13	1 LPAA_PORGI	P81411 porphyromon
21	2	66.7	13	1 PHGR_EUOX	P57793 eubacterium
22	2	66.7	13	1 RPOC_MYCGA	P47716 mycoplasma
23	2	66.7	13	1 YPE2_LALCL	P42021 lactococcus
24	2	66.7	14	1 CAT2_FASHE	P80342 fasciola he
25	2	66.7	14	1 EFTU_CANFA	P54835 canis fami
26	2	66.7	14	1 RS19_CLOPP	Q46228 clover prol
27	2	66.7	14	1 RS19_LOWBP	Q48878 loofah witc
28	2	66.7	14	1 RS19_PRUP	Q44160 prunus arme
29	2	66.7	14	1 TAT_HV1W2	P12509 human immun
30	2	66.7	14	1 TAT_HV1Z8	P12511 human immun
31	2	66.7	15	1 CBPB_PROAT	P19628 protopterus
32	2	66.7	15	1 CKX_WHEAT	P58763 triticum ae
33	2	66.7	15	1 EFLA_MICCR	P81266 microplitis

## ALIGNMENTS

RESULT 1

34	2	66.7	15	1 FIBA_ANAPL	P12801 anas platyr
35	2	66.7	15	1 GR78_HORSE	P16392 equus cabal
36	2	66.7	15	1 MALT_BACTQ	P80072 bacillus th
37	2	66.7	15	1 MK1_PALPR	P80408 palomona pr
38	2	66.7	15	1 MK2A_PALPR	P80409 palomona pr
39	2	66.7	15	1 OBPA_MAMBR	P81285 mamestra br
40	2	66.7	15	1 RS10_BACST	P59683 bacillus st
41	2	66.7	15	1 THL_CLOPA	P81347 clostridium
42	2	66.7	15	1 UC23_MAIZE	P80629 zea mays (m
43	2	66.7	16	1 BAI1_EUBSP	P32371 eubacterium
44	2	66.7	16	1 FIBA_HELME	P14456 meles meles
45	2	66.7	16	1 FIBA_MUSVI	P14458 mustela vis
46	2	66.7	16	1 LE06_BIOGL	P80745 biophalari
47	2	66.7	16	1 MK2B_PALPR	P80410 palomona pr
48	2	66.7	16	1 MK3_PALPR	P80411 palomona pr
49	2	66.7	16	1 MPMX_SOLTU	P80501 solanum tub
50	2	66.7	16	1 ODO2_BOVIN	P11179 bos taurus
51	2	66.7	16	1 ODPB_SOLTU	P81419 solanum tub
52	2	66.7	16	1 PA21_TRIST	P82892 trimeresuru
53	2	66.7	16	1 RL6_VIBPR	Q56715 vibrio prot
54	2	66.7	16	1 TRVP_FELCA	P81071 felis silve
55	2	66.7	17	1 FIBA_PIG	P14460 sus scrofa
56	2	66.7	18	1 CPAX_BOVIN	P22779 bos taurus
57	2	66.7	18	1 D7A1_ACASC	P83402 acanthopagr
58	2	66.7	18	1 FIBA_LAMGL	P14454 lama glama
59	2	66.7	18	1 MLB_SCYCA	P01206 scyllorhinu
60	2	66.7	18	1 PHPT_PSESE	P25271 pseudaletia
61	2	66.7	18	1 RL24_PROVU	P20032 proteus vul
62	2	66.7	19	1 LPGE_ECOLI	P33236 escherichia
63	2	66.7	19	1 NS2_MYCTU	P81136 mycobacteri
64	2	66.7	19	1 RL10_CITFR	P43448 citrobacter
65	2	66.7	19	1 RS19_SPICI	O31159 spiroplasma
66	2	66.7	19	1 SCX6_TITBA	P56610 titus bali
67	2	66.7	19	1 TRPB_KLEAE	P14552 klebsiella
68	2	66.7	19	1 TX3_PHONI	P31010 phonectria
69	2	66.7	20	1 UC31_MAIZE	P80637 zea mays (m
70	2	66.7	20	1 BIP_PHAVU	P80089 phaseolus v
71	2	66.7	20	1 BRA_BASAL	P83186 basella alb
72	2	66.7	20	1 CAT1_FASHE	Q09093 fasciola he
73	2	66.7	20	1 CAT4_FASHE	P80528 fasciola he
74	2	66.7	20	1 CS21_STRTR	P81821 streptococc
75	2	66.7	20	1 EFTU_MYCSY	P81407 mycoplasma
76	2	66.7	20	1 HCY2_PANJA	P82312 panulirus j
77	2	66.7	20	1 HCY6_HOMAM	P82301 homarus ame
78	2	66.7	20	1 HCVA_PANJA	P82310 panulirus j
79	2	66.7	20	1 HCVE_PANJA	P82311 panulirus j
80	2	66.7	20	1 ITRA_ALBUU	P24925 albizzia ju
81	2	66.7	20	1 KORC_METTM	P80906 methanobact
82	2	66.7	20	1 LPTB_BACST	P05658 bacillus st
83	2	66.7	20	1 LPTB_BACSU	P23053 bacillus su
84	2	66.7	20	1 MI17_BOVIN	P35451 bos taurus
85	2	66.7	20	1 PEPT_FUSNP	P81207 fusobacteri
86	2	66.7	20	1 PSAP_MAIZE	P13193 zea mays (m
87	2	66.7	20	1 PSAP_PEA	P20119 pisum sativ
88	2	66.7	20	1 PYRR_PYRAP	P37362 pyrrhocoris
89	2	66.7	20	1 RL10_PROVU	P51411 proteus vul
90	2	66.7	20	1 RT16_BOVIN	P82915 bos taurus
91	2	66.7	20	1 THIO_CANFA	P99505 canis fami
92	2	66.7	20	1 TL14_SFIOI	P82682 spinacia ol
93	2	66.7	20	1 TPX_CLOPA	P81361 clostridium
94	2	66.7	20	1 TRYB_ECOLI	P33789 escherichia
95	2	66.7	20	1 UNQO_EQUAR	P81247 equisetum a
96	2	66.7	20	1 UN05_PINPS	P81674 pinus pinas
97	2	66.7	20	1 YPRE_SERMA	P22581 serratia ma
98	1	33.3	3	1 GRWM_HUMAN	P01157 homo sapien
99	1	33.3	3	1 LUXE_VIBFI	P24272 vibrio fisc
100	1	33.3	4	1 ACHI_ACHFV	P35904 achatina fu

SYK CAMUP STANDARD; PRT; 10 AA.  
 ID Q4646;  
 AC 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine-tRNA ligase) (LysRS) (Fragment).  
 DE (Fragment).  
 GN LYSS.  
 OS Campylobacter upsaliensis.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=28080;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43954;  
 RA MEDLINE=97149302; PubMed=8996110;  
 RX Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;  
 RT "Characterization of Campylobacter upsaliensis fur and its  
 RT localization in a highly conserved region of the Campylobacter  
 RT genome".  
 RL Gene 183:219-224(1996).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate  
 CC + L-lysyl-tRNA(Lys).  
 CC -1- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.  
 CC  
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 CC -----  
 CC EMBL: L77076; BAB41342.1; -  
 DR HMAP; MF\_00252; -; 1.  
 DR InterPro: IPR006195; CRNA\_ligase\_II.  
 DR PROSITE: PS00862; AA\_TRNA\_LIGASE\_II; PARTIAL.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 FT Metal-binding; Magnesium.  
 FT NON\_TER 1 1  
 FT SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;  
 Query Match 100.0%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DKE 3  
 Db 8 DKE 10  
 RESULT 2  
 SAMP\_PLEPL STANDARD; PRT; 20 AA.  
 ID P20677;  
 AC 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Serum amyloid P-component (SAP) (Fragment).  
 DE Pleuronectes platessa (Plaice).  
 OS Pleuronectes platessa (Plaice).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Pleuronectidae; Pleuronectes.  
 OX NCBI\_TaxID=8262;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=82232106; PubMed=7093286;  
 RA Pepys M.B., de Beer F.C., Milstein C.P., March J.F., Feinstein A.,

RA Butress N., Clamp J.R., Taylor J., Bruton C., Fletcher T.C.;  
 RT "C-reactive protein and serum amyloid P component in the plaice  
 RT (Pleuronectes platessa L.), a marine teleost, are homologous with  
 RT their human counterparts";  
 RL Biochim. Biophys. Acta 704:123-133(1982).  
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID  
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
 DR PIR; A05332; A05332.  
 DR InterPro: IPR001759; Pentaxin.  
 DR PROSITE: PS00289; PENTAXIN; PARTIAL.  
 KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.  
 FT DOMAIN 1 >20  
 FT NON\_TER 20 20  
 FT SEQUENCE 20 AA; 2292 MW; B94BB81467BBD75D CRC64;  
 Query Match 100.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DKE 3  
 Db 13 DKE 15  
 RESULT 3  
 ASP2\_LACSN STANDARD; PRT; 6 AA.  
 ID P82655;  
 AC 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Acid shock protein 2 (Fragment).  
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=1625;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=CBI;  
 RX MEDLINE=21322712; PubMed=11429463;  
 RA De Angelis M., Bini L., Pallini V., Coconcelli P.S., Gobetti M.;  
 RT "The acid-stress response in Lactobacillus sanfranciscensis CBI";  
 RL Microbiology 147:1863-1873(2001).  
 CC -1- INDUCTION: Overexpressed in acid environments.  
 FT NON\_TER 6 6  
 FT SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 KE 3  
 Db 2 KE 3  
 RESULT 4  
 WWA3\_ACHF STANDARD; PRT; 7 AA.  
 ID P35921;  
 AC 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Wamide-3.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;



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RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
RT FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 965 MW; 73625B69B132310 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 2 KE 3

RESULT 5
FAR2_MACRS STANDARD; PRT; 8 AA.
AC P83275;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE FMRFamide-like neuropeptide FLP2 (ADKNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eye stalk;
RA Sithigorngul P., Sarathongkum W., Jaidechoey S., Longyant S.,
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -1- MASS SPECTROMETRY: MW=1009.4; METHOD=WALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

Query Match 66.7%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 2 DK 3

RESULT 6
COXE_THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thynnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.

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RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottepeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 66.7%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 1 KE 2

RESULT 7
FAR3_MACRS STANDARD; PRT; 9 AA.
AC P83276;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE FMRFamide-like neuropeptide FLP3 (NYDKNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eye stalk;
RA Sithigorngul P., Sarathongkum W., Jaidechoey S., Longyant S.,
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -1- MASS SPECTROMETRY: MW=1215.4; METHOD=WALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433ABB CRC64;

Query Match 66.7%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 3 DK 4

RESULT 8
FIBB_CERSI STANDARD; PRT; 10 AA.
AC P14537;

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DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
 GN FGB.  
 OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.  
 OX NCBI\_TaxID=9807;  
 RN [1]  
 RP SEQUENCE.  
 RA O'Neill P.B., Doolittle R.F.;  
 RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";  
 RL Syst Zool 22:590-595(1973).  
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 DR InterPro: IPR002181; Fibrinogen C.  
 DR PROSITE: PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.  
 KW Blood coagulation; Plasma. FIBRINOPEPTIDE B.  
 FT PEPTIDE 1 10  
 FT NON TER 1 10  
 SQ SEQUENCE 10 AA; 1097 MW; 9402B2B2CDDDD33A CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DK 2  
 Db 3 DK 4  
 RESULT 9  
 ODP2\_BOVIN STANDARD; PRT; 10 AA.  
 AC P11180;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase  
 DE complex (EC 2.3.1.12) (E2) (Fragment).  
 GN DLAT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=88024154; PubMed=3117054;  
 RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;  
 RT "Primary structure around the lipooate-attachment site on the E2  
 RT component of bovine heart pyruvate dehydrogenase complex.";  
 RL Biochem. J. 245:919-922(1987).  
 CC -1- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall  
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains  
 CC multiple copies of three enzymatic components: pyruvate  
 CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and  
 CC lipoamide dehydrogenase (E3).  
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-  
 CC acetyldihydrolipoamide.  
 CC -1- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL  
 CC COFACTOR.  
 CC -1- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL  
 CC SYMMETRY.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.

CC -1- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.  
 CC -1- SIMILARITY: Contains 2 lipoyl-binding domains.  
 DR InterPro: IPR003016; Lipoyl  
 DR PROSITE: PS00189; LIPOYL; PARTIAL.  
 KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;  
 KW Lipoyl.  
 FT NON TER 1 1  
 FT BINDING 5 5 LIPOYL.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1066 MW; 889BECD1ADD33AB1 CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DK 2  
 Db 4 DK 5  
 RESULT 10  
 TKM1\_SCYCA STANDARD; PRT; 10 AA.  
 ID TKM1\_SCYCA  
 AC P08608;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Scyllorhinin I.  
 DE Scyllorhinin I.  
 OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyllorhinidae; Scyllorhinus.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE.  
 RX TISSUE=Intestine;  
 RC MEDLINE=86192829; PubMed=2422058;  
 RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;  
 RT "Scyllorhinin I and II: two novel tachykinins from dogfish gut.";  
 RL FEBS Lett. 200:111-116(1986).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=93292508; PubMed=7685693;  
 RA Waugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;  
 RT "Primary structures and biological activities of substance-P-related  
 RT peptides from the brain of the dogfish, Scyllorhinus canicula.";  
 RL Eur. J. Biochem. 214:469-474(1993).  
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 CC PIR; A24867; A24867.  
 DR InterPro: IPR002040; Tachykinin.  
 DR PROSITE: PS00267; TACHYKININ\_1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C33AA9 CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DK 2  
 Db 4 DK 5  
 RESULT 11  
 TKS1\_AEDAE STANDARD; PRT; 10 AA.  
 ID TKS1\_AEDAE

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AC P42634;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sialokinin I.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
ON NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RT Champagne D.E., Ribeiro J.M.C.;
RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
RT mosquito Aedes aegypti.";
RT Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC -1- FUNCTION: VASODILATORY PEPTIDE. MAY ACTIVATE MACROPHAGES AT THE
CC SITE OF FEEDING.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A49581; A49581.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1145 MW; 3DCPDE6B59C33AA8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 4 DK 5

RESULT 12
TKS2_AEDAE
ID TKS2_AEDAE STANDARD; PRT; 10 AA.
AC P42635;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sialokinin II.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
ON NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RT Champagne D.E., Ribeiro J.M.C.;
RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
RT mosquito Aedes aegypti.";
RT Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC -1- FUNCTION: VASODILATORY PEPTIDE. MAY ACTIVATE MACROPHAGES AT THE
CC SITE OF FEEDING.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; B49581; B49581.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1146 MW; 3DC77C6B59C33AA8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 4 DK 5

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Db 4 DK 5

RESULT 13
MLG_THETS
ID MLG_THETS STANDARD; PRT; 11 AA.
AC P41989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
ON NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94298944; PubMed=8026574;
RT Salzet M., Watzet C., Bulet P., Malecha J.;
RT "Isolation and structural characterization of a novel peptide related
RT to gamma-melanocyte stimulating hormone from the brain of the leech
RT Theromyzon tessulatum.";
RT FEBS Lett. 348:102-106(1994).
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR PIR; S45698; S45698.
KW Hormone; Amidation.
FT MOD_RES 11 11
FT SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 9 DK 10

RESULT 14
FORD_METTM
ID FORD_METTM STANDARD; PRT; 12 AA.
AC P80903;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyruvate synthase subunit pord (EC 1.2.7.1) (Pyruvate oxidoreductase
DE delta chain) (POR) (Pyruvic-ferredoxin oxidoreductase delta subunit
DE (Fragment)).
GN PORD
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
ON NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RT Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -1- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN.
CC -1- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature
CC of 80 degrees Celsius.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
KW Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT NON_TER 12 12
FT SEQUENCE 12 AA; 1241 MW; 2D54065D1BD1ADD8 CRC64;

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Query Match          66.7%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY      2 KE 3
      ||
DB      9 KE 10

RESULT 15
RS19 CLYPEP
ID   RS19 CLYPEP      STANDARD; PRT; 12 AA.
AC   Q46430;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   30S ribosomal protein S19 (Fragment).
GN   RPSS OR RPS19.
OS   Clover yellow edge phytoplasm.
OC   Bacteria; Firmicutes; Mollicutes; Achaeplastatales;
OC   Achaeplastataceae; Phytoplasma.
OX   NCBI_TaxID=35775;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94350802; PubMed=8071198;
RA   Gunderson D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT   "Phylogeny of mycoplasma-like organisms (phytoplasmatales): a basis for
RT   their classification.";
RL   J. Bacteriol. 176:5244-5254(1994).
CC   -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC   TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
CC   EMBL; L27022; AAA83942.1; -.
DR   HAMAP; MF_00531; 1.
DR   InterPro; IPR002222; Ribosomal S19.
DR   PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW   Ribosomal protein; rRNA-binding.
FT   NON_TER 1
SQ   SEQUENCE 12 AA; 1283 MW; 20C47B9D5833AA8 CRC64;

Query Match          66.7%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY      1 DK 2
      ||
DB      6 DK 7

RESULT 17
RS19 TOBBP
ID   RS19 TOBBP      STANDARD; PRT; 12 AA.
AC   Q56251;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   30S ribosomal protein S19 (Fragment).
GN   RPSS OR RPS19.
OS   Tomato big bud phytoplasm.
OC   Bacteria; Firmicutes; Mollicutes; Achaeplastatales;
OC   Achaeplastataceae; Phytoplasma.
OX   NCBI_TaxID=35770;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94350802; PubMed=8071198;
RA   Gunderson D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT   "Phylogeny of mycoplasma-like organisms (phytoplasmatales): a basis for
RT   their classification.";
RL   J. Bacteriol. 176:5244-5254(1994).
CC   -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC   TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
CC   EMBL; L27004; AAA83952.1; -.
DR   HAMAP; MF_00531; 1.
DR   InterPro; IPR002222; Ribosomal S19.
DR   PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW   Ribosomal protein; rRNA-binding.
FT   NON_TER 1
SQ   SEQUENCE 12 AA; 1409 MW; 4CC478EFC833AA3 CRC64;

Query Match          66.7%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY      1 DK 2
      ||
DB      6 DK 7

RESULT 16
RS19 ELYEP
ID   RS19 ELYEP      STANDARD; PRT; 12 AA.
AC   Q47881;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   30S ribosomal protein S19 (Fragment).
GN   RPSS OR RPS19.
OS   Elm yellows phytoplasm.
OC   Bacteria; Firmicutes; Mollicutes; Achaeplastatales;
OC   Achaeplastataceae; Phytoplasma.
OX   NCBI_TaxID=35774;
RN   [1]

```

SO SEQUENCE 12 AA; 1470 MW; 4CC88BE908333AA3 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2  
||  
Db 6 DK 7

#### RESULT 18

SO15\_BACSU  
ID SO15\_BACSU STANDARD; PRT; 12 AA.  
AC P80863;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Superoxide-inducible protein 5 (SO15) (Fragment).  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=168 / 1858;  
RX MEDLINE=97443988; PubMed=9298659;  
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,  
RT Hecker M.;  
RT "First steps from a two-dimensional protein index towards a response-  
regulation map for Bacillus subtilis.";  
RL Electrophoresis 18:1451-1463(1997).  
CC -1- INDUCTION: By superoxide.  
CC -1- CAUTION: Could not be found in the genome of B. subtilis 168.  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1170 MW; 25718A96B37B1338 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KE 3  
||  
Db 6 KE 7

#### RESULT 19

CRTC\_BOVIN  
ID CRTC\_BOVIN STANDARD; PRT; 13 AA.  
AC P28489;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Calreticulin (CRP5) (Calregulin) (HACBP) (Erp60) (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=91201375; PubMed=2016321;  
RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,  
RA Vance J.E., Opas M., Michalak M.;  
RT "Calreticulin, and not calsequestrin, is the major calcium binding  
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
reticulum.";  
RL J. Biol. Chem. 266:7155-7165(1991).  
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
LOW AFFINITY CALCIUM-BINDING SITES.  
CC -1- SUBUNIT: Monomer (by similarity).  
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

DR PIR; A33208; A33208.  
DR InterPro; IPR001580; Calreticulin.  
DR PROSITE; PS00803; CALRETICULIN\_1; PARTIAL.  
DR PROSITE; PS00804; CALRETICULIN\_2; PARTIAL.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; PARTIAL.  
KW Endoplasmic reticulum; Calcium-binding.  
FT NON TER 13 13  
SQ SEQUENCE 13 AA; 1557 MW; C85DDA6993CA1339 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KE 3  
||  
Db 7 KE 8

#### RESULT 20

LPAA\_PORGI  
ID LPAA\_PORGI STANDARD; PRT; 13 AA.  
AC P81411;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Lipid-A-associated protein (Fragment).  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
OX NCBI\_TaxID=837;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W50;  
RX MEDLINE=99061194; PubMed=9846737;  
RA Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,  
RA Curtis M., Henderson B., Tabona P.;  
RT "A lipid A-associated protein of Porphyromonas gingivalis, derived  
from the haemagglutinating domain of the RI protease gene family, is  
a potent stimulator of interleukin 6 synthesis.";  
RL Microbiology 144:3019-3026(1998).  
CC -1- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID  
CELL. THAT ANCHORS THE LIPOPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE  
CELL.  
FT VARIANT 12 12 G -> F.  
FT NON TER 13 13  
SQ SEQUENCE 13 AA; 1346 MW; 38EA796EAF63AB7 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2  
||  
Db 7 DK 8

#### RESULT 21

PHGR\_EUBOX  
ID PHGR\_EUBOX STANDARD; PRT; 13 AA.  
AC P57793;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Phloroglucinol reductase (EC 1.3.1.57) (Fragment).  
OS Eubacterium oxidoreducens.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae;  
OC Eubacterium.  
OX NCBI\_TaxID=1732;  
RN [1]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC STRAIN=G-41;  
RX MEDLINE=89174692; PubMed=2925649;  
RA Haddock J.D., Ferry J.G.;

RT "Purification and properties of phloroglucinol reductase from  
RT Eubacterium oxidoreducens G-41.";  
RL J. Biol. Chem. 264:4423-4427(1989).  
CC -1- FUNCTION: FUNCTIONS IN THE PATHWAY OF ANAEROBIC DEGRADATION OF  
CC TRIHYDROXYBENZENES BY CATALYZING REDUCTION OF THE AROMATIC NUCLEUS  
CC PRIOR TO RING FISSON.  
CC -1- CATALYTIC ACTIVITY: Dihydrophloroglucinol + NADPH(+) =  
CC phloroglucinol + NADPH.  
CC -1- SUBUNIT: Homodimer.  
CC -1- MISCELLANEOUS: TEMPERATURE AND PH OPTIMA ARE 40 DEGREES CELSIUS  
CC AND 7.8 IN THE FORWARD DIRECTION.  
CC PIR; A32453; A32453.  
CC Aromatic hydrocarbons catabolism; Oxidoreductase; NADP.  
DR KW  
FT NON TER 13 13  
SQ SEQUENCE 13 AA; 1527 MW; 427E2E0833F1CB13 CRC64;  
  
Query Match 66.7%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 KE 3  
||  
DB 6 KE 7  
  
RESULT 22  
RPOC\_MYCGA STANDARD; PRT; 13 AA.  
AC P47716;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase  
DE beta' chain) (RNA polymerase beta' subunit) (Fragment).  
DR KW  
FT NON TER  
GN RPOC.  
OS Mycoplasma gallisepticum.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2096;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A5969Var.B;  
RA Skamrov A.V., Feoktistova E.S., Gol'dman M.A., Feoktistova E.S.,  
RA Bibilashvili R.S.;  
RL Submitted (XX-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS  
CC SUBSTRATES.  
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC (RNA) (N).  
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE  
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1  
CC BETA' CHAIN.  
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.  
CC  
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CC  
CC EMBL; L38402; AAB40952.1; -  
DR KW  
FT NON TER 13 13  
SQ SEQUENCE 13 AA; 1630 MW; 4BEC27C7480D4333 CRC64;  
  
Query Match 66.7%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DK 2  
||  
DB 12 DK 13

Db 2 DK 3  
  
RESULT 23  
YPE2\_LACLC STANDARD; PRT; 13 AA.  
ID YPE2\_LACLC  
AC P42021;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein in PEPT 5' region (ORF2) (Fragment).  
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
DR KW  
FT NON TER  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94245610; PubMed=8188586;  
RA Mierau L., Haandrikman A.J., Velterop O., Tan P.S.T., Leenhouts K.L.,  
RA Konings W.N., Venema G., Kok J.;  
RT "Tripeptidase gene (pept) of Lactococcus lactis: molecular cloning  
RT and nucleotide sequencing of pept and construction of a chromosomal  
RT deletion mutant.";  
RL J. Bacteriol. 176:2854-2861(1994).  
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CC  
CC EMBL; L27596; AAA20625.1; -  
DR KW  
FT NON TER 1  
SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64;  
  
Query Match 66.7%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DK 2  
||  
DB 12 DK 13  
  
RESULT 24  
CAT2\_FASHE STANDARD; PRT; 14 AA.  
ID CAT2\_FASHE  
AC P80342;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cathepsin L2 (EC 3.4.22.15) (Fragment).  
OS Fasciola hepatica (Liver fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
OC Echinostomida; Echinostomata; Fasciolidae; Fasciolidae; Fasciola.  
OX NCBI\_TaxID=6192;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94307282; PubMed=8033913;  
RA Dowd A.J., Smith A.M., McGonigle S., Dalton J.P.;  
RT "Purification and characterisation of a second cathepsin L proteinase  
RT secreted by the parasitic trematode Fasciola hepatica.";  
RL Eur. J. Biochem. 223:91-98(1994).  
CC -1- FUNCTION: THIOL PROTEASE THAT ASSISTS THE PARASITE IN BURROWING  
CC THROUGH THE GUT WALL AND LIVER OF ITS MAMMALIAN HOST.  
CC -1- CATALYTIC ACTIVITY: Specificity close to that of papain. As  
CC compared to cathepsin B, cathepsin L exhibits higher activity  
CC towards protein substrates, but has little activity on Z-Arg-Arg-  
CC NHMeC, and no peptidyl-dipeptidase activity.  
CC -1- SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE  
CC BONDS.  
CC

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CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR PIR; S45655; S45655.
DR MEROPS; C01.033; -.
DR InterPro; IPR000169; SHprot_acsite.
DR PROSITE; PS001139; THIOLESTERASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOLESTERASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOLESTERASE_ASN; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON TER 14
SQ SEQUENCE 14 AA; 1605 MW; 9CAEAB74E9D110A CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 4 DK 5

RESULT 25
EFTU_CANFA STANDARD; PRT; 14 AA.
AC P54835;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor Tu, mitochondrial (EF-Tu) (Fragment).
GN TUFM.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-TU/EF-1A SUBFAMILY.
DR HSC-2DPAGE; P54835; DOG.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFATOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; Mitochondrion; GTP-binding.
FT NON TER 14
SQ SEQUENCE 14 AA; 1600 MW; 8CAF0B6AE7CCDE41 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 11 DK 12

RESULT 26
RS19_CLOPP STANDARD; PRT; 14 AA.
AC Q46228;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19.

OS Clover proliferation phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Achleoplasmatales;
OC Achleoplasmataceae; Phytoplasma.
OX NCBI_TaxID=35776;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=80711198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification.";
RL J. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
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CC
CC EMBL; L27011; AAA83938.1; -.
DR HAMAP; MF_00531; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON TER 1
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 8 DK 9

RESULT 27
RS19_LOWBP STANDARD; PRT; 14 AA.
AC Q48878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19.
OS Lofah witches'-broom phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Achleoplasmatales;
OC Achleoplasmataceae; Phytoplasma.
OX NCBI_TaxID=35773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=80711198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification.";
RL J. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
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CC
CC EMBL; L27027; AAA83944.1; -.

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DR HAMAP: MF 00531; -, 1.
DR InterPro: IPR002222; Ribosomal S19.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 8 DK 9

RESULT 28
RS19 PRUAP
ID RS19 PRUAP STANDARD; PRT; 14 AA.
AC Q44150;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS OR RPS19.
OS Prunus armeniaca phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=36589;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gunderson D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RL J. Bacteriol. 176:5244-5254 (1994).
CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL: L26994; AAA83934.1; -.
DR HAMAP: MF_00531; -, 1.
DR InterPro: IPR002222; Ribosomal S19.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1756 MW; 4CC029EF8FFFE4A3 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 5 DK 6

RESULT 29
TAT_HV1W2
ID TAT_HV1W2 STANDARD; PRT; 14 AA.
AC P12509;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
FT NON_TER 1
SQ SEQUENCE 14 AA; 1756 MW; 4CC029EF8FFFE4A3 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 13 KE 14

RESULT 30
TAT_HV1Z8
ID TAT_HV1Z8 STANDARD; PRT; 14 AA.
AC P12511;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
FT NON_TER 1
SQ SEQUENCE 14 AA; 1467 MW; 37CC737BF6F67AA8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 13 KE 14

TAT.
Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11705;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS."
RL Science 232:1548-1553 (1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
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CC -----
DR EMBL: M12507; AAB12991.1; -.
DR HIV: M12507; TATSMWJ2.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1467 MW; 37CC737BF6F67AA8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 13 KE 14

TAT.
Human immunodeficiency virus type 1 (2-84 isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11681;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=88281278; PubMed=3395517;
RA Yorno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1."
RL AIDS Res. Hum. Retroviruses 4:165-173 (1988).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -1- MISCELLANEOUS: THE 2-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
```



CC ZAIRAN MALE.  
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 CC -----

DR EMBL: J03653; AAA44685.1; --  
 DR HIV: J03653; TAT5JY1.  
 KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
 KW AIDS.  
 FT NON TER 1 1  
 FT SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 DB 13 KE 14

RESULT 31  
 CBPB\_PROAT STANDARD; PRT; 15 AA.  
 AC P1962B;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Carboxypeptidase B (EC 3.4.17.2) (Fragment).  
 OS Protopterus aethiopicus (Marbled lungfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Dipnoi; Lepidosireniiformes; Protopteriidae; Protopterus.  
 OX NCBI\_TaxID=7886;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=73025047; PubMed=5079891;  
 RA Reeck G.R., Neurath H.;  
 RT "Isolation and characterization of pancreatic procarboxypeptidase B  
 RT and carboxypeptidase B of the African lungfish."  
 RL Biochemistry 11:3947-3955(1972)  
 CC -1- CATALYTIC ACTIVITY: Peptidyl-L-lysine(or L-arginine) + H(2)O =  
 CC peptide + L-lysine(or L-arginine).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M14.  
 DR PIR: A26212; A26212.  
 DR MEROPS: M14.003; --  
 DR InterPro: IPR000834; Zn\_carboxypept.  
 DR PROSITE: PS00132; CARBOXYPEPT\_ZN\_1; PARTIAL.  
 DR PROSITE: PS00133; CARBOXYPEPT\_ZN\_2; PARTIAL.  
 KW Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Zymogen.  
 FT PROPEP 1 >15 ACTIVATION PEPTIDE.  
 FT NON TER 15 15  
 FT SEQUENCE 15 AA; 1749 MW; 124C910D937BED65 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 DB 10 DK 11

RESULT 32  
 CKX\_WHEAT STANDARD; PRT; 15 AA.  
 AC P58763;  
 DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Cytokinin oxidase (EC 1.4.3.-) (CKO) (Fragment).  
 OS Triticum aestivum (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC STRAIN=cv. Samantha;  
 RX MEDLINE=21099312; PubMed=11168382;  
 RA Galuszka P., Frebort I., Sebel M., Sauer P., Jacobsen S., Pec P.;  
 RT "Cytokinin oxidase or dehydrogenase? Mechanism of cytokinin  
 RT degradation in cereals."  
 RL Eur. J. Biochem. 268:450-461(2001).  
 CC -1- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-  
 CC substituted adenine derivatives that are plant hormones, where the  
 CC substituent is an isopentenyl group. Substrate preference is 2-(2-  
 CC Hydroxyethylamino)-9-methyl-N(6)-isopentenyladenine >>  
 CC isopentenyladenine > cis-zeatin = isopentenyladenosine = zeatin >>  
 CC zeatin riboside.  
 CC -1- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-enyl)adenine + H(2)O +  
 CC O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).  
 CC -1- COFACTOR: FAD.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Extracellular (By similarity).  
 CC -1- MISCELLANEOUS: Optimal pH is 6.5.  
 CC -1- SIMILARITY: Belongs to the oxygen-dependent FAD-linked  
 CC oxidoreductase family.  
 KW Oxidoreductase; Flavoprotein; FAD.  
 FT UNSURE 1 1  
 FT UNSURE 13 15  
 FT NON TER 15 15  
 FT SEQUENCE 15 AA; 1709 MW; 85B589BDS3FCEDEF CRC64;

QY 1 DK 2  
 ||  
 DB 12 DK 13

RESULT 33

EFIA\_MICCR

ID EFIA\_MICCR STANDARD; PRT; 15 AA.  
 AC P81266;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Elongation factor 1-alpha (EF-1-alpha) (Fragment).  
 OS Microplitis croceipes.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;  
 OC Braconidae; Microgasterinae; Microplitis.  
 OX NCBI\_TaxID=72115;  
 RN [1]

Query Match 66.7%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

DB 12 DK 13

SEQUENCE.  
 RX MEDLINE=99033459; PubMed=9816671;  
 RA Stuart M.K.;  
 RT "An antibody diagnostic for hymenopteran parasitism is specific for a  
 RT homologue of elongation factor-1 alpha."  
 RL Arch. Insect Biochem. Physiol. 39:1-8(1998).  
 CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF  
 CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN  
 CC BIOSYNTHESIS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 CC EF-TU/EF-1A SUBFAMILY.  
 DR InterPro: IPR000795; EF\_GTPbind.  
 DR PROSITE: PS00301; EFACTOR\_GTP; PARTIAL.

KW Elongation factor; Protein biosynthesis; GTP-binding.  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1670 MW; 1EB7DA05B09BJ751 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
DB 2 KE 3

RESULT 34  
FIBA\_ANAPL STANDARD; PRT; 15 AA.  
ID FIBA\_ANAPL  
AC P12801;

DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).  
GN FGA.

OS Anas platyrhynchos (Domestic duck).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
OX NCBI\_TaxID=8839;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=85168193; PubMed=3983613;

RA Min Y., Ping Z., Yasoshi Z.;  
RT "Purification and primary structures of duck fibrinopeptides A and B".  
RL Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).  
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COPACTOR IN PLATELET AGGREGATION.

CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

PIR; JP0101; JP0101.  
KW Blood coagulation; Plasma; Pyrrolidone carboxylic acid.  
FT PEPTIDE 1 15 FIBRINOPEPTIDE A.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1580 MW; D78A51FF88B40373 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
DB 9 KE 10

RESULT 35  
GR78\_HORSE STANDARD; PRT; 15 AA.  
ID GR78\_HORSE  
AC P16392;

DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE 78 kDa Glucose-regulated protein (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP). (Fragment).  
GN HSPA5 OR GRP78.

OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=90147817; PubMed=1689156;  
RA Ohlbas B., Boyd N.D., Luber-Narod J., Reyes V.E., Leeman S.E.;  
RT "Isolation and identification of a polypeptide in the Hsp 70 family that binds substance P.";  
RL Biochem. Biophys. Res. Commun. 166:978-983(1990).  
CC -1- FUNCTION: Probably plays a role in facilitating the assembly of multimeric protein complexes inside the ER.  
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.

CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

DR InterPro; IPR001023; Hsp70.  
DR PROSITE; PS00297; HSP70\_1; PARTIAL.  
DR PROSITE; PS00329; HSP70\_2; PARTIAL.  
DR PROSITE; PS01036; HSP70\_3; PARTIAL.  
KW ATP-binding; Endoplasmic reticulum.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1647 MW; 81119D21D0EC26DB CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
DB 4 DK 5

RESULT 36  
MALT\_BACTQ

ID MALT\_BACTQ STANDARD; PRT; 15 AA.  
AC P80072;

DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Maltase (EC 3.2.1.20) (Alpha-glucosidase I) (Fragment).  
OS Bacillus thermoamyloliquefaciens.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=1425;

RN [1]

RP SEQUENCE.  
RC STRAIN=KP1071 / FERM P8477;

RX MEDLINE=92209510; PubMed=155585;

RA Suzuki Y., Yonezawa K., Hattori M., Takii Y.;  
RT "Assignment of Bacillus thermoamyloliquefaciens KP1071 alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence and in structural parameters calculated from the amino acid composition.";

RL Eur. J. Biochem. 205:249-256(1992).

CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.

CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.

CC PIR; S21240; S21240.

DR Hydrolase; Glycosidase.

FT NON\_TER 15 15

SQ SEQUENCE 15 AA; 1929 MW; 62B4CE501F2D3042 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
DB 7 KE 8

RESULT 37  
MK1\_PALPR

ID MK1\_PALPR STANDARD; PRT; 15 AA.  
AC P80408;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Metanikowin I.  
 OS Palomena prasina (Green shield bug).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 OC Panheteroptera; Pentatomomorpha; Pentatomolidea; Pentatomidae;  
 OC Palomena.  
 OX NCBI\_TaxID=55431;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RX Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
 RA "The inducible antibacterial peptides of the hemipteran insect  
 RT Palomena prasina: identification of a unique family of proline-rich  
 RT peptides and of a novel insect defensin.";  
 RL J. Insect Physiol. 42:81-89(1996).  
 CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE  
 CC BACTERIA.  
 CC -!- INDUCTION: By bacterial infection.  
 KW Antibiotic; Insect immunity.  
 SQ SEQUENCE 15 AA; 1838 MW; 21407B663CE46299 CRC64;  
  
 Query Match 66.7%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 DK 2  
 ||  
 DB 2 DK 3  
  
 RESULT 38  
 MK2A\_PALPR STANDARD; PRT; 15 AA.  
 AC P80409;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Metanikowin IIA.  
 OS Palomena prasina (Green shield bug).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 OC Panheteroptera; Pentatomomorpha; Pentatomolidea; Pentatomidae;  
 OC Palomena.  
 OX NCBI\_TaxID=55431;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RX Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
 RA "The inducible antibacterial peptides of the hemipteran insect  
 RT Palomena prasina: identification of a unique family of proline-rich  
 RT peptides and of a novel insect defensin.";  
 RL J. Insect Physiol. 42:81-89(1996).  
 CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE  
 CC BACTERIA.  
 CC -!- INDUCTION: By bacterial infection.  
 KW Antibiotic; Insect immunity.  
 SQ SEQUENCE 15 AA; 1838 MW; 23835D063B946299 CRC64;  
  
 Query Match 66.7%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 DK 2  
 ||  
 DB 2 DK 3  
  
 RESULT 39  
 OBPA\_MAMBR STANDARD; PRT; 15 AA.  
 AC P81285;  
 DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 38, Last annotation update)  
 DE Antennal odorant-binding protein (AOBP) (Fragment).  
 OS Mamestra brassicae.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
 OC Noctuidae; Hadeninae; Mamestra.  
 OX NCBI\_TaxID=55057;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Antenna;  
 RX MEDLINE=99097262; PubMed=9878563;  
 RA Bohbot J., Sobrio F., Lucas P., Nagnan-Le Meillour P.;  
 RT "Functional characterization of a new class of odorant-binding  
 RT proteins in the moth Mamestra brassicae.";  
 RL Biochem. Biophys. Res. Commun. 253:489-494(1998).  
 CC -!- TISSUE SPECIFICITY: ANTENNA.  
 DR InterPro; IPR005055; A10\_OS-D.  
 DR Pfam; PF03392; OS-D; 1.  
 KW Olfaction; Transport.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1875 MW; 1EE9B36E65A74BAA CRC64;  
  
 Query Match 66.7%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 DK 2  
 ||  
 DB 2 DK 3  
  
 RESULT 40  
 RS10\_BACST STANDARD; PRT; 15 AA.  
 ID RS10\_BACST  
 AC P59683;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE 30S ribosomal protein S10 (BS13) (Fragment).  
 GN RPSJ.  
 OS Bacillus stearothermophilus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.  
 OX NCBI\_TaxID=1422;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=10;  
 RX PubMed=4607606;  
 RA Yaguchi M., Matheson A.T., Visentin L.P.;  
 RT "Procarvotic ribosomal proteins: N-terminal sequence homologies and  
 RT structural correspondence of 30 S ribosomal proteins from Escherichia  
 RT coli and Bacillus stearothermophilus.";  
 RL FEBS Lett. 46:296-300(1974).  
 CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By  
 CC similarity).  
 CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.  
 DR HAMAP; MF 00508; -; 1.  
 DR PROSITE; PS00361; RIBOSOMAL\_S10; PARTIAL.  
 KW Ribosomal protein.  
 FT INIT\_MET 0 0  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1897 MW; 746B2ACEAF9AC031 CRC64;  
  
 Query Match 66.7%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 KE 3  
 ||  
 DB 2 KE 3  
  
 RESULT 41

THL\_CLOPA STANDARD; PRT; 15 AA.

AC P81347; 1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Acetyl-CoA acetyltransferase (EC 2.3.1.9) (Acetoacetyl-CoA thiolase)

DE (CP 13) (Fragment).

GN THL.

OS Clostridium pasteurianum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI\_TaxID=1501;

RN [1]

RP SEQUENCE.

RC STRAIN=W5;

RX MEDLINE=98291870; PubMed=96229918;

RA Flengrud R., Skjeldal L.;

RT "Two-dimensional gel electrophoresis separation and N-terminal

RT sequence analysis of proteins from Clostridium pasteurianum W5. ";

RL Electrophoresis 19:802-806(1998).

CC -1- CATALYTIC ACTIVITY: 2 acetyl-CoA = CoA + acetoacetyl-CoA.

CC -1- PATHWAY: JUNCTION IN THE PATHWAY LEADING TO THE PRODUCTION OF

CC EITHER ACIDS (ACETATE OR BUTYRATE) OR SOLVENTS (ACETONE, BUTANOL

CC OR ETHANOL).

CC -1- SUBUNIT: Homotetramer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: BELONGS TO THE THIOLEASE FAMILY.

DR InterPro; IPR002155; Thiolease.

DR PROSITE; PS00098; THIOLEASE 1; PARTIAL.

DR PROSITE; PS00737; THIOLEASE 2; PARTIAL.

DR PROSITE; PS00099; THIOLEASE 3; PARTIAL.

KW Transferase; Acyltransferase.

FT NON\_TER 15

SQ SEQUENCE 15 AA; 1496 MW; 9735820D61BB35FC CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

DB 2 KE 3

RESULT 42

UC23 MAIZE STANDARD; PRT; 15 AA.

AC P80629;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 502)

DE (Fragment).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI\_TaxID=4577;

RN [1]

RP SEQUENCE.

RC TISSUE=Coleoptile;

RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

RA Pernollet J.-C., Zivy M., de Vienne D.;

RT "The maize two dimensional gel protein database: towards an integrated

RT genome analysis program."

RL Theor. Appl. Genet. 93:997-1005(1996).

CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 6.2, ITS MW IS: 45.0 kDa.

DR Maize-2DPAGE; P80629; COLEOPTILE.

DR MaizeDB; 123955; --

FT NON\_TER 1 1

FT NON\_TER 15 15

SQ SEQUENCE 15 AA; 1557 MW; C974ED33E9A4EC28 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

DB 3 DK 4

RESULT 43

BALI EUBSP STANDARD; PRT; 16 AA.

AC P32371;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bile acid-inducible operon protein I (Fragment).

GN BALI.

OS Eubacterium sp. (strain VPI 12708).

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI\_TaxID=29347;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93259945; PubMed=8491719;

RA Franklund C.V.; Baron S.F.; Hylemon P.B.;

RT "Characterization of the baih gene encoding a bile acid-inducible

RT NADH:flavin oxidoreductase from Eubacterium sp. strain VPI 12708. ";

RL J. Bacteriol. 175:3002-3012(1993).

CC -1- PATHWAY: Bile acid catabolism.

CC -----

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CC -----

CC EMBL; U57489; AAC45418.1; --

DR Bile acid catabolism.

KW NON\_TER 16

SQ SEQUENCE 16 AA; 1721 MW; B9BAAE7B8746B4F4 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 4.9e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

DB 10 DK 11

RESULT 44

FIBA MELME STANDARD; PRT; 16 AA.

AC P14456;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).

GN FGA.

OS Meles meles (Eurasian badger).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;

OC Meles.

OX NCBI\_TaxID=9662;

RN [1]

RP SEQUENCE.

RA Blomback B., Grondahl N.J.;

RT "Studies on fibrinopeptides from mammals. ";

```

RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1708 MW; 09433547919EC7C4 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 4 KE 5

RESULT 45
FIBA_MUSVI STANDARD; PRT; 16 AA.
ID FIBA_MUSVI
AC P144Eg;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain (Contains: Fibrinopeptide A) (Fragment).
GN FGA.
OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1679 MW; 09432A57919ECF66 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 4 KE 5

RESULT 46
LE06_BIOGL STANDARD; PRT; 16 AA.
ID LE06_BIOGL
AC P80745;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Hemolymph 65 kDa lectin BG06 (Fragment).
GN BG06.
OS Blomphalaria glabrata (Bloodfluke planorb).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeoides; Planorbidae; Blomphalaria.
OX NCBI_TaxID=6526;
RN [1]
RP SEQUENCE.
RC STRAIN=M-LINE; TISSUE=Hemolymph;
RX MEDLINE=97385165; PubMed=9238039;
RA Adema C.M., Hertel L.A., Miller R.D., Loker E.S.;
RT "A family of fibrinogen-related proteins that precipitates parasite-
RT derived molecules is produced by an invertebrate after infection.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:8691-8696(1997).
CC -1- FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE
CC ECHINOSTOMA PARAENSEI.
CC -1- SUBCELLULAR LOCATION: SECRETED IN THE HEMOLYMPH.
CC -1- INDUCTION: By infection.
KW Lectin.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1964 MW; A1665754589EF82C CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 6 DK 7

RESULT 47
MK2B_PALPR STANDARD; PRT; 16 AA.
ID MK2B_PALPR
AC P80410;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metalnikowin IIB.
OS Palomona prasina (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomioidea; Pentatomidae;
OC Palomona.
OX NCBI_TaxID=55431;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
RT Palomona prasina: identification of a unique family of proline-rich
RT peptides and of a novel insect defensin.";
RL J. Insect Physiol. 42:81-89(1996).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -1- INDUCTION: By bacterial infection.
KW Antibiotic; Insect immunity.
SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 2 DK 3

RESULT 48
MK3_PALPR STANDARD; PRT; 16 AA.
ID MK3_PALPR
AC P80411;

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DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Metanikowin III.  
 OS Palomena prasina (Green shield bug).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 OC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;  
 OC Palomena.  
 OX NCBI\_TaxID=55431;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
 RT "The inducible antibacterial peptides of the hemipteran insect  
 RT Palomena prasina: identification of a unique family of proline-rich  
 RT peptides and of a novel insect defensin.";  
 RL J. Insect Physiol. 42:81-89(1996).  
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE  
 CC BACTERIA.  
 CC -1- INDUCTION: By bacterial infection.  
 KW Antibiotic; Insect immunity.  
 SQ SEQUENCE 16 AA; 2024 MW; A9B3835D063B9462 CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DK 2  
 DB 2 DK 3  
 RESULT 49  
 MMPX SOLTU  
 ID WMPX SOLTU STANDARD; PRT; 16 AA.  
 AC P80501;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Unidentified mitochondrial matrix protein (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Tuber;  
 RA MEDLINE=9707345; PubMed=8919912;  
 RA Jansch L., Kluft V., Schmitz U.K., Braun H.P.;  
 RT "New insights into the composition, molecular mass and stoichiometry  
 RT of the protein complexes of plant mitochondria.";  
 RL Plant J. 9:357-368(1996).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 KW Mitochondrion.  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1768 MW; C58D4DB48AA18B8D CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KE 3  
 DB 6 KE 7  
 RESULT 50  
 ODO2 BOVIN  
 ID ODO2 BOVIN STANDARD; PRT; 16 AA.  
 AC P11179;  
 DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Dihydrolipoamide succinyltransferase component of 2-oxoglutarate  
 DE dehydrogenase complex (EC 2.3.1.61) (E2) (Fragment).  
 GN DLST.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Kidney;  
 RA MEDLINE=88005143; PubMed=3115829;  
 RA Bradford A.P., Aicken A., Bsg F., Cook K.G., Yeaman S.J.;  
 RT "Amino acid sequence surrounding the lipioic acid cofactor of bovine  
 RT kidney 2-oxoglutarate dehydrogenase complex.";  
 RL FEBS Lett. 222:211-214(1987).  
 CC -1- FUNCTION: The 2-oxoglutarate dehydrogenase complex catalyzes the  
 CC overall conversion of 2-oxoglutarate to succinyl-CoA and CO(2). It  
 CC contains multiple copies of 3 enzymatic components: 2-oxoglutarate  
 CC dehydrogenase (E1), dihydrolipoamide succinyltransferase (E2) and  
 CC lipoamide dehydrogenase (E3).  
 CC -1- CATALYTIC ACTIVITY: Succinyl-CoA + dihydrolipoamide = CoA + S-  
 CC succinyl-dihydrolipoamide.  
 CC COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL  
 CC COFACTOR. Tricarboxylic acid cycle.  
 CC -1- PATHWAY: Tricarboxylic acid cycle.  
 CC -1- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL  
 CC SYMMETRY.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.  
 CC -1- SIMILARITY: Contains 1 lipoyl-binding domain.  
 CC PIR; S00123; S00123.  
 DR InterPro; IPR003016; Lipoyl.  
 DR PROSITE; PS00189; LIPOYL; PARTIAL.  
 KW Tricarboxylic acid cycle; Transferase; Acyltransferase; Lipoyl;  
 KW Mitochondrion.  
 FT NON\_TER 1 1  
 FT BINDING 5 5 LIPOYL.  
 FT NON\_TER 16 16  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1643 MW; E34CD29B86B3239D CRC64;  
 Query Match 66.7%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DK 2  
 DB 4 DK 5  
 RESULT 51  
 ODPB SOLTU  
 ID ODPB SOLTU STANDARD; PRT; 16 AA.  
 AC P81419;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial  
 DE (EC 1.2.4.1) (PDHE1-B) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Romano; TISSUE=Tuber;  
 RX MEDLINE=98399821; PubMed=9729464;  
 RA Millar A.H., Knorr C., Leaver C.J., Hill S.A.;  
 RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and  
 RT identification of catalytic components in potato.";

RL Biochem. J. 334:571-576(1998).  
 CC -1- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall  
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains  
 CC multiple copies of three enzymatic components: pyruvate  
 CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and  
 CC lipoamide dehydrogenase (E3).  
 CC -1- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-  
 CC acetyldihydrolipoamide + CO(2).  
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.  
 CC -1- SUBUNIT: Tetramer of two alpha and two beta subunits (by  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;  
 KW Phosphorylation; Mitochondrion.  
 FT NON TER 16 16  
 SQ SEQUENCE 16 AA; 1705 MW; FF6ED80EC804F797 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 5 KE 6

RESULT 52  
 ID PA21 TRIST STANDARD; PRT; 16 AA.  
 AC P2892;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phospholipase A2, basic 1 (EC 3.1.1.4) (PA2-I) (PLA2-I)  
 DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).  
 OS Trimeresurus stejnegeri (Chinese green tree viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Trimeresurus.  
 OX NCBI\_TaxID=39682;  
 [1]  
 RN SEQUENCE.

RA Li S.Y., Wang W.Y., Xiong Y.L.;  
 RC "Isolation, sequence and characterization of five variants of  
 RT phospholipase A2 from venom of snake Trimeresurus stejnegeri.";  
 RL Submitted (DEC-2000) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
 CC acyl groups in 3-sn-phosphoglycerides.  
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 CC acylglycerophosphocholine + a fatty acid anion.  
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II  
 CC SUBFAMILY.  
 DR InterPro: IPR001211; PhospholipaseA2.  
 DR PROSITE: PS00119; PA2 ASP; PARTIAL.  
 DR PROSITE: PS00118; PA2\_HIS; PARTIAL.  
 KW Hydrolase; Lipid degradation; Calcium; Multigene family.  
 FT NON TER 16 16  
 SQ SEQUENCE 16 AA; 2012 MW; 4EF2D4959E981117 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 15 KE 16

RESULT 53  
 RL6\_VIBPR

ID RL6\_VIBPR STANDARD; PRT; 16 AA.  
 AC Q56715;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE 50S ribosomal protein L6 (Fragment).  
 GN RELF.  
 OS Vibrio proteolyticus (Aeromonas proteolytica).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=671;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=ATCC 15338;  
 RC MEDLINE=97149305; PubMed=8996113;  
 RA Satterquist R.A., Smith G.K., Oakley T.H., Lee Y.H., Fox G.E.;  
 RT "Sequence, overproduction and purification of Vibrio proteolyticus  
 RT ribosomal protein L18 for in vitro and in vivo studies.";  
 RL Gene 183:237-242(1996).  
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS  
 CC LOCATED AT THE AMINOACYL-TRNA BINDING SITE OF THE  
 CC PEPTIDYLTRANSFERASE CENTER (BY SIMILARITY)  
 CC -1- SIMILARITY: BELONGS TO THE L6P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL: U38943; AAB41328.1;  
 DR InterPro: IPR002358; Ribosomal\_L6\_1.  
 DR PROSITE: PS00525; RIBOSOMAL\_L6\_1; PARTIAL.  
 KW Ribosomal protein; rRNA-binding.  
 FT NON TER 1 1  
 SQ SEQUENCE 16 AA; 1935 MW; ABC19078DF581B6C CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 11 KE 12

RESULT 54  
 ID TRYP\_FELCA STANDARD; PRT; 16 AA.  
 AC P81071;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Trypsin precursor (EC 3.4.21.4) (Fragment).  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 [1]  
 RN SEQUENCE.  
 RP TISSUE=Pancreas;  
 RC MEDLINE=97235546; PubMed=9080665;  
 RA Steiner J.M., Medinger T.L., Williams D.A.;  
 RT "Purification and partial characterization of feline trypsin.";  
 RL Comp. Biochem. Physiol. 116B:87-93(1997).  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg|-Xaa, Lys|-Xaa.  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR PROSITE: P850240; TRYPSIN\_DOM; PARTIAL.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; PARTIAL.

```

DR PROSITE; PS00135; TRYPSIN SER; PARTIAL.
KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.
FT PROPER 1 8 ACTIVATION PEPTIDE.
FT CHAIN 9 >16 TRYPSIN.
FT NON_TER 16 16
SQ SEQUENCE -16 AA; 1825 MW; A6D751BB58760A86 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.9e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 1 DK 2
DB 7 DK 8

RESULT 55
FIBA_PIG STANDARD; PRT; 17 AA.
AC P14460;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN - [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COPOLYMER IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; E29501; E29501.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1762 MW; 232EFEBB8B6B0A0C CRC64;

Query Match 66.7%; Score 2; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 1 DK 2
DB 5 DK 6

RESULT 56
CPAX_BOVIN STANDARD; PRT; 18 AA.
AC P22779;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cytochrome P450 2A (Olf2) (Olfactive) (P52) (EC 1.14.14.1) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN - [1]
RP SEQUENCE.

```

```

RX MEDLINE=91027757; PubMed=2121272;
RA Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;
RT "Identification and biochemical analysis of novel olfactory-specific
RT cytochrome P-450IIA and UDP-glucuronosyl transferase.";
RL Biochemistry 29:7433-7440(1990).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR PIR; A35704; A35704.
DR InterPro; IPR001128; Cytochrome P450.
DR PROSITE; PS00086; CYTOCHROME_P450; PARTIAL.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum; Olfaction.
FT NON_TER 1 1
FT VARIANT 6 6 G -> D.
FT VARIANT 11 11 A -> E.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2058 MW; F80746F76CCD77FF CRC64;

Query Match 66.7%; Score 2; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 KE 3
DB 13 KE 14

RESULT 57
D7A1_ACASC STANDARD; PRT; 18 AA.
AC P83402;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1)
DE (Fragment).
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI_TaxID=72011;
RN [1]
RP SEQUENCE, ACTIVITY, COFACTOR, AND SUBUNIT.
RC TISSUE=Liver;
RX MEDLINE=21956475; PubMed=11959129;
RA Tang W.-K., Cheng C.H.K., Fong W.-P.;
RT "First purification of the antiquitin protein and demonstration of its
RT enzymatic activity.";
RL FEBS Lett. 516:183-186(2002).
CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid +
CC NADH.
CC -1- SUBUNIT: Homotetramer.
CC -1- MISCELLANEOUS: Optimal pH is 9-10. The Km for acetaldehyde is
CC 2.0 mM and Vmax is 1.3 micromol/min x mg enzyme.
CC -1- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
DR GO; GO:0004029; F:aldehyde dehydrogenase (NAD+) activity; IDA.
DR GO; GO:0006081; P:aldehyde metabolism; IDA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; PARTIAL.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; PARTIAL.
KW Oxidoreductase; NAD.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2059 MW; BFF8C3EF1A9B4047 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 18;

```



Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
Db 14 KE 15

## RESULT 58

FIBA\_LAMGL  
ID FIBA\_LAMGL STANDARD; PRT; 18 AA.  
AC P14454;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).  
GN FGA.  
OS Lama glama (Llama), and  
OS Lama vicugna (Vicugna) (Vicugna vicugna).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.  
OX NCBI\_TaxID=9844, 9843;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=L.vicugna;  
RA Blomback B., Blomback M., Grondahl N.J.;  
RT "Studies on fibrinopeptides from mammals."  
RL Acta Chem. Scand. 19:1789-1791(1965).  
RN [2]  
RP SEQUENCE.

RA Moss G.A., Doolittle R.F.;  
RC "Amino acid sequence studies on artiodactyl fibrinopeptides."  
RT Arch. Biochem. Biophys. 122:674-684(1967)  
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

KW Blood coagulation; Plasma.  
FT PEPTIDE 1 18 FIBRINOPEPTIDE A.  
FT NON TER 18  
SQ SEQUENCE 18 AA; 1834 MW; 2444487B8B7F4CC6 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 6 DK 7

## RESULT 59

MLB\_SCYCA  
ID MLB\_SCYCA STANDARD; PRT; 18 AA.  
AC P01206;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Melanotropin beta (beta-MSH).  
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidei; Carcharhiniformes;  
OC Scyllorhinidae; Scyllorhinus.  
OX NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE.

RA MEDLINE=75113445; PubMed=4452470;

RA Love R.M., Pickering B.T.;  
RT "A beta-MSH in the pituitary gland of the spotted dogfish  
RT (Scyllorhinus canicula): isolation and structure."  
RL Gen. Comp. Endocrinol. 24:398-404(1974).  
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.  
DR PIR; A01470; MTDIBC.  
KW Hormone.

SQ SEQUENCE 18 AA; 2195 MW; 353C93A30C314DF4 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 17 DK 18

## RESULT 60

PHPT\_PSESE  
ID PHPT\_PSESE STANDARD; PRT; 18 AA.  
AC P25271;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-MAY-1992 (Rel. 22, Last annotation update)  
DE Pheromonotropin (PSS-PT).  
OS Pseudaletia separata (Armyworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Hadeninae; Pseudaletia.  
OX NCBI\_TaxID=7105;  
RN [1]  
RP SEQUENCE.

RT TISSUE=Head;  
RX MEDLINE=92134266; PubMed=1734867;  
RA Matsumoto S., Fonagy A., Kurihara M., Uchiumi K., Nagamine T.,  
RA Chijimatsu M., Mitsui T.;  
RT "Isolation and primary structure of a novel pheromonotropic  
RT neuropeptide structurally related to leucopyrokinin from the armyworm  
RT larvae, Pseudaletia separata."  
RL Biochem. Biophys. Res. Commun. 182:534-539(1992).  
CC -1- FUNCTION: HORMONE THAT CONTROLS SEX PHEROMONE PRODUCTION IN  
CC LARVAE.

CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR PIR; JS0647; JS0647.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Hormone; Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 18 18 AMIDATION.  
SQ SEQUENCE 18 AA; 2200 MW; DDF3A1B75ACB18FF CRC64;

Query Match 66.7%; Score 2; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 6 DK 7

## RESULT 61

RL24\_PROVU  
ID RL24\_PROVU STANDARD; PRT; 18 AA.  
AC P20032;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE 50S ribosomal protein L24 (Fragment).  
GN RPLX.  
OS Proteus vulgaris.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Proteus.  
OX NCBI\_TaxID=585;

```

RN  SEQUENCE FROM N.A.
RP  MEDLINE=99125589; PubMed=2464692;
RX  Carretti D.P., Mattheakis L.C., Kearney K.R., Vu L., Nomura M.;
RA  "Translational regulation of the spc operon in Escherichia coli.
RT  Identification and structural analysis of the target site for S8
RT  repressor protein.";
RL  J. Mol. Biol. 204:309-329(1998).
CC  -1- FUNCTION: THIS PROTEIN IS FOUND IN THE RIBONUCLEOPROTEIN CORE AND
CC  IS INVOLVED IN THE EARLY ASSEMBLY OF THE 50S SUBUNIT. IT IS NOT
CC  INVOLVED IN THE FUNCTIONS OF THE MATURE 50S SUBUNIT.
CC  -1- SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.
CC  -----
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CC  -----
DR  EMBL; M36264; AAA25661.1; -.
DR  InterPro; IPR005825; Ribosomal_L24_26.
DR  PROSITE; PS01108; RIBOSOMAL_L24; PARTIAL.
KW  Ribosomal protein.
FT  NON_TER 1
FT  SEQUENCE 18 AA; 2202 MW; 43606F53C5CBA57C CRC64;
SQ  SEQUENCE 18 AA; 2202 MW; 43606F53C5CBA57C CRC64;

Query Match 66.7%; Score 2; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 14 KE 15

RESULT 62
LPGE_ECOLI
ID LPGE_ECOLI STANDARD; PRT; 19 AA.
AC P33236;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gef leader peptide.
DE GEFL OR B0018.
GN Escherichia coli.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92048481; PubMed=1943701;
RA Poulsen L.K., Refn A., Molin S., Andersson P.;
RT "The gef gene from Escherichia coli is regulated at the level of
RT translation.";
RL Mol. Microbiol. 5:1639-1648(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1233-1238(1997).
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CC -----
DR  EMBL; AS000112; AAC73129.1; ALT_TERM.
DR  EcoGene; EGI2074; gefL.
KW  Leader peptide; Complete proteome.
SQ  SEQUENCE 19 AA; 2259 MW; 19B3EDF371EB0BEB CRC64;

Query Match 66.7%; Score 2; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 15 KE 16

RESULT 63
NS2_MYCTU
ID NS2_MYCTU STANDARD; PRT; 19 AA.
AC P81136;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 2 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -1- SIMILARITY: STRONG, TO THE N-TERMINALS OF C.ELEGANS F20A1.4
CC AND H.INFLUENZAE HI0967.
CC -1- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON_TER 19
FT SEQUENCE 19 AA; 2211 MW; A8C1854BF1FF1F70 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2
DB 8 DK 9

RESULT 64
RL10_CITFR
ID RL10_CITFR STANDARD; PRT; 19 AA.
AC P43448;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S05 ribosomal protein L10 (Fragment).
GN RPLJ.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhyvoloup A.N.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----

DR EMBL: X74448; CAA52459.1; --  
DR PIR: S35970; S35970.  
DR HAMAP: MF\_00362; --; 1.  
DR InterPro: IPR002363; Ribosomal\_L10eub.  
DR PROSITE: PS01109; RIBOSOMAL\_L10; PARTIAL.  
KW Ribosomal protein.  
FT INIT\_MET 0 0 BY SIMILARITY.  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2026 MW; E20A02CD7851DB16 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DK 2  
||  
Db 6 DK 7

RESULT 65  
RS19 SPIC1 STANDARD; PRT; 19 AA.  
AC Q31159;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 30S ribosomal protein S19 (Fragment).  
GN RPSS.  
OS Spiroplasma citri.  
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;  
OC Spiroplasmataceae; Spiroplasma.  
OX NCBI\_TaxID=2133;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 27556 / RBA2;  
RX MEDLINE=98406077; PubMed=9733727;  
RA Le Dantec L., Castroviejo M., Bove J.M., Saillard C.;  
RT "Purification, cloning, and preliminary characterization of a  
RT Spiroplasma citri ribosomal protein with DNA binding capacity.";  
RL J. Biol. Chem. 273:24379-24386(1998).  
CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY  
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
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CC -----

DR EMBL: AF031160; AAC35868.1; --  
DR HAMAP: MF\_00531; --; 1.  
DR InterPro: IPR002222; Ribosomal\_S19.  
DR Pfam: PF00203; Ribosomal\_S19; 1.  
DR PROSITE: PS00323; RIBOSOMAL\_S19; PARTIAL.  
KW Ribosomal protein.  
FT NON\_TER 1 1  
SQ SEQUENCE 19 AA; 2190 MW; 517818B405DA70E9 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DK 2  
||  
Db 14 DK 15

## RESULT 66

SCX6 TITBA STANDARD; PRT; 19 AA.  
AC P56610;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Toxin TBTX-VI (Fragment).  
OS Tityus bahiensis (Brazilian scorpion).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;  
OC Buthoidea; Buthidae; Tityus.  
OX NCBI\_TaxID=50343;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=96190713; PubMed=8611151;  
RA Becerril B., Corona M., Coronas F.I., Zamudio F.,  
RA Calderon-Aranda E.S., Fletcher P.L. Jr., Martin B.M., Possani L.D.;  
RT "Toxic peptides and genes encoding toxin gamma of the Brazilian  
RT scorpions Tityus bahiensis and Tityus stigmurus.";  
RL Biochem. J. 313:753-760(1996).  
CC -!- FUNCTION: Not toxic to mice.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.  
CC ALPHA-TOXIN SUBFAMILY.  
CC PIR: S62864; S62864.  
DR InterPro: IPR002061; Scorpion\_toxinL.  
DR Pfam: PF00537; toxin\_3; 1.  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2151 MW; 3535A2F1E5E67D14 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KE 3  
||  
Db 2 KE 3

## RESULT 67

TRPB KLEAE STANDARD; PRT; 19 AA.  
AC P14552;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tryptophan synthase beta chain (EC 4.2.1.20) (Fragment).  
GN TRPB.  
OS Klebsiella aerogenes.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=28451;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81199002; PubMed=6262736;  
RA Nichols B.P., Blumenberg M., Yanofsky C.;  
RT "Comparison of the nucleoside sequence of trpA and sequences  
RT immediately beyond the trp operon of Klebsiella aerogenes. Salmonella  
RT typhimurium and Escherichia coli".  
RL Nucleic Acids Res. 9:1743-1755(1981).  
CC -!- FUNCTION: The beta subunit is responsible for the synthesis of L-  
CC tryptophan from indole and L-serine.  
CC -!- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)glycerol 3-phosphate  
CC = L-tryptophan + glyceraldehyde 3-phosphate.  
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).  
CC -!- PATHWAY: Tryptophan biosynthesis; fifth (last) step.  
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By  
CC similarity).  
CC -!- SIMILARITY: BELONGS TO THE TRPB FAMILY.

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CC use by non-profit institutions as long as its content is in no way  
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DR EMBL; V00630; CAA23901.1; -;  
DR EMBL; J01738; AAA25144.1; -;  
DR HSSP; P00933; 2TYS;  
DR HAMAP; MF\_00133; 1;  
DR InterPro; IPR006653; Trp\_synth\_b\_rel.  
DR PROSITE; PS00168; TRP\_SYNTHASE\_BETA; PARTIAL.  
KW Tryptophan biosynthesis; Pyridoxal phosphate; Lyase.  
FT NON\_TER 1  
SQ SEQUENCE 19 AA; 2183 MW; 82864627BF574E2C CRC64;

Query Match 66.7%; Score 2; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
DB 3 DK 4

RESULT 68  
TX3\_PHONI STANDARD; PRT; 19 AA.  
AC P31010;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neurotoxin Tx3 (Fragment).  
OS Phoneutria nigriventer (Brazilian armed spider).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.  
OX NCBI\_TaxID=6918;  
RN 1;  
RP SEQUENCE  
RC TISSUE=Venom;  
RX MEDLINE=92196803; PubMed=1801316;  
RA Rezende L. Jr., Cordeiro M.N., Oliveira E.B., Diniz C.R.;  
RT "Isolation of neurotoxic peptides from the venom of the 'armed'  
RT spider Phoneutria nigriventer.";  
RL Toxicon 29:1225-1233(1991).  
CC -1- FUNCTION: ANTAGONIST OF L-TYPE CALCIUM CHANNELS (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -1- SIMILARITY: BELONGS TO THE SPIDER TOXIN TX3 FAMILY.  
DR PTR; C39305; C39305.  
KW Calcium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor.  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2244 MW; 3214E89CF10F7587 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
DB 18 KE 19

RESULT 69  
UC31\_MAIZE STANDARD; PRT; 19 AA.  
AC P80637;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT\* 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 67)  
DE (Fragments).  
DE Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN 1;  
RP SEQUENCE  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
RT genome analysis program.";  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.8, ITS MW IS: 41.7 kDa.  
CC -1- CAUTION: THE ORDER OF THE PEPTIDES SHOWN IS UNCERTAIN.  
DR Maize-2DPAGE; P80637; COLEOPTILE.  
FT NON\_TER 1  
FT NON\_CONS 10 11  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2439 MW; DFB2ASC15E50E5F5 CRC64;

Query Match 66.7%; Score 2; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
DB 9 DK 10

RESULT 70  
BIP\_PHAVU STANDARD; PRT; 20 AA.  
AC P80089;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Luminal binding protein (78 kDa glucose-regulated protein homolog)  
DE (GRP 78) (Fragment).  
OS Phaseolus vulgaris (Kidney bean) (French bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
OX NCBI\_TaxID=3885;  
RN 1;  
RP SEQUENCE  
RC STRAIN=cv. Greensleeves; TISSUE=Cotyledon;  
RX MEDLINE=94221084; PubMed=1344885;  
RA D'Amico L., Valasaina B., Damiani M.G., Fabbri M.S., Nitti G.,  
RA Bollini R., Ceriotti A., Vitale A.;  
RT "Bean homologs of the mammalian glucose-regulated proteins: induction  
RT by tunicamycin and interaction with newly synthesized seed storage  
RT proteins in the endoplasmic reticulum.";  
RL Plant J. 2:443-455(1992).  
CC -1- FUNCTION: PROBABLY PLAYS A ROLE IN FACILITATING THE ASSEMBLY OF  
CC MULTIMERIC PROTEIN COMPLEXES INSIDE THE ER.  
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -1- INDUCTION: By tunicamycin.  
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
DR InterPro; IPR001023; Hsp70.  
DR PROSITE; PS00297; HSP70\_1; PARTIAL.  
DR PROSITE; PS00329; HSP70\_2; PARTIAL.  
DR PROSITE; PS01036; HSP70\_3; PARTIAL.  
KW ATP-binding; Endoplasmic reticulum.  
FT UNSURE 4 4 OR T.  
FT UNSURE 18 18 OR T.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2147 MW; 809D43AF21A21476 CRC64;

Query\_Match 66.7%; Score 2; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 1 KE 2

RESULT 71  
 BRA\_BASAL STANDARD; PRT; 20 AA.  
 AC P83186;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-basurbrin (Fragment).  
 OS Basella alba (Malabar spinach) (Ceylon spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Basellaceae; Basella.  
 OX NCBI\_TaxID=3589;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Seed;  
 RX MEDLINE=21547763; PubMed=11688973;  
 RA Wang H., Ng T.B.;  
 RT "Novel antifungal peptides from ceylon spinach seeds.";  
 RL Biochem. Biophys. Res. Commun. 288:765-770(2001).  
 CC -!- FUNCTION: Possesses antifungal activity against B.cinerea,  
 CC M.arachidicola and F.oxysporum but not C.comatus and R.solani.  
 CC Inhibits HIV-1 reverse transcriptase and cell-free translation.  
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.  
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IDA.  
 KW Fungicide.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2354 MW; D9B40A0B85CD0973 CRC64;

Query\_Match 66.7%; Score 2; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 9 KE 10

RESULT 72  
 CAT1\_FASHE STANDARD; PRT; 20 AA.  
 AC Q09093;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cathepsin L1 (EC 3.4.22.15) (Fragment).  
 OS Fasciola hepatica (Liver fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
 OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.  
 OX NCBI\_TaxID=6192;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94158959; PubMed=8114809;  
 RA Smith A.M., Dowd A.J., McGonigle S., Brennan G.,  
 RA Trudgett A., Dalton J.P.;  
 RT "Purification of a cathepsin L-like proteinase secreted by adult  
 RT Fasciola hepatica.";  
 RL Mol. Biochem. Parasitol. 62:1-8(1993).  
 CC -!- FUNCTION: THIOL PROTEASE THAT ASSISTS THE PARASITE IN BURROWING  
 CC THROUGH THE GUT WALL AND LIVER OF ITS MAMMALIAN HOST.  
 CC -!- CATALYTIC ACTIVITY: Specificity close to that of papain. As  
 CC compared to cathepsin B, cathepsin L exhibits higher activity  
 CC towards protein substrates, but has little activity on Z-Arg-Arg-  
 CC NHMeC, and no peptidyl-dipeptidase activity.

CC -!- SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE  
 CC BONDS.  
 CC -!- SUBCELLULAR LOCATION: Lysosomal.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 CC PIR; S68785; S68785.  
 DR MEROPS; C01.033; -;  
 DR InterPro; IPR000668; Peptidase\_C1.  
 DR InterPro; IPR000169; SHprot\_acsite.  
 DR Pfam; PF00112; Peptidase\_C1\_1.  
 DR PROSITE; PS00139; THIOL\_PROTEASE\_CYS; PARTIAL.  
 DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; PARTIAL.  
 DR PROSITE; PS00640; THIOL\_PROTEASE\_ASN; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2174 MW; 97CDEDB33055BCAE CRC64;

Query\_Match 66.7%; Score 2; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 4 DK 5

RESULT 73  
 CAT4\_FASHE STANDARD; PRT; 20 AA.  
 ID CAT4\_FASHE  
 AC P80528;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cathepsin L-like cysteine proteinase (EC 3.4.22.-) (Newly excysted  
 DE juvenile protein 4) (Fragment).  
 OS Fasciola hepatica (Liver fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
 OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.  
 OX NCBI\_TaxID=6192;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95366993; PubMed=7639732;  
 RA Tkalcovic J., Ashman K., Meusen E.;  
 RT "Fasciola hepatica: rapid identification of newly excysted juvenile  
 RT proteins.";  
 RL Biochem. Biophys. Res. Commun. 213:169-174(1995).  
 CC -!- FUNCTION: THIOL PROTEASE.  
 CC -!- SUBCELLULAR LOCATION: Lysosomal (Potential).  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT THE NEWLY EXCYSTED JUVENILE  
 CC STAGE.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 DR MEROPS; C01.033; -;  
 DR InterPro; IPR000169; SHprot\_acsite.  
 DR PROSITE; PS00139; THIOL\_PROTEASE\_CYS; PARTIAL.  
 DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; PARTIAL.  
 DR PROSITE; PS00640; THIOL\_PROTEASE\_ASN; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2515 MW; D6F75BCA63C91FD6 CRC64;

Query\_Match 66.7%; Score 2; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 15 KE 16

RESULT 74  
 CS21\_STRTR STANDARD; PRT; 20 AA.  
 ID CS21\_STRTR  
 AC P81621;  
 DT 15-JUL-1999 (Rel. 38, Created)

Job time : 2.45213 secs

DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 21 kDa cold-shock induced protein (Fragment).  
OS Streptococcus thermophilus.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OX NCBI\_TaxID=1308;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=PB18;  
RX MEDLINE=99456673; PubMed=10525839;  
RA Perrin C., Guimont C., Bracqurt P., Gaillard J.L.;  
RT "Expression of a new cold shock protein of 21.5 kDa and of the major  
RT cold shock protein by Streptococcus thermophilus after cold shock.";  
RL Curr. Microbiol. 39:342-347(1999).  
CC -!- INDUCTION: By cold shock.  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2390 MW; 9C2CA57F266B80AD CRC64;  
  
Query Match 66.7%; Score 2; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 KE 3  
Db 5 KE 6  
  
RESULT 75  
EFTU MYCSY  
ID EFTU MYCSY STANDARD; PRT; 20 AA.  
AC P81407;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Elongation factor Tu (EF-Tu) (Fragment).  
GN TUF.  
OS Mycoplasma synoviae.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2109;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=ULB 925 / Isolate KF9;  
RX MEDLINE=99237234; PubMed=10220885;  
RA Bencina D., Narat M., Dovc P., Drobnic-valic M., Habe F., Kleven S.H.;  
RT "The characterization of Mycoplasma synoviae EF-Tu protein and  
RT proteins involved in hemadherence and their N-terminal amino acid  
RT sequences.";  
RL FEMS Microbiol. Lett. 173:85-94(1999).  
CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF  
CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN  
CC BIOSYNTHESIS.  
CC -!- SUBUNIT: Monomer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
CC EF-TU/EF-1A SUBFAMILY.  
DR HAMAP; MF\_00118; -; 1.  
DR InterPro; IPR000795; EF\_GTPbind.  
DR PROSITE; PS00301; EFACFOTR GTP; PARTIAL.  
KW Elongation factor; Protein biosynthesis; GTP-binding.  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2222 MW; C3C92564B740ACC6 CRC64;  
  
Query Match 66.7%; Score 2; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 KE 3  
Db 9 KE 10

Search completed: November 25, 2003, 18:17:31

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 2.76064 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-11

Perfect score: 3

Sequence: 1 DXE 3

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	100.0	15	I49407	placental calcium-
2	3	100.0	18	B48408	21K high mobility
3	3	100.0	19	A48408	21K high mobility
4	3	100.0	20	A05332	serum amyloid P-co
5	2	66.7	5	PQ0689	photosystem I 10.4
6	2	66.7	5	PT0660	T-cell receptor be
7	2	66.7	6	A61419	sarcosine dehydrog
8	2	66.7	6	S78764	ribosomal protein
9	2	66.7	6	PT0511	T-cell receptor be
10	2	66.7	6	S29881	Na+/K+-exchanging
11	2	66.7	7	S52774	triacylglycerol li
12	2	66.7	7	PS0254	18K protein 5507 -
13	2	66.7	7	S33244	neuromodulatory pe
14	2	66.7	7	PT0520	T-cell receptor be
15	2	66.7	8	A21440	variant surface gl
16	2	66.7	8	A61328	trypsin (EC 3.4.21
17	2	66.7	8	PT0653	T-cell receptor be
18	2	66.7	8	A61597	cytochrome P450 AL
19	2	66.7	9	JQ1202	leader peptide - p
20	2	66.7	9	S77984	cytochrome-c oxida
21	2	66.7	9	PH0321	T-cell receptor be
22	2	66.7	9	I57650	hemoglobin alpha c
23	2	66.7	10	S33844	alpha-2-macroglobu
24	2	66.7	10	A49581	sialokinin I - yel
25	2	66.7	10	B49581	sialokinin II - ye
26	2	66.7	10	A24867	scyllorhinin I - s
27	2	66.7	10	A24407	amicyanin - Paraco
28	2	66.7	10	F44644	neurotoxin-associ
29	2	66.7	10	S62880	polygalacturonase

30	2	66.7	10	2	H61308	hemocyanin subunit
31	2	66.7	10	2	PH0946	T-cell receptor be
32	2	66.7	10	2	PC4374	telomeric and tetr
33	2	66.7	10	2	PQ0785	NADH2 dehydrogenas
34	2	66.7	11	2	PQ0682	photosystem I 17.5
35	2	66.7	11	2	JQ0395	hypothetical prote
36	2	66.7	11	2	B39853	luxC protein - Pho
37	2	66.7	11	2	PT0081	protein QA300023 -
38	2	66.7	11	2	S45698	gamma-MSH-like pro
39	2	66.7	11	2	S23373	T-cell receptor al
40	2	66.7	11	2	PH1376	T antigen variant
41	2	66.7	11	2	H84082	hypothetical prote
42	2	66.7	12	2	C49215	urease (EC 3.5.1.5
43	2	66.7	12	2	G49410	t-complex polypept
44	2	66.7	12	2	S01222	translation elonga
45	2	66.7	12	2	A58501	24K kidney and bla
46	2	66.7	12	2	G49215	urease (EC 3.5.1.5
47	2	66.7	12	2	E64573	hypothetical prote
48	2	66.7	12	2	A60757	enterotoxin C-1 -
49	2	66.7	12	2	PA0047	protein QA100045 -
50	2	66.7	12	2	S18722	matk protein - bee
51	2	66.7	12	2	A56878	light yellow cell
52	2	66.7	12	2	C61308	hemocyanin chain 6
53	2	66.7	12	2	S47360	T-cell antigen rec
54	2	66.7	12	2	C49033	T-cell receptor de
55	2	66.7	12	2	S68402	NAD(+)-glycohydrol
56	2	66.7	13	2	S39413	tubulin beta chain
57	2	66.7	13	2	A33208	calreticulin, hepa
58	2	66.7	13	2	E39778	lactose phosphotra
59	2	66.7	13	2	A59387	VCAM-1 5'UTR bindi
60	2	66.7	13	2	A61288	spore proteinase g
61	2	66.7	13	2	G44644	neurotoxin-associ
62	2	66.7	13	2	A32453	phloroglucinol red
63	2	66.7	13	2	PC4055	hypothetical 13 pr
64	2	66.7	13	2	PA0023	protein QA300052 -
65	2	66.7	13	2	S28425	20K protein - rape
66	2	66.7	13	2	JQ2309	hypothetical 1.6K
67	2	66.7	13	2	JQ2319	hypothetical 1.6K
68	2	66.7	13	2	PN0168	phosphopyruvate hy
69	2	66.7	13	2	S03879	6-phosphofructokin
70	2	66.7	13	2	A86126	hypothetical prote
71	2	66.7	14	2	PC2373	probable IMP dehyd
72	2	66.7	14	2	I54945	gene C protein - E
73	2	66.7	14	2	S60353	amylopolulanase -
74	2	66.7	14	2	PN0147	omega-gliadine 1 a
75	2	66.7	14	2	PN0151	omega-gliadine 2,
76	2	66.7	14	2	S45655	cathepsin L (EC 3.
77	2	66.7	14	2	PC1215	homeotic protein E
78	2	66.7	14	2	A61308	hemocyanin chain 2
79	2	66.7	14	2	B61308	hemocyanin chain 4
80	2	66.7	14	2	D61308	hemocyanin chain 5
81	2	66.7	14	2	S00150	ovostatin - duck (
82	2	66.7	14	2	PH1763	T cell receptor al
83	2	66.7	14	2	D35141	T-cell receptor de
84	2	66.7	14	2	C35141	T-cell receptor de
85	2	66.7	14	2	E35141	T-cell receptor de
86	2	66.7	14	2	F49037	Tcr delta chain V-
87	2	66.7	14	2	PC7079	unidentified 27.2K
88	2	66.7	14	2	PC4376	telomeric and tetr
89	2	66.7	14	2	PC4382	dehydrin 4.5K poly
90	2	66.7	14	2	B83836	hypothetical prote
91	2	66.7	14	2	F31160	H+-transporting tw
92	2	66.7	14	2	S21747	glutamate dehydrog
93	2	66.7	15	2	S21241	oligo-1,6-glucosid
94	2	66.7	15	2	S21240	alpha-glucosidase
95	2	66.7	15	2	S21202	glucan 1,4-alpha-g
96	2	66.7	15	2	S36888	ribosomal protein
97	2	66.7	15	2	I46512	troponin - rabbit
98	2	66.7	15	2	B33208	calreticulin, uter
99	2	66.7	15	2	JP0101	fibrinogen alpha c
100	2	66.7	15	2	S65717	prostaglandin D-sy

## ALIGNMENTS

## RESULT 1

I49407  
 placental calcium-binding protein - western wild mouse (fragment)  
 C;Species: Mus spretus (western wild mouse)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 29-Sep-1999  
 C;Accession: I49407  
 R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.  
 Mamm. Genome 5, 349-355, 1994  
 A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
 A;Reference number: I48334; MUID:94319082; PMID:8043949  
 A;Accession: I49407  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-15 <RES>  
 A;Cross-references: EMBL:U05696; NID:G497016; PIDN:AAA61936.1; PID:G497017  
 C;Superfamily: S-100 protein; calmodulin repeat homology  
 C;Keywords: calcium binding; EF hand

Query Match 100.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 DB 9 DKE 11

## RESULT 2

B48408  
 21K high mobility group protein, hepatic (isoform 2) - Atlantic salmon (fragment)  
 C;Species: Salmo salar (Atlantic salmon)  
 C;Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 07-Feb-1997  
 C;Accession: B48408  
 R;Waters, S.; Khamis, M.; Von Der Decken, A.  
 Cell. Mol. Biol. 38, 783-789, 1992  
 A;Title: Purification of the Atlantic salmon hepatic 21 kDa protein and classification  
 A;Reference number: A48408  
 A;Accession: B48408  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-18 <WAT>  
 C;Keywords: liver

Query Match 100.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 DB 10 DKE 12

## RESULT 3

A48408  
 21K high mobility group protein, hepatic (isoform 1) - Atlantic salmon (fragment)  
 C;Species: Salmo salar (Atlantic salmon)  
 C;Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 07-Feb-1997  
 C;Accession: A48408  
 R;Waters, S.; Khamis, M.; Von Der Decken, A.  
 Cell. Mol. Biol. 38, 783-789, 1992  
 A;Title: Purification of the Atlantic salmon hepatic 21 kDa protein and classification  
 A;Reference number: A48408  
 A;Accession: A48408  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-19 <WAT>  
 C;Keywords: liver

Query Match 100.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DKE 3  
 |||  
 DB 11 DKE 13

## RESULT 4

A05332  
 serum amyloid P-component - plaice (fragment)  
 N;Alternate names: SAP  
 C;Species: Pleuronectes platessa (plaice)  
 C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 22-Apr-1995  
 C;Accession: A05332  
 R;Pepps, M.B.; de Beer, F.C.; Milstein, C.P.; March, J.F.; Feinstein, A.; Butress, N.;  
 Biochim. Biophys. Acta 704, 123-133, 1982  
 A;Reference number: A90642; MUID:82232106; PMID:7093286  
 A;Contents: tentative sequence  
 A;Accession: A05332  
 A;Molecule type: protein  
 A;Residues: 1-20 <PEP>  
 C;Superfamily: C-reactive protein  
 C;Keywords: amyloid; glycoprotein; pentraxin; plasma

Query Match 100.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DKE 3  
 |||  
 DB 13 DKE 15

## RESULT 5

PQ0689.  
 photosystem I 10.4K H1 chain - common tobacco (fragment)  
 C;Species: Nicotiana tabacum (common tobacco)  
 C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
 C;Accession: PQ0689  
 R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiyura, M.  
 Plant Physiol. 102, 1259-1267, 1993  
 A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are  
 A;Reference number: PQ0667; MUID:94105345; PMID:8278548  
 A;Accession: PQ0689  
 A;Molecule type: protein  
 A;Residues: 1-5 <OSO>  
 C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 66.7%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 |||  
 DB 4 DK 5

## RESULT 6

PT0660  
 T-cell receptor beta chain V-D-J region (121-181) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PT0660  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0660  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-5 <FEE>  
 A;Experimental source: day 4 postnatal thymus, strain BAUB/c  
 C;Keywords: T-cell receptor



Query Match 66.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 4 DK 5

## RESULT 7

A61419  
sarcosine dehydrogenase (EC 1.5.99.1) - Pseudomonas sp. (strain WRF) (fragment)  
C;Species: Pseudomonas sp.  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
C;Accession: A61419  
R;Pinto, J.T.; Frisell, W.R., 483-491, 1975  
Arch. Biochem. Biophys. 169,  
A;Title: Characterization of the peptide-bound flavin of a bacterial sarcosine dehydrogenase  
A;Reference number: A61419; MUID:76038634; PMID:241294  
A;Accession: A61419  
A;Molecule type: protein  
A;Residues: 1-6 <PIN>  
C;Keywords: FAD; flavoprotein; oxidoreductase; phosphoprotein  
F;6/Modified site: 3'-FAD-histidine (His) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 1 DK 2

## RESULT 8

S78764  
ribosomal protein MRP-S23, mitochondrial - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: S78764  
R;Graack, H.R.

submitted to the Protein Sequence Database, July 1999

A;Reference number: S78760  
A;Accession: S78764  
A;Molecule type: protein  
A;Residues: 1-6 <GRA>  
C;Keywords: mitochondrial  
F;1-6/Product: ribosomal protein MRP-S23 (fragment) #status experimental <MAT>

Query Match 66.7%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 4 DK 5

## RESULT 9

PT0511  
T-cell receptor beta chain V-D-J region (100-4A) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0511  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0511

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FEE>

A;Experimental source: adult thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 66.7%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 4 DK 5

## RESULT 10

S29881  
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)  
C;Species: Canis lupus familiaris (dog)  
C;Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 19-Apr-2002  
C;Accession: S29881  
R;Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.  
J. Biol. Chem. 260, 3852-3859, 1985  
A;Title: Structural relatedness of three ion-transport adenosine triphosphatases around  
A;Reference number: S29881; MUID:85131201; PMID:3156136  
A;Accession: S29881  
A;Molecule type: protein  
A;Residues: 1-6 <WAL>  
A;Experimental source: kidney  
C;Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;  
F;4/Active site: Asp (aspartylphosphate intermediate) #status Predicted

Query Match 66.7%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 4 DK 5

## RESULT 11

S57274  
triacylglycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)  
C;Species: Psychrobacter immobilis  
C;Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 03-Nov-1995  
C;Accession: S57274  
R;Arpigny, J.L.; Feller, G.; Gerday, C.  
Biochim. Biophys. Acta 1263, 103, 1995  
A;Title: Corrigendum to "Cloning, sequence and structural features of a lipase from the  
A;Reference number: S57274; MUID:95359197; PMID:7632728  
A;Accession: S57274  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-7 <ARP>  
A;Cross-references: EMBL:X67712  
C;Keywords: carboxylic ester hydrolase

Query Match 66.7%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 3 DK 4

## RESULT 12

PS0254  
18K protein 5507 - rice (strain Nihonbare) (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Mar-1995  
C;Accession: PS0254  
R;Tsugita, A.  
submitted to JPIID, April 1993  
A;Reference number: PS0206

A;Accession: PS0254  
 A;Molecule type: protein  
 A;Residues: 1-7 <TSU>  
 A;Experimental source: leaf, chloroplast, strain Nihonbare  
 A;Note: molecular weight 18k, pI 4.4

Query Match 66.7%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KE 3  
 ||  
 Db 5 KE 6

## RESULT 13

S33244  
 neuromodulatory peptide Wamide-1 - giant African snail  
 C;Species: Achatina fulica (giant African snail)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
 C;Accession: S33244  
 R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.  
 FEBS Lett. 323, 104-108, 1993  
 A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of b  
 A;Reference number: S33244; MUID:93265912; PMID:8495720  
 A;Accession: S33244  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-7 <MIN>

Query Match 66.7%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KE 3  
 ||  
 Db 2 KE 3

## RESULT 14

PT0520  
 T-cell receptor beta chain V-D-J region (100-4F) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PT0520  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0520  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-7 <PEE>  
 A;Experimental source: adult thymus, strain BALB/c  
 C;Keywords: T-cell receptor

Query Match 66.7%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2  
 ||  
 Db 4 DK 5

## RESULT 15

A21440  
 variant surface glycoprotein pSLc1 - Trypanosoma brucei (fragment)  
 C;Species: Trypanosoma brucei  
 C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Mar-1998  
 C;Accession: A21440  
 R;Parsons, M.; Nelson, R.G.; Watkins, K.P.; Agabian, N.  
 Cell 38, 309-316, 1984

A;Title: Trypanosome mRNAs share a common 5' spliced leader sequence.  
 A;Reference number: A90853; MUID:84282716; PMID:6088073  
 A;Accession: A21440  
 A;Molecule type: mRNA  
 A;Residues: 1-8 <PAR>  
 A;Cross-references: GB:K02195; NID:gl62150; PID:gl62151  
 C;Keywords: glycoprotein

Query Match 66.7%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KE 3  
 ||  
 Db 4 KE 5

## RESULT 16

A61328  
 trypsin (EC 3.4.21.4) precursor - minke whale (fragment)  
 C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)  
 C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
 C;Accession: A61328  
 R;Brictoux-Gregoire, S.; Schyns, R.; Florkin, M.; Emmens, M.; Welling, G.W.; Beintema,  
 Biochim. Biophys. Acta 386, 244-255, 1975  
 A;Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaen  
 creas.

A;Reference number: A61328; MUID:75146765; PMID:1125273  
 A;Accession: A61328  
 A;Molecule type: protein  
 A;Residues: 1-8 <BRI>  
 C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen  
 F;1-8/Domain: activation peptide #status experimental <APT>

Query Match 66.7%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2  
 ||  
 Db 7 DK 8

## RESULT 17

PT0653  
 T-cell receptor beta chain V-D-J region (121-3H) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PT0653  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0653  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-8 <PEE>  
 A;Experimental source: day 4 postnatal thymus, strain BALB/c  
 C;Keywords: T-cell receptor

Query Match 66.7%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2  
 ||  
 Db 4 DK 5

## RESULT 18

A61597  
 cytochrome P450 AL-1 - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

R;Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.

Drug Metab. Dispos. 19, 291-297, 1991

A;Title: Purification and aminopyrine monooxygenase activity of liver microsomal cytochrome P-450

A;Reference number: A61597

A;Accession: A61597

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <SHI>

Query Match 66.7%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

DB 6 KE 7

RESULT 19

leader peptide - Pseudomonas sp. plasmid R1033 transposon Tn1696

C;Species: Pseudomonas sp.

C;Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 12-Dec-1997

C;Accession: JQ1202

R;Stokes, H.W.; Hall, R.M.

Plasmid 26, 10-19, 1991

A;Title: Sequence analysis of the inducible chloramphenicol resistance determinant in the plasmid R1033

A;Reference number: JQ1201; MUID:92052679; PMID:1658833

A;Accession: JQ1202

A;Molecule type: DNA

A;Residues: 1-9 <STO>

A;Cross-references: GB:M60454

C;Comment: This peptide is a potential translational attenuation signal for cmlA gene.

C;Genetics:

A;Genome: plasmid

C;Superfamily: unassigned leader peptides

Query Match 66.7%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

DB 8 DK 9

RESULT 20

S77984

Cytochrome-c oxidase (EC 1.9.3.1) chain VIa - bigeye tuna (fragment)

C;Species: Thunnus obesus (bigeye tuna)

C;Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 30-Jan-1998

C;Accession: S77984

R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A;Reference number: S77980

A;Accession: S77984

A;Molecule type: protein

A;Residues: 1-9 <ARN>

A;Experimental source: heart

C;Genetics:

A;Genome: nuclear

C;Function:

A;Pathway: oxidative phosphorylation; respiratory chain

C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 66.7%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

DB 6 KE 7

Db 1 KE 2

RESULT 21

PH0921

T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0921

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0921

A;Molecule type: mRNA

A;Residues: 1-9 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 66.7%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

DB 8 DK 9

RESULT 22

I57650

hemoglobin alpha chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence\_revision 31-Jul-1997 #text\_change 20-Apr-2000

C;Accession: I57650

R;Whiteclaw, E.; Hogben, P.; Hanscombe, O.; Proudfoot, N.J.

Mol. Cell. Biol. 9, 241-251, 1989

A;Title: Transcriptional promiscuity of the human alpha-globin gene.

A;Reference number: I57650; MUID:89181576; PMID:2538719

A;Accession: I57650

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-9 <WHI>

A;Cross-references: GB:M23454; NID:G340922; PIDN:AAAS2629.1; PID:G553329

A;Note: engineered sequence; this sequence was not determined in this report

C;Genetics:

A;Gene: GDB:HBA1

A;Cross-references: GDB:119293

A;Map position: 16p13.3-16p13.3

Query Match 66.7%; Score 2; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

DB 7 DK 8

RESULT 23

S33844

alpha-2-macroglobulin - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 22-Nov-1993 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000

C;Accession: S33844

R;Warburton, M.J.; Coles, B.; Dundas, S.R.; Gusterson, B.A.; O'Hare, M.J.

Eur. J. Biochem. 214, 803-809, 1993

A;Title: Hydrocortisone induces the synthesis of alpha(2)-macroglobulin by rat mammary

A;Reference number: S33843; MUID:93307297; PMID:7686489

A;Accession: S33844

A;Molecule type: protein

A;Residues: 1-10 <WAR>

C;Superfamily: alpha-2-macroglobulin

C;Keywords: glycoprotein; plasma; proteinase inhibitor; thiolester bond

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 5 KE 6

RESULT 24  
 A49581  
 sialokinin I - yellow fever mosquito  
 C;Species: Aedes aegypti (yellow fever mosquito)  
 C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 18-Aug-2000  
 C;Accession: A49581  
 R;Champagne, D.E.; Ribeiro, J.M.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994  
 A;Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito A49581  
 A;Reference number: A49581; MUID:94105119; PMID:8278354  
 A;Accession: A49581  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <CHA>  
 A;Experimental source: Rockefeller, salivary gland  
 A;Note: sequence extracted from NCBI backbone (NCBIP:141841)  
 C;Superfamily: unassigned animal peptides

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 4 DK 5

RESULT 25  
 B49581  
 sialokinin II - yellow fever mosquito  
 C;Species: Aedes aegypti (yellow fever mosquito)  
 C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 18-Aug-2000  
 C;Accession: B49581  
 R;Champagne, D.E.; Ribeiro, J.M.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994  
 A;Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito A49581  
 A;Reference number: A49581; MUID:94105119; PMID:8278354  
 A;Accession: B49581  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <CHA>  
 A;Experimental source: Rockefeller, salivary gland  
 A;Note: sequence extracted from NCBI backbone (NCBIP:141842)  
 C;Superfamily: unassigned animal peptides

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 4 DK 5

RESULT 26  
 A24867  
 scyllorhinin I - smaller spotted catehawk  
 C;Species: Scyllorhinus canicula (smaller spotted dogfish)  
 C;Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 18-Aug-2000  
 C;Accession: A24867; S33301  
 R;Conlon, J.M.; Deacon, C.F.; O'Toole, L.; Thim, L.  
 FEBS Lett. 200, 111-116, 1986  
 A;Title: Scyllorhinin I and II: two novel tachykinins from dogfish gut.

A;Reference number: A91359; MUID:86192829; PMID:2422058  
 A;Accession: A24867  
 A;Molecule type: protein  
 A;Residues: 1-10 <CON>  
 R;Wang, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.  
 Eur. J. Biochem. 214, 469-474, 1993  
 A;Title: Primary structures and biological activities of substance-P-related peptides f  
 A;Reference number: S33300; MUID:93292508; PMID:7685693  
 A;Accession: S33301  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <WAU>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end; neuropeptide  
 F;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 4 DK 5

RESULT 27  
 A24407  
 amicyanin - Paracoccus denitrificans (fragment)  
 C;Species: Paracoccus denitrificans  
 C;Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 18-Jun-1993  
 C;Accession: A24407  
 R;Husain, M.; Davidson, V.L.  
 Biochemistry 25, 2431-2436, 1986  
 A;Title: Properties of Paracoccus denitrificans amicyanin.  
 A;Reference number: A24407; MUID:86243362; PMID:3718960  
 A;Accession: A24407  
 A;Molecule type: protein  
 A;Residues: 1-10 <HUS>

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 1 DK 2

RESULT 28  
 F44644  
 neurotoxin-associated protein type B Hn+ 35K chain, band 3a - Clostridium botulinum (fr  
 C;Species: Clostridium botulinum  
 C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
 C;Accession: F44644  
 R;Somers, E.; DasGupta, B.R.  
 J. Protein Chem. 10, 415-425, 1991  
 A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without h  
 A;Reference number: A44644; MUID:92143938; PMID:1781887  
 A;Contents: type B  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <SOM>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:83787)  
 C;Keywords: hemagglutinin

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 7 DK 8

Db 9 DK 10

## RESULT 29

S62880  
 polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)  
 C:Species: Aspergillus sp.  
 C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
 C:Accession: S62880  
 R:Stratilova, E.; Dzuova, M.; Markovic, O.; Joernvall, H.  
 FEBS Lett. 382, 164-166, 1996  
 A:Title: An essential tyrosine residue of Aspergillus polygalacturonase.  
 A:Reference number: S62880; MUID:96196586; PMID:8612742  
 A:Accession: S62880  
 A:Molecule type: protein  
 A:Residues: 1-10 <STR>  
 C:Keywords: glycosidase; hydrolase  
 F:4/Active site: Tyr #status predicted

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

Db 7 KE 8  
 ||  
 ||

## RESULT 30

H61308  
 hemocyanin subunit IV - Atlantic horseshoe crab (fragment)  
 C:Species: Limulus polyphemus (Atlantic horseshoe crab)  
 C:Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
 C:Accession: H61308  
 R:Jolles, J.; Jolles, P.; Lamv, J.; Lamv, J.  
 FEBS Lett. 106, 289-291, 1979  
 A:Title: Structural characterization of seven different subunits in Androctonus australis  
 A:Reference number: A61308; MUID:80047238; PMID:499512  
 A:Accession: H61308  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <JOL>

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

Db 3 KE 4  
 ||  
 ||

## RESULT 31

PH0946  
 T-cell receptor beta chain V-D-J region (clone BB12) - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C:Accession: PH0946  
 R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A:Reference number: PH0891; MUID:92078857; PMID:1836012  
 A:Accession: PH0946  
 A:Molecule type: mRNA  
 A:Residues: 1-10 <GOL>  
 A:Experimental source: myelin basic protein fragment-reactive T-cell, recovered from exp  
 C:Keywords: T-cell receptor

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

||  
 ||

## RESULT 32

PC4374  
 telomeric and tetraplex DNA binding protein qTBP42 IV - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 07-May-1999  
 C:Accession: PC4374  
 R:Sarig, G.; Weisman-Shomer, P.; Fry, M.  
 Biochem. Biophys. Res. Commun. 237, 617-623, 1997  
 A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the C  
 A:Reference number: PC4371; MUID:97445086; PMID:9299414  
 A:Accession: PC4374  
 A:Molecule type: protein  
 A:Residues: 1-10 <SAR>  
 C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

Db 6 KE 7  
 ||  
 ||

## RESULT 33

PQ0785  
 NADH2 dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrion (fragment)  
 N:Alternate names: complex I 27K chain; NADH-ubiquinone reductase 27K chain  
 C:Species: mitochondrion Vicia faba (fava bean)  
 C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 03-Jun-2002  
 C:Accession: PQ0785  
 R:Letierme, S.; Boutry, M.  
 Plant Physiol. 102, 435-443, 1993  
 A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH  
 A:Reference number: PQ0775; MUID:94151437; PMID:8108509  
 A:Accession: PQ0785  
 A:Molecule type: protein  
 A:Residues: 1-10 <DET>  
 C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the ti  
 ranging from 5K to 75K.  
 C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone b  
 C:Genetics:  
 A:Genome: mitochondrion  
 C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 66.7%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

Db 7 KE 8  
 ||  
 ||

## RESULT 34

PQ0682  
 photosystem I 17.5K D2 chain - common tobacco (fragment)  
 C:Species: Nicotiana tabacum (common tobacco)  
 C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
 C:Accession: PQ0682  
 R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiyura, M.  
 Plant Physiol. 102, 1259-1267, 1993  
 A:Title: Molecular heterogeneity of photosystem I. psad, psaE, psaF, psaH and psal are  
 A:Reference number: PQ0667; MUID:94105345; PMID:8278548  
 A:Accession: PQ0682  
 A:Molecule type: protein  
 A:Residues: 1-11 <OBO>  
 C:Superfamily: photosystem I chain II  
 C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 66.7%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 7 KE 8

## RESULT 35

JQ0395  
 hypothetical protein (nodB 3' region) - Azorhizobium caulinodans  
 N;Alternate names: hypothetical 1.4K protein  
 C;Species: Azorhizobium caulinodans  
 A;Note: host Sesbania rostrata  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 03-Feb-1994  
 C;Accession: JQ0395  
 R;Goethals, K.; Gao, M.; Tönkepe, K.; Van Montagu, M.; Holsters, M.  
 Mol. Gen. Genet. 219, 289-298, 1989  
 A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans: nucleotide sequence  
 A;Reference number: JQ0393; MUID:90136519; PMID:2615763  
 A;Accession: JQ0395  
 A;Molecule type: DNA  
 A;Residues: 1-11 <GOE>  
 A;Cross-references: GB:118897  
 A;Experimental source: strain ORS571

Query Match 66.7%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 5 DK 6

## RESULT 36

B39853  
 LuxC protein - Photobacterium phosphoreum (fragment)  
 C;Species: Photobacterium phosphoreum  
 C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 08-Oct-1999  
 C;Accession: B39853  
 R;Ferri, S.R.; Meighan, E.A.  
 J. Biol. Chem. 266, 12852-12857, 1991  
 A;Title: A lux-specific myristoyl transferase in luminescent bacteria related to eukaryotic  
 A;Reference number: A39853; MUID:91302295; PMID:2071574  
 A;Accession: B39853  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-11 <FER>  
 A;Cross-references: GB:M64224; NID:g150701; PIDN:AAA25625.1; PID:g150702

Query Match 66.7%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 4 DK 5

## RESULT 37

PT0081  
 protein QA300023 - Arabidopsis thaliana (fragment)  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 07-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 24-Nov-1999  
 C;Accession: PT0081  
 R;Tsugata, A.; Kano, M.; Kawakami, M.; Ohki, Y.  
 submitted to JIPID, December 1995  
 A;Description: Two dimensional electrophoresis of plant proteins and standardization of  
 A;Reference number: PN0173  
 A;Accession: PT0081  
 A;Molecule type: protein

A;Residues: 1-11 <TSU>  
 A;Experimental source: leaf  
 C;Keywords: acetylated amino end  
 F;Modified site: acetylated amino end (Ser) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
 ||  
 Db 2 KE 3

## RESULT 38

S45698  
 gamma-MSH-like protein - duck leech  
 C;Species: Theromyzon tessulatatum (duck leech)  
 C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 25-Apr-1997  
 C;Accession: S45698  
 R;Salzet, M.; Watter, C.; Bulet, P.; Malecha, J.  
 FEBS Lett. 348, 102-106, 1994  
 A;Title: Isolation and structural characterization of a novel peptide related to gamma-MSH  
 A;Reference number: S45698; MUID:94298944; PMID:8026574  
 A;Accession: S45698  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-11 <SAL>

Query Match 66.7%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 9 DK 10

## RESULT 39

S23373  
 T-cell receptor alpha chain J region - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
 C;Accession: S23373  
 R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichmann, J.  
 Eur. J. Immunol. 21, 2749-2754, 1991  
 A;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheumatoid  
 A;Reference number: S23364; MUID:92037820; PMID:1657615  
 A;Accession: S23373  
 A;Status: preliminary; translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-11 <PLU>  
 A;Cross-references: EMBL:X58168  
 C;Keywords: T-cell receptor

Query Match 66.7%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
 ||  
 Db 7 DK 8

## RESULT 40

PH1376  
 T antigen variant K-3 - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-May-2000  
 C;Accession: PH1376  
 R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.  
 J. Exp. Med. 176, 449-457, 1992  
 A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for

A;Reference number: PH1373; MUID:92364547; PMID:1380062

A;Accession: PH1376

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <L1>

Query Match 66.7%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 6 KE 7

#### RESULT 41

H84082

hypothetical protein BH3464 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C;Accession: H84082

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: H84082

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <STO>

A;Cross-references: GB:AP001518; GB:BA000004; NID:gl0175792; PIDN:BAB07183.1; GSPDB:GNOC

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH3464

Query Match 66.7%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 4 KE 5

#### RESULT 42

C49215

urease (EC 3.5.1.5) large subunit UreB - Helicobacter felis (fragment)

C;Species: Helicobacter felis

C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 06-Jan-2003

C;Accession: C49215

R;Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.

Infect. Immun. 60, 5259-5266, 1992

A;Title: Purification and characterization of the urease enzymes of Helicobacter species

A;Reference number: A49215; MUID:93084378; PMID:1452339

A;Accession: C49215

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <TUR>

A;Experimental source: ATCC 49179

A;Note: sequence extracted from NCBI backbone (NCBIP:119484)

C;Superfamily: urease, alpha subunit; urease 62K chain homology

C;Keywords: hydrolase

Query Match 66.7%; Score 2; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 8.2e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 7 KE 8

#### RESULT 43

G49410

t-complex polypeptide 1 homolog (peak 6b fraction) - rabbit (fragment)

N;Alternate names: chaperonin homolog (peak 6b)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 04-Sep-1998

C;Accession: G49410

R;Romelaere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.; A

Proc. Natl. Acad. Sci. U.S.A. 90, 11975-11979, 1993

A;Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven rel

A;Reference number: A49410; MUID:94089752; PMID:7903455

A;Accession: G49410

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <ROM>

A;Experimental source: reticulocyte

C;Superfamily: molecular chaperone t-complex-type

Query Match 66.7%; Score 2; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 8.2e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

||

Db 11 DK 12

#### RESULT 44

S01222

translation elongation factor EF-Tu - Pseudomonas aeruginosa (fragment)

C;Species: Pseudomonas aeruginosa

C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 26-Aug-1999

C;Accession: S01222

R;Hughes, M.A.; Jones, D.S.

Nucleic Acids Res. 16, 7193, 1988

A;Title: A fragment of the Pseudomonas aeruginosa genome contains five tRNA genes, four

A;Reference number: S01222; MUID:88303352; PMID:3136442

A;Accession: S01222

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-12 <HUG>

A;Cross-references: EMBL:X07950; NID:g45426; PIDN:CAA30775.1; PID:g45427

C;Genetics:

A;Gene: tuftB

C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homol

C;Keywords: GTP binding; protein biosynthesis

Query Match 66.7%; Score 2; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 8.2e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 3 KE 4

#### RESULT 45

A58501

24K kidney and bladder stone protein 1 - unidentified bacterium (fragment)

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998

C;Accession: A58501

R;Binette, J.P.; Binette, M.B.

submitted to The Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: A58501

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <BIN>

A;Experimental source: human kidney and bladder stones

A;Note: tentative identification of 2-Ser

Query Match 66.7%; Score 2; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 8.2e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
Db 3 KE 4

## RESULT 46

G49215  
urease (EC 3.5.1.5) small subunit UreA - Helicobacter felis (fragment)  
C;Species: Helicobacter felis  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 26-May-1995  
C;Accession: G49215  
R;Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.  
Infect. Immun. 60, 5259-5266, 1992  
A;Title: Purification and characterization of the urease enzymes of Helicobacter species  
A;Reference number: A49215; MUID:93084378; PMID:1452359  
A;Accession: G49215  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <TUR>  
A;Experimental source: ATCC 49179  
A;Note: sequence extracted from NCBI backbone (NCBIP:119489)  
C;Keywords: hydrolase

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
Db 6 KE 7

## RESULT 47

E64573  
hypothetical protein HP0429 - Helicobacter pylori (strain 26695)  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999  
C;Accession: E64573  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: E64573  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-12 <TOM>  
A;Cross-references: GB:AF000559; GB:AF000511; NID:G2313536; PIDN:AAD07512.1; PID:G231355

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
Db 7 KE 8

## RESULT 48

A60757  
enterotoxin C-1 - Staphylococcus aureus (fragments)  
C;Species: Staphylococcus aureus  
C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 30-Sep-1993  
C;Accession: A60757  
R;Bohach, G.A.; Handley, J.P.; Schlievert, P.M.  
Infect. Immun. 57, 23-28, 1989  
A;Title: Biological and immunological properties of the carboxyl terminus of staphylococcal enterotoxin C-1.  
A;Reference number: A60757; MUID:89079292; PMID:2909489  
A;Accession: A60757

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <BOH>

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 3 DK 4

## RESULT 49

PA0047  
protein QM10045 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C;Accession: PA0047  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
A;Reference number: PA0001  
A;Accession: PA0047  
A;Molecule type: protein  
A;Residues: 1-12 <KAM>

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 6 DK 7

## RESULT 50

S18722  
cmtK protein - beechdrops plastid (fragment)  
C;Species: Plastid Epifagus virginiana (beechdrops)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Feb-1995  
C;Accession: S18722  
R;Morden, C.W.; Wolfe, K.H.; dePamphilis, C.W.; Palmer, J.D.  
EMBO J. 10, 3281-3288, 1991  
A;Title: Plastid translation and transcription genes in a non-photosynthetic plant: intA.  
A;Reference number: S17794; MUID:92007779; PMID:1315295  
A;Accession: S18722  
A;Molecule type: DNA  
A;Residues: 1-12 <MOR>  
A;Cross-references: EMBL:X61798  
C;Genetics:  
A;Gene: cmtK  
A;Genome: plastid  
C;Keywords: plastid

Query Match 66.7%; Score 2; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 2 DK 3

## RESULT 51

A56878  
light yellow cell peptide A - great pond snail  
N;Contains: light yellow cell peptide B  
C;Species: Lymnaea stagnalis (great pond snail)  
C;Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 20-Aug-1999  
C;Accession: A56878  
R;Hoek, R.M.; Li, K.W.; van Minnen, J.; Geraerts, W.P.  
Brain Res. Mol. Brain Res. 16, 71-74, 1992



A;Title: Chemical characterization of a novel peptide from the neuroendocrine light yell  
A;Reference number: A56878; MUID:93095719; PMID:1334202  
A;Accession: A56878  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <H>E>  
A;Cross-references: PIDN:AB24433.1; PID:G261422  
A;Note: sequence extracted from NCBI backbone (NCBIIP:120090)  
C;Keywords: neuropeptide  
F;1-12/Product: light yellow cell peptide A #status experimental <YCPA>  
F;2-12/Product: light yellow cell peptide B #status experimental <YCPB>

Query Match 66.7%; Score 2; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 8.2e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

||

Db 4 DK 5

RESULT 52

C61308

hemocyanin chain 6 - Sahara scorpion (fragment)

C;Species: Androctonus australis (Sahara scorpion)

C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999

C;Accession: C61308

R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.

FEBS Lett. 106, 289-291, 1979

A;Title: Structural characterization of seven different subunits in Androctonus australis

A;Reference number: A61308; MUID:80047238; PMID:499512

A;Accession: C61308

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <J>L>

Query Match

Best Local Similarity 66.7%; Score 2; DB 2; Length 12;

C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

||

Db 4 DK 5

RESULT 53

S47360

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999

C;Accession: S47360

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T

A;Reference number: S47355

A;Accession: S47360

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-12 <L>E>H>

A;Cross-references: EMBL:235684; NID:G527457; PIDN:CAA84753.1; PID:G527458

C;Keywords: T-cell receptor

Query Match

Best Local Similarity 66.7%; Score 2; DB 2; Length 12;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 7 KE 8

RESULT 54

C49033

T-cell receptor delta chain V-D-J region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Dec-1993 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
C;Accession: C49033  
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.  
Eur. J. Immunol. 21, 2999-3007, 1991

A;Title: Functionally distinct subsets of human gamma/delta T cells.

A;Reference number: A49033; MUID:92083926; PMID:1684157

A;Accession: C49033

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 <M>O>R>

A;Cross-references: GB:S72583; NID:G240694; PIDN:AAB20629.1; PID:G240695

A;Note: sequence extracted from NCBI backbone (NCBIIP:72583, NCBIIP:72585)

C;Keywords: T-cell receptor

Query Match

Best Local Similarity 66.7%; Score 2; DB 2; Length 12;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

||

Db 10 DK 11

RESULT 55

S68402

NAD(+)-glycohydrolase - bovine (fragments)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 12-Dec-1997

C;Accession: S68402

R;Zhang, J.; Ziegler, M.; Schneider, R.; Klocker, H.; Auer, B.; Schweiger, M.

FEBS Lett. 377, 530-534, 1995

A;Title: Identification and purification of a bovine liver mitochondrial NAD(+)-glycohy

A;Reference number: S68402; MUID:96140583; PMID:8549791

A;Accession: S68402

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7,8-12 <Z>H>A>

C;Genetics:

A;Genome: nuclear

C;Keywords: mitochondrion; NAD

Query Match

Best Local Similarity 66.7%; Score 2; DB 2; Length 12;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 8 KE 9

RESULT 56

S39413

tubulin beta chain - turkey (fragment)

C;Species: Meleagris gallopavo (common turkey)

C;Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07-May-1999

C;Accession: S39413

R;Ruediger, M.; Weber, K.

Eur. J. Biochem. 218, 107-116, 1993

A;Title: Characterization of the post-translational modifications in tubulin from the m

A;Reference number: S39412; MUID:94062821; PMID:8243458

A;Accession: S39413

A;Molecule type: protein

A;Residues: 1-13 <R>U>E>

C;Superfamily: tubulin

C;Keywords: heterodimer; microtubule

Query Match

Best Local Similarity 66.7%; Score 2; DB 2; Length 13;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 2 KE 3

Db 11 KE 12  
||

## RESULT 57

A33208  
calreticulin, hepatic - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 31-Oct-1997  
C:Accession: A33208  
R:Milner, R.E.; Bakh, S.; Shenanko, C.; Carpenter, M.R.; Vance, J.E.; Opa  
J. Biol. Chem. 266, 7155-7165, 1991  
A:Title: Calreticulin, and not calnexin, is the major calcium binding protein of sm  
A:Reference number: A33208; MUID:91201375; PMID:2016321  
A:Accession: A33208  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <MIL>  
C:Superfamily: calreticulin  
C:Keywords: liver

Query Match 66.7%; Score 2; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 8.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 7 KE 8

## RESULT 58

E39778  
lactose phosphotransferase system lacR protein - Lactococcus lactis (fragment)

C:Species: Lactococcus lactis

C>Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 11-Jan-2000

C:Accession: E39778

R:van Rooijen, R.J.; van Schalkwijk, S.; de Vos, W.M.

J. Biol. Chem. 266, 7176-7181, 1991

A:Title: Molecular cloning, characterization, and nucleotide sequence of the tagatose 6-

A:Reference number: A39778; MUID:91201377; PMID:1901863

A:Accession: E39778

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-13 <VAN>

A:Cross-references: GB:J05748

C:Superfamily: regulatory protein gutr

C:Keywords: DNA binding; transcription regulation

Query Match 66.7%; Score 2; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 8.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 2 KE 3

## RESULT 59

A59387  
VCAM-1 5'UTR binding protein - Rana pipiens (fragment)

C:Species: Rana pipiens

C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001

C:Accession: A59387

R:BANERJEE, H.

submitted to the Protein Sequence Database, February 2001

A:Description: Identification and characterization of a novel VCAM-1 5'UTR.

A:Reference number: A59387

A:Accession: A59387

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <BAN>

A:Experimental source: CCL-145

A>Note: VCAM-1 5' untranslated region binding protein with a probable translation inhibi

Query Match 66.7%; Score 2; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 8.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 10 KE 11

## RESULT 60

A61288

spore proteinase gpr (EC 3.4.-.-) - Bacillus megaterium (fragments)

C:Species: Bacillus megaterium

C>Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 21-Mar-1996

C:Accession: A61288

R:Sanchez-Salas, J.L.; Setlow, P.

J. Bacteriol. 175, 2568-2577, 1993

A:Title: Proteolytic processing of the protease which initiates degradation of small, a

A:Reference number: A61288; MUID:93239682; PMID:8478323

A:Accession: A61288

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <SAN>

C:Keywords: hydrolase

Query Match 66.7%; Score 2; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 8.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3

||

Db 3 KE 4

## RESULT 61

G44644

neurotoxin-associated protein type B Hn+ 35K chain, band 3b - Clostridium botulinum (fr

C:Species: Clostridium botulinum

C>Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994

C:Accession: G44644

R:Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A:Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without h

A:Reference number: A44644; MUID:92143938; PMID:1781887

A:Contents: type B

A:Accession: G44644

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <SOM>

A>Note: sequence extracted from NCBI backbone (NCBIP:83785)

C:Keywords: hemagglutinin

Query Match 66.7%; Score 2; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 8.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2

||

Db 10 DK 11

## RESULT 62

A32453

phloroglucinol reductase (EC 1.-.-.-) - Eubacterium oxidoreducens (fragment)

C:Species: Eubacterium oxidoreducens

C>Date: 26-Oct-1989 #sequence\_revision 26-Oct-1989 #text\_change 24-Oct-1998

C:Accession: A32453

R:Haddock, J.D.; Ferry, J.G.

J. Biol. Chem. 264, 4423-4427, 1989

A:Title: Purification and properties of phloroglucinol reductase from Eubacterium oxid

A:Reference number: A32453; MUID:89174692; PMID:2925649.

A:Accession: A32453

A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <HAD>  
C:Keywords: oxidoreductase

Query Match 66.7%; Score 2; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
Db 6 KE 7

## RESULT 63

PC4055  
hypothetical 13 protein - Frankia sp. (fragment)  
C:Species: Frankia sp.  
C:Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 27-Oct-1995  
C:Accession: PC4055  
R:Harriott, O.T.; Hosted, T.J.; Benson, D.R.  
Gene 161, 63-67, 1995  
A:Title: Sequences of nifX, nifW, nifZ, nifB and two ORF in the Frankia nitrogen fixation  
A:Reference number: JC4203; MUID:95369734; PMID:7642138  
A:Accession: PC4055  
A:Molecule type: DNA  
A:Residues: 1-13 <HAR>  
A:Cross-references: GB:L29299

Query Match 66.7%; Score 2; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DK 2  
||  
Db 12 DK 13

## RESULT 64

PA0023  
protein OA300052 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 11-Jul-1997  
C:Accession: PA0023  
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional  
A:Reference number: PA0001  
A:Accession: PA0023  
A:Molecule type: protein  
A:Residues: 1-13 <KAM>  
A:Experimental source: seed  
C:Keywords: pyroglutamic acid; seed  
F:/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 66.7%; Score 2; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
Db 5 KE 6

## RESULT 65

S28425  
20K protein - rape (fragment)  
C:Species: Brassica napus (rape)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
C:Accession: S28425  
R:Heiliger, A.; Leadlay, P.F.; Slabas, A.R.  
Plant Mol. Biol. 20, 763-780, 1992  
A:Title: Induction, purification and characterisation of acyl-ACP thioesterase from deve

A:Reference number: S28424; MUID:93099229; PMID:1301073  
A:Accession: S28425  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <HEL>

Query Match 66.7%; Score 2; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
Db 10 KE 11

## RESULT 66

JQ2309  
hypothetical 1.6K protein - tomato chloroplast (strain Toko)  
C:Species: chloroplast Lycopersicon esculentum (tomato)  
C:Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 23-Mar-1995  
C:Accession: JQ2309  
R:Kawagoe, Y.; Kikuta, Y.  
Theor. Appl. Genet. 81, 13-20, 1991  
A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).  
A:Reference number: JQ2306  
A:Accession: JQ2309  
A:Molecule type: DNA  
A:Residues: 1-13 <KAW>  
A:Experimental source: strain Toko  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 66.7%; Score 2; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
Db 2 KE 3

## RESULT 67

JQ2319  
hypothetical 1.6K protein - potato chloroplast  
C:Species: chloroplast Solanum tuberosum (potato)  
C:Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Jan-1996  
C:Accession: JQ2319; JQ2314  
R:Kawagoe, Y.; Kikuta, Y.  
Theor. Appl. Genet. 81, 13-20, 1991  
A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).  
A:Reference number: JQ2306  
A:Accession: JQ2319  
A:Molecule type: DNA  
A:Residues: 1-13 <KW1>  
A:Experimental source: cv. W553-4  
A:Accession: JQ2314  
A:Molecule type: DNA  
A:Residues: 1-13 <KW2>  
A:Experimental source: cv. 150  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 66.7%; Score 2; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3  
||  
Db 2 KE 3



Query Match 66.7%; Score 2; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DK 2  
 ||  
 Db 4 DK 5

## RESULT 74

PN0147

omega-gliadine 1 and 2 - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PN0147; PN0146

R;Odintsova, T.I.; Egorov, T.A.

Biokhimia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of

A;Reference number: PN0146; PMID:90283493; PMID:2354218

A;Accession: PN0147

A;Molecule type: protein

A;Residues: 1-14 &lt;ODI&gt;

A;Experimental source: strain K-202

A;Note: Omega-gliadine 2 (amino-terminal fragment)

A;Accession: PN0146

A;Molecule type: protein

A;Residues: 1-9 &lt;OD2&gt;

A;Experimental source: strain K-202

A;Note: omega-gliadine 1 (amino-terminal fragment)

Query Match 66.7%; Score 2; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KE 3  
 ||  
 Db 9 KE 10

## RESULT 75

PN0151

omega-gliadine 2' - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PN0151

R;Odintsova, T.I.; Egorov, T.A.

Biokhimia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of

A;Reference number: PN0146; PMID:90283493; PMID:2354218

A;Accession: PN0151

A;Molecule type: protein

A;Residues: 1-14 &lt;ODI&gt;

A;Experimental source: strain K-907

Query Match 66.7%; Score 2; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KE 3  
 ||  
 Db 9 KE 10

Search completed: November 25, 2003, 18:28:21  
 Job time : 3.76064 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 4.60106 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-12

Perfect score: 5

Sequence: 1 PPPPK 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96169682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	80.0	20	A42267	J-kappa recombinat
2	3	60.0	7	S71299	ICL2 protein - Par
3	3	60.0	10	B59272	peptide-N4-(N-acet
4	3	60.0	10	A36454	trypsin-modulating
5	3	60.0	10	C30572	T-cell receptor be
6	3	60.0	11	D45900	complement C3b rec
7	3	60.0	12	PN0663	dystrophin-associa
8	3	60.0	12	B39690	neural cell adhesi
9	3	60.0	12	S71380	lebetin 1 isoform
10	3	60.0	13	D39690	neural cell adhesi
11	3	60.0	13	S21152	trypsin-modulating
12	3	60.0	13	A05174	trypsin-modulating
13	3	60.0	13	S09716	2S albumin large c
14	3	60.0	14	H64008	hypothetical prote
15	3	60.0	14	S12904	protein kinase (EC
16	3	60.0	14	S11129	phosphoprotein, bo
17	3	60.0	15	A54397	ubiquitin-carrier
18	3	60.0	15	PT0037	light harvesting c
19	3	60.0	16	JH0517	insulin-like growt
20	3	60.0	17	S57991	hydroxyproline-ric
21	3	60.0	17	S59481	hydroxyproline-ric
22	3	60.0	18	PC2280	prolylendopeptidas
23	3	60.0	18	A54195	Na+/K+-exchanging
24	3	60.0	19	G56819	PS I complex subun
25	3	60.0	19	PH1352	Ig heavy chain DJ
26	3	60.0	19	S25715	hypothetical prote
27	3	60.0	20	A33878	myosin light chain
28	3	60.0	20	A45806	T-cell receptor be
29	3	60.0	20	S06150	photosystem I chai

30	3	60.0	20	2	S03954	acidic fibroblast
31	3	60.0	20	2	A1516	lectin, galactose/
32	3	40.0	20	2	S53508	starvation-induced
33	2	40.0	5	2	C41225	copper resistance
34	2	40.0	5	2	B37988	acid proteinase li
35	2	40.0	6	2	A61049	halo-toxin - Pseud
36	2	40.0	6	2	B60110	repetitive protein
37	2	40.0	6	2	A61140	sperm acrosomal pr
38	2	40.0	7	2	S36662	dermorphin (Lys-7)
39	2	40.0	7	2	PH1408	Ig heavy chain V r
40	2	40.0	7	2	A61081	tryptophyllin, bas
41	2	40.0	7	2	A44428	platelet aggregati
42	2	40.0	7	2	PT0283	Ig heavy chain CRD
43	2	40.0	8	2	PH1407	Ig heavy chain V r
44	2	40.0	8	2	PL0184	capsid protein VP-
45	2	40.0	8	2	B39745	endoglycosylcerami
46	2	40.0	8	2	S16324	hypothetical prote
47	2	40.0	8	2	S21288	lecitin - potato (f
48	2	40.0	8	2	A63306	spasmogenic toxin
49	2	40.0	8	2	S66646	cardioacceleratory
50	2	40.0	8	2	A39892	p element, P cytot
51	2	40.0	8	2	E47393	neuropeptide calla
52	2	40.0	8	2	A14683	aspartate transami
53	2	40.0	8	2	A61328	trypsin (EC 3.4.21
54	2	40.0	8	2	S10783	enamelin f - bovin
55	2	40.0	8	2	A28719	thymic humoral fac
56	2	40.0	8	2	PT0559	T-cell receptor be
57	2	40.0	9	2	A28495	conopressin G - co
58	2	40.0	9	2	S35338	ribosomal protein
59	2	40.0	9	2	A61230	calsequestrin, car
60	2	40.0	9	2	JS0302	xenopsin-related p
61	2	40.0	9	2	A60320	xenopsin-related p
62	2	40.0	9	2	A61358	bradykinin-like pe
63	2	40.0	9	2	A61057	Thr-6 bradykinin -
64	2	40.0	9	2	A26744	bradykinin-like pe
65	2	40.0	9	2	A61363	bradykinin - Commo
66	2	40.0	9	2	A60579	bradykinin-like pe
67	2	40.0	9	2	B60246	ornitho-kinin - ch
68	2	40.0	9	2	S66607	quinoline 2-oxidor
69	2	40.0	9	2	B41983	orf dowstream to b
70	2	40.0	9	2	S65433	bradykinin - horn
71	2	40.0	9	2	B20569	serum amyloid P-co
72	2	40.0	9	2	S66635	alpha-2-macroglobu
73	2	40.0	9	2	S66636	alpha-2-macroglobu
74	2	40.0	9	2	S26508	collagen alpha 2(V
75	2	40.0	9	2	S10784	enamelin i - bovin
76	2	40.0	9	2	I45023	growth hormone rec
77	2	40.0	9	2	PC7078	unidentified 48.7K
78	2	40.0	9	2	B30572	T-cell receptor be
79	2	40.0	9	2	A43065	hydroxyproline-3-b
80	2	40.0	9	2	S39040	lysine-conopressin
81	2	40.0	9	2	PC7073	ubiquinol-cytochro
82	2	40.0	10	1	XAV16B	angiotensin-conver
83	2	40.0	10	1	XASNPC	angiotensin-conver
84	2	40.0	10	2	JC1367	thyloliberin poten
85	2	40.0	10	2	A60410	beta-neoendorphin
86	2	40.0	10	2	PC2171	triacylglycerol li
87	2	40.0	10	2	B31710	ornithine decarbox
88	2	40.0	10	2	S39030	lysyl-bradykinin -
89	2	40.0	10	2	B33143	pneumadin - human
90	2	40.0	10	2	A33143	pneumadin - rat
91	2	40.0	10	2	S18396	probable glucose-6
92	2	40.0	10	2	C35389	urease (EC 3.5.1.5
93	2	40.0	10	2	A60476	S-layer protein -
94	2	40.0	10	2	F41839	ribosomal protein
95	2	40.0	10	2	H28027	protein P11 - curl
96	2	40.0	10	2	PQ0753	beta-fructofuranos
97	2	40.0	10	2	B37196	bradykinin-potent
98	2	40.0	10	2	H37196	bradykinin-potent
99	2	40.0	10	2	S26506	collagen alpha 1(V
100	2	40.0	10	2	S71948	matrix metalloprot

## ALIGNMENTS

## RESULT 1

A42267  
J-kappa recombination sequence-binding protein RBP-2N - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C;Accession: A42267; S23798  
R;Kawaiuchi, M.; Oka, C.; Shibayama, S.; Koromilas, A.E.; Matsunami, N.; Hameguchi, Y.; H  
J. Biol. Chem. 267, 4016-4022, 1992  
A;Title: Genomic organization of mouse J-kappa recombination signal binding protein (RBP  
A;Reference number: A42267; MUID:92156146; PMID:1740450  
A;Accession: A42267  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-20 <KAW>  
A;Cross-references: GB:M81866

Query Match 80.0%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 PPPK 5

DB

13 PPPK 16

## RESULT 2

S71299  
ICL2 protein - Paramoecium tetraurelia (fragment)  
C;Species: Paramoecium tetraurelia  
C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999  
R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.  
Eur. J. Biochem. 238, 121-128, 1996  
A;Title: Characterization of centrin genes in Paramoecium.  
A;Reference number: S71299; MUID:96248429; PMID:8665928  
A;Accession: S71299  
A;Molecule type: protein  
A;Residues: 1-7 <MAD>  
A;Experimental source: strain d4-2  
C;Genetics:  
A;Genetic code: SGCS

Query Match 60.0%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 PPP 4

DB

3 PPP 5

## RESULT 3

B59272  
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain  
N;Alternate names: peptidase N-glycosidase  
C;Species: Prunus dulcis var. sativa (sweet almond)  
C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 19-May-2000  
C;Accession: B59272  
R;Altmann, F.; Paschinger, K.; Dalik, T.; Voraauer, K.  
Eur. J. Biochem. 252, 118-123, 1998  
A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A  
A;Reference number: A59272; MUID:98181894; PMID:9523720  
A;Accession: B59272  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <ALT>  
C;Keywords: hydrolase

Query Match 60.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;

QY

3 PPK 5

DB

8 PPK 10

Matches

3; Conservative

0; Mismatches

0; Indels

0; Gaps

QY

1 PPP 3

DB

8 PPP 10

## RESULT 4

A36454  
Trypsin-modulating oostatic factor - yellow fever mosquito  
C;Species: Aedes aegypti (yellow fever mosquito)  
C;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 24-May-1996  
C;Accession: A36454; A61630  
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
FASEB J. 4, 3015-3020, 1990  
A;Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme b  
A;Reference number: A36454; MUID:90367888; PMID:2394318  
A;Accession: A36454  
A;Molecule type: protein  
A;Residues: 1-10 <BOR>  
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
Insect Biochem. Mol. Biol. 23, 703-712, 1993  
A;Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oos  
A;Reference number: A61630; MUID:93357794; PMID:8353526  
A;Accession: A61630  
A;Molecule type: protein  
A;Residues: 1-10 <BO2>  
A;Note: none of the amino acids is modified  
A;Function:  
A;Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut e  
C;Keywords: hormone

Query Match 60.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 PPP 4

DB

5 PPP 7

## RESULT 5

C30572  
T-cell receptor beta chain C region (CRTB49) - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-Apr-1989 #sequence\_revision 03-Apr-1989 #text\_change 30-May-1997  
C;Accession: C30572  
R;Williams, C.B.; Gutman, G.A.  
J. Immunol. 142, 1027-1035, 1989  
A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utili  
A;Reference number: A30563; MUID:89110038; PMID:2563271  
A;Accession: C30572  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-10 <WIL>  
C;Keywords: T-cell receptor

Query Match 60.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

3 PPK 5

DB

8 PPK 10

## RESULT 6

D45900  
complement C3b receptor type 2 - mouse (clone 12) (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: D45900  
R;Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.



J. Immunol. 144, 3581-3591, 1990

A;Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene  
A;Reference number: A45900; MUID:90229754; PMID:2139460  
A;Accession: D45900  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A;Molecule type: mRNA  
A;Residues: 1-11 <KUR>

Query Match 60.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

Db 9 PPP 11

#### RESULT 7

PN0663

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C;Accession: PN0663

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained  
A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0663

A;Molecule type: protein

A;Residues: 1-12 <YOS>

A;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match

Best Local Similarity 60.0%; Score 3; DB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

Db 5 PPP 7

#### RESULT 8

B39690

neural cell adhesion molecule, cardiac splice form +, -, - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999

C;Accession: B39690

R;Reyes, A.A.; Small, S.J.; Akeson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991

A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule m

A;Reference number: A39690; MUID:91141516; PMID:1996115

A;Accession: B39690

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: mRNA

A;Residues: 1-12 <REV>

A;Cross-references: GB:M63970

C;Keywords: cardiac muscle; cell adhesion; heart

Query Match

Best Local Similarity 60.0%; Score 3; DB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

Db 6 PPP 8

#### RESULT 9

S71380

lebetin 1 isoform beta - Vipera lebetina

C;Species: Vipera lebetina

C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C;Accession: S71380

R;Barbouche, R.; Marrakchi, N.; Mansuelle, P.; Krifi, M.; Fenouillet, E.; Rochat, H.; E

FEBS Lett. 392, 6-10, 1996

A;Title: Novel anti-platelet aggregation polypeptides from Vipera lebetina venom: isola

A;Reference number: S71379; MUID:96354866; PMID:8769304

A;Accession: S71380

A;Molecule type: protein

A;Residues: 1-12 <BAR>

A;Experimental source: venom

C;Keywords: anticoagulant; venom

Query Match

Best Local Similarity 60.0%; Score 3; DB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5

Db 4 PPP 6

#### RESULT 10

D39690

neural cell adhesion molecule, cardiac splice form +, -, - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999

C;Accession: D39690

R;Reyes, A.A.; Small, S.J.; Akeson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991

A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule m

A;Reference number: A39690; MUID:91141516; PMID:1996115

A;Accession: D39690

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A;Molecule type: mRNA

A;Residues: 1-13 <REV>

A;Cross-references: GB:M63970

C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm

C;Keywords: cardiac muscle; cell adhesion; heart

Query Match

Best Local Similarity 60.0%; Score 3; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

Db 6 PPP 8

#### RESULT 11

S21152

cryptophyllin-related peptide - two-colored leaf frog

C;Species: Phyllomedusa bicolor (two-colored leaf frog)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C;Accession: S21152

R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G

FEBS Lett. 302, 151-154, 1992

A;Title: Identification and characterization of two dermorphins from skin extracts of t

A;Reference number: S21152; MUID:92339502; PMID:1633846

A;Accession: S21152

A;Molecule type: protein

A;Residues: 1-13 <MIG>

A;Experimental source: skin

C;Superfamily: unassigned animal peptides

Query Match

Best Local Similarity 60.0%; Score 3; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

Db 7 PPP 9

#### RESULT 12

## A05174

cryptophyllin-13 - Rohde's leaf frog  
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 18-Aug-2000  
C;Accession: A05174  
R;Montecucchi, P.C.; Gozzini, L.; Erspamer, V.  
Int. J. Pept. Protein Res. 27, 175-182, 1986  
A;Reference number: A05174  
A;Accession: A05174  
A;Molecule type: protein  
A;Residues: 1-13 <MON>  
C;Superfamily: unassigned animal peptides  
C;Keywords: pyroglutamic acid; skin  
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 60.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 7 PPP 9

## RESULT 13

## S09716

2S albumin large chain (1 and 2) nII - rape (fragments)  
N;Alternate names: 2S albumin large chain nIII  
C;Species: Brassica napus (rape)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Aug-1998  
C;Accession: S09716; S09718; S09717  
R;Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.  
FEBS Lett. 263, 209-212, 1990  
A;Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins  
A;Reference number: S09720; MUID:90242974; PMID:2185951

A;Accession: S09716  
A;Molecule type: protein  
A;Residues: 1-9;10-13 <MON>  
A;Experimental source: seed  
A;Note: 3-Ser was also found  
A;Accession: S09718  
A;Molecule type: protein  
A;Residues: 1-9;10-13 <MO2>  
A;Experimental source: seed  
A;Accession: S09717  
A;Molecule type: protein  
A;Residues: 1-9;10-13 <MO3>  
A;Experimental source: seed

Query Match 60.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 8 PPP 10

## RESULT 14

## H64008

hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)  
C;Species: Haemophilus influenzae  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 30-Jun-1998  
C;Accession: H64008  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630; PMID:7542800  
A;Accession: H64008  
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <TIGR>

A;Cross-references: GB:U32731; GB:L42023; NID:G1573465; PID:G1573478; TIGR:HI0492

Query Match 60.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5  
|||  
Db 9 PPK 11

## RESULT 15

## S12904

protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)

C;Species: Pisaster ochraceus

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997

C;Accession: S12904

R;Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.

FEBS Lett. 273, 223-226, 1990

A;Title: Identification of the sites in myelin basic protein that are phosphorylated by

A;Reference number: S12904; MUID:91032186; PMID:1699809

A;Accession: S12904

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <SAN>

C;Keywords: phosphotransferase

Query Match 60.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 8 PPP 10

## RESULT 16

## S11129

phosphoprotein, bone - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 25-Oct-1996

C;Accession: S11129

R;Wakuni-Takagaki, Y.; Glimcher, M.J.

Biochem. J. 268, 585-591, 1990

A;Title: Post-translational processing of chicken bone phosphoproteins. Identification

A;Reference number: S11127; MUID:90303246; PMID:2363696

A;Accession: S11129

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <MIK>

C;Keywords: phosphoprotein

Query Match 60.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 5 PPP 7

## RESULT 17

## A54397

ubiquitin-carrier protein E2-F1 - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 11-Jan-2000

C;Accession: A54397

R;Blumenfeld, N.; Gonen, H.; Mayer, A.; Smith, C.E.; Siegel, N.R.; Schwartz, A.L.; Cieci

J. Biol. Chem. 269, 9574-9581, 1994

A;Title: Purification and characterization of a novel species of ubiquitin-carrier prot

A;Reference number: A54397; MUID:94193635; PMID:8144544

A:Accession: A54397

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <BLU>

A:Experimental source: reticulocyte

A>Note: sequence extracted from NCBI backbone (NCBIP:146038)

C:Superfamily: human ubiquitin-protein ligase E2

Query Match 60.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5

DB 13 PPK 15

RESULT 18

PT0037

light harvesting complex chain III/b, photosystem I - rice (fragment)

C:Species: Oryza sativa (rice)

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993

C:Accession: PT0037; PS0205

R:Uchiyama, Y.; Tsugita, A.

submitted to JIPID, June 1991

A:Reference number: PS0189

A:Accession: PT0037

A:Molecule type: protein

A:Residues: 1-15 <UCH>

Query Match 60.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

DB 8 PPP 10

RESULT 19

JH0517

insulin-like growth factor-binding protein 4 - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 23-Mar-1995

C:Accession: JH0517

R:Coleman, M.E.; Pan, Y.C.E.; Ethernon, T.D.

Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991

A>Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth

A:Reference number: JH0515; MUID:92109718; PMID:1722398

A:Accession: JH0517

A:Molecule type: protein

A:Residues: 1-16 <COL>

A:Experimental source: serum

Query Match 60.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

DB 7 PPP 9

RESULT 20

S57991

hydroxyproline-rich protein - Sesbania rostrata (fragment)

C:Species: Sesbania rostrata

C>Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 11-Jan-2000

C:Accession: S57991

R:Goormachtig, S.; Valerio-Lepintec, M.; Szczylowski, K.; van Montagu, M.; Holsters, M.

submitted to the EMBL Data Library, March 1995

A:Description: Use of differential display to identify novel Sesbania rostrata genes enh

A:Reference number: S57991

A:Accession: S57991

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-17 <GOO>

A:Cross-references: EMBL:Z48673; NID:G899484; PID:G899485

C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 60.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

DB 10 PPP 12

RESULT 21

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C:Species: Phaseolus vulgaris (kidney bean)

C>Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998

C:Accession: S59481

R:Wojtaszek, P.; Trzethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A>Title: Specificity in the immobilisation of cell wall proteins in response to differ

A:Reference number: S59481; MUID:96011753; PMID:7548825

A:Accession: S59481

A:Molecule type: protein

A:Residues: 1-17 <WOJ>

C:Keywords: glycoprotein; hydroxyproline

F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 60.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

DB 8 PPP 10

RESULT 22

PC2280

prolylendopeptidase-inhibiting peptide - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 28-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-May-1997

C:Accession: PC2280

R:Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.

Biochem. Biophys. Res. Commun. 202, 809-815, 1994

A>Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.

A:Reference number: PC2280; MUID:94324971; PMID:8048952

A:Accession: PC2280

A:Molecule type: protein

A:Residues: 1-18 <OHM>

A:Experimental source: brain

C:Superfamily: cytoskeletal keratin

Query Match 60.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

DB 2 PPP 4

RESULT 23

A54195

Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)

C:Species: Squalus acanthias (spiny dogfish)

C>Date: 13-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 19-Apr-2002

C:Accession: A54195

R:Esmann, M.; Karlsh, S.J.; Sottrup-Jensen, L.; Marsh, D.

Biochemistry 33, 8044-8050, 1994  
A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase  
A:Reference number: A54195; MUID:94297020; PMID:8025109  
A:Accession: A54195  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <ESM>  
A:Experimental source: rectal gland  
A>Note: sequence extracted from NCBI backbone (NCBIP:149363)  
C:Keywords: hydrolase

Query Match 60.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
DB 8 PPP 10

RESULT 24  
G56819  
PS I complex subunit 6 - cucumber (fragment)  
C:Species: Cucumis sativus (cucumber)  
C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
C:Accession: G56819  
R:Tsawaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.  
Biochim. Biophys. Acta 1059, 141-148, 1991  
A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-terminal sequencing  
A:Reference number: A56819; MUID:91355209; PMID:1883835  
A:Accession: G56819  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-19 <IWA>  
A>Note: sequence extracted from NCBI backbone (NCBIP:58604)

Query Match 60.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
DB 6 PPP 8

RESULT 25  
PH1352  
IG heavy chain DJ region (clone C100-115) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1352  
R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1352  
A:Molecule type: DNA  
A:Residues: 1-19 <WAS>  
A>Note: the authors translated the stop codon for residue 2 as X  
C:Keywords: heterotetramer; immunoglobulin

Query Match 60.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
DB 7 PPP 9

RESULT\*26  
S25715  
hypothetical protein - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S25715; S21390  
R:Bowtell, D.; Fu, P.; Simon, M.; Senior, P.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6511-6515, 1992  
A:Title: Identification of murine homologues of the Drosophila Son of sevenless gene: p75<sup>src</sup>  
A:Reference number: S25714; MUID:92335328; PMID:1631150  
A:Accession: S25715  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-19 <BOW>  
A:Cross-references: EMBL:Z11578; NID:G54132; PIDN:CAA77665.1; PID:G54133  
R:Bowtell, D.D.; Fu, P.; Simon, M.A.; Senior, P.V.  
submitted to the EMBL Data Library, January 1992  
A:Description: Identification of murine homologues of the Drosophila Son of sevenless gene  
A:Reference number: S21390  
A:Accession: S21390  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-19 <BO2>  
A:Cross-references: EMBL:Z11578; NID:G54132; PIDN:CAA77665.1; PID:G54133

Query Match 60.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
DB 2 PPP 4

RESULT 27  
A33878  
myosin light chain kinase, smooth muscle - turkey (fragment)  
C:Species: Meleagris gallopavo (common turkey)  
C:Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 07-Nov-1997  
C:Accession: A33878  
R:Kebe, M.; Maruta, S.; Reardon, S.  
J. Biol. Chem. 264, 6967-6971, 1989  
A:Title: Location of the inhibitory region of smooth muscle myosin light chain kinase.  
A:Reference number: A33878; MUID:89214114; PMID:2708351  
A:Accession: A33878  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <IKE>  
A:Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat homology  
C:Keywords: smooth muscle

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
|||  
DB 8 PPP 10

RESULT 28  
A45806  
T-cell receptor beta chain C region type 1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Jul-1999  
C:Accession: A45806  
R:Dent, A.L.; Fink, P.J.; Hedrick, S.M.  
J. Immunol. 143, 322-328, 1989  
A:Title: Characterization of an alternative exon of the murine T cell receptor beta chain  
A:Reference number: A45806; MUID:89278666; PMID:2525149  
A:Accession: A45806  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-20 <DEN>  
A:Cross-references: GB:M27225; NID:G339373; PIDN:AAA61099.1; PID:G553781  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPP 3  
DB 6 PPP 8  
RESULT 29  
S06150  
Photosystem I chain III - maize (fragment)  
C:Species: Zea mays (maize)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
C:Accession: S06150  
R.Anandan, S.; Vainstein, A.; Thornber, J.P.  
FEBS Lett. 256, 150-154, 1989  
A:Title: Correlation of some published amino acid sequences for photosystem I polypeptide  
A:Reference number: S06149; MUID:90033290; PMID:2680596  
A:Accession: S06150  
A:Molecule type: protein  
A:Residues: 1-20 <ANA>  
A:Note: the authors identified this protein as light-harvesting complex I 17K protein  
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PPK 5  
DB 7 PPK 9

RESULT 30  
S03954  
acidic fibroblast growth factor - pig (fragment)  
N:Alternate names: alpha-endothelial cell growth factor  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993  
C:Accession: S03954  
R.Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Schape  
Eur. J. Biochem. 181, 67-73, 1989  
A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea  
A:Reference number: S03953; MUID:89231704; PMID:2714282  
A:Accession: S03954  
A:Molecule type: protein  
A:Residues: 1-20 <QUI>  
C:Keywords: growth factor

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PPK 5  
DB 4 PPK 6

RESULT 31  
A31516  
lectin, galactose/N-acetylgalactosamine-specific - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993  
C:Accession: A31516  
R.Ii, M.; Kawasaki, T.; Yamashina, I.  
Biochem. Biophys. Res. Commun. 155, 720-725, 1988  
A:Title: Structural similarity between the macrophage lectin specific for galactose/N-ac  
A:Reference number: A31516; MUID:88339956; PMID:3421964  
A:Accession: A31516  
A:Molecule type: protein

A:Residues: 1-20 <IIX>

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
DB 16 PPP 18

RESULT 32  
S53508  
starvation-induced ribonuclease - tomato  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
C:Accession: S53508  
R.Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.  
Plant Mol. Biol. 27, 477-485, 1995  
A:Title: cDNA structure and regulatory properties of a family of starvation-induced rib  
A:Reference number: S53506; MUID:95201242; PMID:7894013  
A:Accession: S53508  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-4 <KOE>

Query Match 40.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FP 2  
DB 1 FP 2

RESULT 33  
C41225  
copper resistance protein - Pseudomonas syringae pv. tomato (fragment)  
C:Species: Pseudomonas syringae pv. tomato  
C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
C:Accession: C41225  
R.Cha, J.S.; Cooksey, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem  
A:Reference number: A41225; MUID:92020361; PMID:1924351  
A:Accession: C41225  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <CHA>

Query Match 40.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PK 5  
DB 2 PK 3

RESULT 34  
B37988  
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
C:Species: Physarum polycephalum  
C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
R.Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-O  
J. Biol. Chem. 265, 19898-19903, 1990  
A:Title: Purification and characterization of a novel intracellular acid proteinase from  
A:Reference number: A37988; MUID:91060608; PMID:2246266  
A:Accession: B37988  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <MUR>

Query Match 40.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 ||  
 3 PP 4

Db

RESULT 35  
 A61049  
 halo-toxin - Pseudomonas syringae pv. mori  
 C:Species: Pseudomonas syringae pv. mori  
 A:Note: host mulberry tree  
 C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Jan-1997  
 C:Accession: A61049  
 R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;  
 Chem. Lett. 00, 679-680, 1989  
 A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri  
 A:Reference number: A61049  
 A:Accession: A61049  
 A:Molecule type: protein  
 A:Residues: 1-6 <KAJ>  
 A:Note: sequence confirmed by synthesis  
 C:Comment: This toxin is one of the etiological agents of halo bright disease in mulber  
 C:Keywords: toxin

Query Match 40.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2  
 ||  
 2 FP 3

Db

RESULT 36  
 B60110  
 repetitive protein antigen 61 - Trypanosoma cruzi (fragment)  
 C:Species: Trypanosoma cruzi  
 C>Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 18-Jun-1993  
 C:Accession: B60110  
 R:Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.B.  
 Infect. Immun. 57, 1959-1967, 1989  
 A:Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.  
 A:Reference number: A60110; MUID:89277508; PMID:2659529  
 A:Accession: B60110  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-6 <HOF>  
 A:Note: this is an example of a five residue tandem repeat from this protein; the actual  
 C:Keywords: tandem repeat

Query Match 40.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
 ||  
 3 PK 4

Db

RESULT 37  
 A61140  
 sperm acrosomal protein - spoonworm (Urechis caupo) (fragment)  
 C:Species: Urechis caupo  
 C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-Apr-1994  
 C:Accession: A61140  
 R:Gould, M.C.; Stephano, J.L.  
 Dev. Biol. 146, 509-518, 1991  
 A:Title: Peptides from sperm acrosomal protein that initiate egg development.  
 A:Reference number: A61140; MUID:91323672; PMID:1864468

A:Accession: A61140  
 A:Molecule type: protein  
 A:Residues: 1-6 <GOU>

Query Match 40.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
 ||  
 5 PK 6

Db

RESULT 38  
 S36662  
 demorphin (lys-7) [validated] - two-colored leaf frog  
 C:Species: Phyllomedusa bicolor (two-colored leaf frog)  
 C>Date: 10-Dec-1993 #sequence\_revision 13-Mar-1997 #text\_change 18-Aug-2000  
 C:Accession: S36662  
 R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G  
 FEBS Lett. 302, 151-154, 1992  
 A:Title: Identification and characterization of two dermorphins from skin extracts of t  
 A:Reference number: S21152; MUID:92339502; PMID:1633846  
 A:Accession: S36662  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <MIG>  
 C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
 ||  
 6 PK 7

Db

RESULT 39  
 PH1408  
 Ig heavy chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C:Accession: PH1408; PH1405  
 R:Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; T  
 J. Exp. Med. 176, 1209-1214, 1992  
 A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in  
 ia virus.

A:Reference number: PH1403; MUID:93018837; PMID:1402663  
 A:Accession: PH1408  
 A:Molecule type: DNA  
 A:Residues: 1-7 <SHI>  
 A:Experimental source: clone micro m+ 46-12-2  
 A:Accession: PH1405  
 A:Molecule type: DNA  
 A:Residues: 1-7 <SHI>  
 A:Experimental source: clone micro m+ 46-6  
 A:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2  
 ||  
 6 FP 7

Db

RESULT 40  
 A61081  
 cryptophyllin, basic - Rohde's leaf frog  
 C:Species: Phyllomedusa rohdei (Rohde's leaf frog)



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Db          ||
           2 PP 3

RESULT 46
S16324
hypothetical protein 2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C:Accession: S16324
R:Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A>Title: A novel class of plant proteins containing a homeodomain with a closely linked
A:Reference number: S16323; MUID:91266907; PMID:1675603
A:Accession: S16324
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <RUB>
A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match          40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 PP 3
Db          ||
           7 PP 8

RESULT 47
S21288
lectin - potato (fragment)
C:Species: Solanum tuberosum (potato)
C>Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
C:Accession: S21288
R:Willar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1992
A>Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
A:Reference number: S21288; MUID:92272683; PMID:1590771
A:Accession: S21288
A:Molecule type: protein
A:Residues: 1-8 <MIL>
A:Experimental source: var. Ulster Sceptre
A:Function:
A:Description: may be involved in defence mechanism of the plant
C:Keywords: hydroxyproline; lectin

Query Match          40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 PP 3
Db          ||
           7 PP 8

RESULT 48
A46306
spasmogenic toxin PNVI - spider (Phoneutria nigriventer) (fragment)
C:Species: Phoneutria nigriventer
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C:Accession: A46306
R:Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.
Toxicol. 31, 377-384, 1993
A>Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide
A:Reference number: A46306; MUID:93276438; PMID:8503129
A:Accession: A46306
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MAR>

Query Match          40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 PP 3
Db          ||
           7 PP 8

RESULT 49
S66646
cardioacceleratory protein 2b - tobacco hornworm
C:Species: Manduca sexta (tobacco hornworm)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S66646
R:Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderek, K.M.; Tublitz, N.J.
FEBS Lett. 371, 311-314, 1995
A>Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the
A:Reference number: S66646; MUID:96013159; PMID:7556618
A:Accession: S66646
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <HUE>

Query Match          40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FP 2
           ||
Db          3 FP 4

RESULT 50
A39892
P element, P cytotpe-determining - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Feb-1997
C:Accession: A39892
R:Nitaseaka, E.; Mukai, T.; Yamazaki, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987
A>Title: Repressor of P elements in Drosophila melanogaster: cytotpe determination by
A:Reference number: A39892
A:Accession: A39892
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <NIT>
C:Genetics:
A:Gene: FlyBase:P-element
A:Cross-references: FlyBase:FBgn0003055

Query Match          40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FP 2
           ||
Db          5 FP 6

RESULT 51
E47393
neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C:Accession: E47393
R:Duve, H.; Johnson, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A>Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequen
A:Reference number: A47393; MUID:93211980; PMID:8460157
A:Accession: E47393
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <DUV>
A:Experimental source: whole flies

```



A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 52

A14683

aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragment)

N;Alternate names: aspartate aminotransferase, mitochondrial

C;Species: Gallus gallus (chicken)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000

C;Accession: A14683

R;Wilson, K.J.; Hunziker, P.; Hughes, G.J.

FEBS Lett. 108, 98-102, 1979

A;Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.

A;Reference number: A14683; MUID:80092116; PMID:520566

A;Accession: A14683

A;Molecule type: protein

A;Residues: 1-8 <WIL>

C;Keywords: aminotransferase; mitochondrion

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
||  
Db 7 PK 8

## RESULT 53

A61328

trypsin (EC 3.4.21.4) precursor - minke whale (fragment)

C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)

C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999

C;Accession: A61328

R;Brictoux-Gregoire, S.; Schyns, R.; Florquin, M.; Emmens, M.; Welling, G.W.; Beintema, J.

Biochim. Biophys. Acta 386, 244-255, 1975

A;Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaenoptera acutorostrata

A;Reference number: A61328; MUID:75146765; PMID:1125273

A;Accession: A61328

A;Molecule type: protein

A;Residues: 1-8 <BRI>

C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen

F;1-8/Domain: activation peptide #status experimental <APT>

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2  
||  
Db 1 FP 2

## RESULT 54

S10783

enamelin f - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998

C;Accession: S10783

R;Strawich, E.; Glincher, M.J.

Eur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin

A;Reference number: S10780; MUID:90336641; PMID:2379503

A;Accession: S10783

A;Molecule type: protein

A;Residues: 1-8 <STR>

C;Keywords: enamel; phosphoprotein

Query Match 40.0%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 4 PP 5

## RESULT 55

A28719

thymic humoral factor gamma-2 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 18-Jun-1993

C;Accession: A28719

R;Burstein, Y.; Buchner, V.; Pecht, M.; Trainin, N.

Biochemistry 27, 4066-4071, 1988

A;Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an immunoreactive

A;Reference number: A28719; MUID:88326920; PMID:3261994

A;Accession: A28719

A;Molecule type: protein

A;Residues: 1-8 <BUR>

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
||  
Db 5 PK 6

## RESULT 56

PT0559

T-cell receptor beta chain V-D-J region (126-18H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0559

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0559

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-8 <FEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 4 PP 5

## RESULT 57

A28495

conopressin G - cone shell (Conus geographus)

N;Alternate names: Lys-conopressin-G

C;Species: Conus geographus (geography cone)

C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 25-Apr-1997

C;Accession: A28495

R;Cruz, L.J.; de Santos, V.; Zafaralla, G.C.; Ramilo, C.A.; Zeikus, R.; Gray, W.R.; Oli

J. Biol. Chem. 262, 15821-15824, 1987

A;Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from

A;Reference number: A92617; MUID:88058932; PMID:3680228

A;Accession: A28495  
A;Molecule type: protein  
A;Residues: 1-9 <CRU>  
C;Superfamily: oxytocin-neurophysin  
C;Keywords: amidated carboxyl end; venom  
F;1-6/Disulfide bonds: #status experimental  
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
||  
Db 7 PK 8

RESULT 58  
S35538  
ribosomal protein S7 - Mycobacterium intracellulare (fragment)  
C;Species: Mycobacterium intracellulare  
C;Date: 09-Dec-1993 #sequence\_revision 14-Nov-1997 #text\_change 13-Aug-1999  
C;Accession: S35538  
R;Nair, J.; Rouse, D.; Morris, S.  
Nucleic Acids Res. 21, 1039, 1993  
A;Title: Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium intracellulare  
A;Reference number: S35537; MUID:93197130; PMID:8451173  
A;Accession: S35538  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-9 <NAI>  
A;Cross-references: EMBL:L08171; NID:g149994; PIDN:AAA25376.1; PID:g551901  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1993  
C;Superfamily: Escherichia coli ribosomal protein S7  
C;Keywords: protein biosynthesis; ribosome

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
||  
Db 8 PK 9

RESULT 59  
A61230  
calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (fragment)  
N;Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin-  
C;Species: Rana pipiens (northern leopard frog)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 16-Jul-1999  
C;Accession: A61230  
R;McLeod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.  
Circ. Res. 69, 344-359, 1991  
A;Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular distribution.  
A;Reference number: A61230; MUID:91316784; PMID:1860177  
A;Accession: A61230  
A;Molecule type: protein  
A;Residues: 1-9 <MCL>  
C;Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protein  
C;Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to calsequestrin  
C;Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vivo  
C;Superfamily: calsequestrin  
C;Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; skeletal muscle

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PK 2  
||  
Db 6 PK 7

## RESULT 60

JS0302  
xenopsin-related peptide 2 - turkey  
N;Contains: xenopsin-related peptide 1  
C;Species: Meleagris gallopavo (common turkey)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 18-Aug-2000  
C;Accession: JS0302  
R;Carraway, R.E.; Cochran, D.E.; Mitra, S.P.  
Regul. Pept. 22, 303-314, 1988  
A;Title: Xenopsin-related peptide generated in avian gastric extracts.  
A;Reference number: JS0302; MUID:89042995; PMID:2460902  
A;Accession: JS0302  
A;Molecule type: protein  
A;Residues: 1-9 <CAR>

C;Comment: The peptides are present within several tissues primarily in large molecular weight fractions of turkey stomach and intestine.  
C;Superfamily: yeast coatomer complex alpha chain; WD repeat homology  
C;Keywords: neuropeptide  
F;1-9/Product: xenopsin-related peptide 2 #status experimental <XP2>  
F;2-9/Product: xenopsin-related peptide 1 #status experimental <XP1>

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
||  
Db 3 PK 4

## RESULT 61

A60320  
xenopsin-related peptide 2 - rat  
N;Contains: xenopsin-related peptide 1  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 18-Aug-2000  
C;Accession: A60320  
R;Carraway, R.E.; Mitra, S.P.; Muraki, K.  
Regul. Pept. 29, 229-239, 1990  
A;Title: Isolation and structures of xenopsin-related peptides from rat stomach, liver and spleen.  
A;Reference number: A60320; MUID:91018491; PMID:2217904  
A;Accession: A60320  
A;Molecule type: protein  
A;Residues: 1-9 <CAR>

C;Comment: The authors purified these peptides from pepsin-treated extracts of stomach, liver and spleen.  
C;Superfamily: yeast coatomer complex alpha chain; WD repeat homology  
C;Keywords: neuropeptide  
F;1-9/Product: xenopsin-related peptide 2 #status experimental <MAT1>  
F;2-9/Product: xenopsin-related peptide 1 #status experimental <MAT2>

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
||  
Db 3 PK 4

## RESULT 62

A61358  
bradykinin-like peptide I - Japanese pond frog  
C;Species: Rana nigromaculata (Japanese pond frog)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 02-Sep-2000  
C;Accession: A61358  
R;Nakajima, T.  
Chem. Pharm. Bull. 16, 769-770, 1968  
A;Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin of Japanese pond frog.  
A;Reference number: A61358; MUID:68412013; PMID:5677638  
A;Accession: A61358  
A;Status: preliminary

A:Molecule type: protein  
A:Residues: 1-9 <NAK>  
C:Superfamily: unassigned animal peptides  
C:Keywords: skin

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 63

A61057  
Thr-6 bradykinin - scoliid wasp (Colpa interrupta)  
C:Species: Colpa interrupta  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Aug-2000  
C:Accession: A61057  
R:Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.  
Comp. Biochem. Physiol. C 96, 157-162, 1990  
A:Title: Threonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynapt  
A:Reference number: A61057; MUID:91130217; PMID:1980872  
A:Accession: A61057  
A:Molecule type: protein  
A:Residues: 1-9 <PIE>  
C:Superfamily: unassigned animal peptides  
C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 64

A26744  
bradykinin-like peptide - garden dagger wasp  
N:Alternate names: Thr-6-bradykinin  
C:Species: Megascolia flavifrons (garden dagger wasp)  
C:Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 18-Aug-2000  
C:Accession: A26744  
R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.  
Toxicon 25, 527-535, 1987  
A:Title: Two kinins isolated from an extract of the venom reservoirs of the solitary was  
A:Reference number: A94322; MUID:87293024; PMID:3617088  
A:Accession: A26744  
A:Molecule type: protein  
A:Residues: 1-9 <YAS>  
C:Superfamily: unassigned animal peptides

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 65

A61363  
bradykinin - common frog  
C:Species: Rana temporaria (common frog)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
C:Accession: A61363  
R:Anastasi, A.; Erspamer, V.; Bertaccini, G.  
Comp. Biochem. Physiol. A 14, 43-52, 1965  
A:Title: Occurrence of bradykinin in the skin of Rana temporaria.

A:Reference number: A61363  
A:Accession: A61363  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <ANA>  
C:Superfamily: unassigned animal peptides  
C:Keywords: skin

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 66

A60579  
bradykinin-like peptide - slider turtle  
C:Species: Pseudemys scripta (slider)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
C:Accession: A60579  
R:Conlon, J.M.; Hicks, J.W.; Smith, D.D.  
Endocrinology 126, 985-991, 1990  
A:Title: Isolation and biological activity of a novel kinin ([Thr(6)]bradykinin) from t  
A:Reference number: A60579; MUID:90126625; PMID:2298179  
A:Accession: A60579  
A:Molecule type: protein  
A:Residues: 1-9 <CON>  
C:Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammalian  
C:Superfamily: unassigned animal peptides  
C:Keywords: plasma

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 67

B60246  
ornitho-kinin - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 18-Aug-2000  
C:Accession: B60246  
R:Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.  
Adv. Exp. Med. Biol. 247A, 359-367, 1989  
A:Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemical  
A:Reference number: A60246; MUID:90102072; PMID:2603803  
A:Accession: B60246  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <KIM>  
C:Superfamily: unassigned animal peptides

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 68

S66607  
guinoline 2-oxidoeductase beta chain - Comamonas testosteroni (fragment)  
C:Species: Comamonas testosteroni  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C;Accession: S66607

R;Schach, S.; Tehisnaka, B.; Fetzner, S.; Lingens, F.

Eur. J. Biochem. 232, 536-544, 1995

A;Title: Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from

A;Reference number: S66606; MUID:96035889; PMID:7556204

A;Accession: S66607

A;Molecule type: protein

A;Residues: 1-9 <SCH>

A;Experimental source: strain 63

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2

DB 3 FP 4

RESULT 69

B41983

ori downstream to bacterioferritin - Azotobacter vinelandii (fragment)

C;Species: Azotobacter vinelandii

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999

C;Accession: B41983

R;Crossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.

Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992

A;Title: Unification of the ferritin family of proteins.

A;Reference number: A41983; MUID:92196129; PMID:1549605

A;Accession: B41983

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid; protein

A;Residues: 1-9 <GRO>

A;Cross-references: GB:M83692; NID:G142297; PIDN:AAA22122.1; PID:G142299

A;Note: sequence extracted from NCBI backbone (NCBIP:88442)

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3

DB 3 PP 4

RESULT 70

S65433

bradykinin - horn fly (fragment)

C;Species: Haematobia irritans (horn fly)

C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997

C;Accession: S65433

R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, P.

Eur. J. Biochem. 237, 414-423, 1996

A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran

A;Reference number: S65431; MUID:96215437; PMID:8647080

A;Accession: S65433

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <WIG>

A;Note: the source is designated as Haematobia irritans exigua

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3

DB 2 PP 3

RESULT 71

B20569

serum amyloid P-component - smooth dogfish (fragment)

C;Species: Mustelus canis (smooth dogfish)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 18-Jun-1993

C;Accession: B20569; A05074

R;Robey, F.A.; Tanaka, T.; Liu, T.Y.

J. Biol. Chem. 258, 3889-3894, 1983

A;Title: Isolation and characterization of two major serum proteins from the dogfish, M

A;Reference number: A92419; MUID:83160932; PMID:6403520

A;Accession: B20569

A;Molecule type: protein

A;Residues: 1-9 <ROB>

C;Keywords: amyloid

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2

DB 2 FP 3

RESULT 72

S66635

alpha-2-macroglobulin isoform 1 - bovine (fragment)

C;Species: Bos primigenius indicus (zebu cattle)

C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C;Accession: S66635

R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottiri

FBS Lett. 372, 93-95, 1995

A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain

A;Reference number: S66634; MUID:96032553; PMID:7556651

A;Accession: S66635

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <DOL>

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2

DB 4 FP 5

RESULT 73

S66636

alpha-2-macroglobulin isoform 2 - bovine (fragment)

C;Species: Bos primigenius indicus (zebu cattle)

C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 17-Mar-1999

C;Accession: S66636

R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottiri

FBS Lett. 372, 93-95, 1995

A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain

A;Reference number: S66634; MUID:96032553; PMID:7556651

A;Accession: S66636

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <DOL>

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5

DB 5 PK 6

RESULT 74

S26508

collagen alpha 2(VI) chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Dec-1998

C;Accession: S26508

R;Jander, R.; Rautenberg, J.; Glanville, R.W.

Eur. J. Biochem. 133, 39-46, 1983

A;Title: Further characterization of the three polypeptide chains of bovine and human sh

A;Reference number: S26506; MUID:83209648; PMID:6852033

A;Accession: S26508

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <JAN>

C;Keywords: hydroxyproline

F;7/Modified site: hydroxyproline (Pro) #status experimental

Query Match

40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3

DB 6 PP 7

RESULT 75

S10784

enamelin i - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998

C;Accession: S10784

R;Strawich, E.; Glincher, M.J.

Eur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu

A;Reference number: S10780; MUID:90336641; PMID:2379503

A;Accession: S10784

A;Molecule type: protein

A;Residues: 1-9 <STR>

C;Keywords: enamel; phosphoprotein

Query Match

40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PP 2

DB 1 PP 2

Search completed: November 25, 2003, 18:28:22

Job time : 5.60106 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 2.42021 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-12

Perfect score: 5

Sequence: 1 FPPPK 5

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	60.0	10	1	TM0F_AEDAE
2	3	60.0	13	1	TY13_PHYRO
3	3	60.0	15	1	PRP_MYCBO
4	3	60.0	16	1	IBP4_PIG
5	3	60.0	17	1	APID_BOMPA
6	3	60.0	19	1	PSAE_CUCSA
7	3	60.0	20	1	PSAF_MAIZE
8	2	40.0	5	1	PAP2_PARMA
9	2	40.0	7	1	TPFY_PACDA
10	2	40.0	7	1	UF04_MOUSE
11	2	40.0	8	1	ALL5_CALVO
12	2	40.0	8	1	PPK2_PPRAM
13	2	40.0	8	1	RS7_MYCIT
14	2	40.0	9	1	CONO_CONGE
15	2	40.0	9	1	KNL3_BOWVA
16	2	40.0	9	1	SAMP_MUSCA
17	2	40.0	9	1	UPA3_HUMAN
18	2	40.0	9	1	YBFR_AZOVI
19	2	40.0	10	1	AH3_PRUSE
20	2	40.0	10	1	BPP2_BOTIN
21	2	40.0	10	1	BPP2_BOTJA
22	2	40.0	10	1	BPP8_BOTIN
23	2	40.0	10	1	BPP_VIPAS
24	2	40.0	10	1	BRK_ONCMY
25	2	40.0	10	1	PNEU_HUMAN
26	2	40.0	10	1	PNEU_RAT
27	2	40.0	10	1	PVK_LOGMI
28	2	40.0	10	1	Q20E_COMTE
29	2	40.0	10	1	RL16_ACHLA
30	2	40.0	10	1	SLAP_BACTG
31	2	40.0	10	1	UPA2_HUMAN
32	2	40.0	10	1	UPA5_HUMAN
33	2	40.0	10	1	URE3_MORMO
34	2	40.0	11	1	BPP3_BOTIN
35	2	40.0	11	1	BPP4_BOTIN
36	2	40.0	11	1	BPPB_AKHA
37	2	40.0	11	1	BPP_AKHP
38	2	40.0	11	1	BRK_MEGFL
39	2	40.0	11	1	LADD_ONCMY
40	2	40.0	11	1	MORN_HUMAN
41	2	40.0	11	1	TKN2_UPERU
42	2	40.0	11	1	TKNA_HORSE
43	2	40.0	12	1	FAR7_PENMO
44	2	40.0	12	1	FIF1_SARBU
45	2	40.0	12	1	TKN1_KASMA
46	2	40.0	12	1	TKN2_KASMA
47	2	40.0	12	1	TKN_KASSE
48	2	40.0	13	1	AH4_PRUSE
49	2	40.0	13	1	BPP1_BOTJA
50	2	40.0	13	1	BRK_FARID
51	2	40.0	13	1	MPI_MICOC
52	2	40.0	13	1	PSPB_PINPS
53	2	40.0	13	1	RS19_ASHYP
54	2	40.0	14	1	JAP1_RANJA
55	2	40.0	14	1	LPER_BACLI
56	2	40.0	14	1	PHI_PRUSE
57	2	40.0	14	1	TAT_HVIW2
58	2	40.0	14	1	TAT_HVI28
59	2	40.0	15	1	AFIL_MALPA
60	2	40.0	15	1	AH2_PRUSE
61	2	40.0	15	1	CHI1_PEA
62	2	40.0	15	1	CKA_WHEAT
63	2	40.0	15	1	CXA2_CONAL
64	2	40.0	15	1	DCMM_PSECH
65	2	40.0	15	1	FGF1_CANFA
66	2	40.0	15	1	LPF_ECOLI
67	2	40.0	15	1	MK1_PALPR
68	2	40.0	15	1	NUO8_SOLTU
69	2	40.0	15	1	PH3_PRUSE
70	2	40.0	15	1	RBS_PHYPA
71	2	40.0	15	1	SODM_STRGR
72	2	40.0	15	1	UC06_MAIZE
73	2	40.0	15	1	UC19_MAIZE
74	2	40.0	15	1	UC25_MAIZE
75	2	40.0	15	1	UE15_HORVU
76	2	40.0	15	1	UP01_METAN
77	2	40.0	16	1	AFIS_MALPA
78	2	40.0	16	1	AF2S_MALPA
79	2	40.0	16	1	AH1_PRUSE
80	2	40.0	16	1	CXA1_CONAL
81	2	40.0	16	1	CXA3_CONAL
82	2	40.0	16	1	CXAA_CONPE
83	2	40.0	16	1	CXAB_CONPE
84	2	40.0	16	1	H5_COTJA
85	2	40.0	16	1	MMEX_SOLTU
86	2	40.0	16	1	PH2_PRUSE
87	2	40.0	16	1	TRYP_FELCA
88	2	40.0	17	1	A45K_MYCBO
89	2	40.0	17	1	GSHX_PINPS
90	2	40.0	17	1	H2B3_ICTPU
91	2	40.0	17	1	SRY_URSAR
92	2	40.0	17	1	TRP2_LEUMA
93	2	40.0	17	1	VESP_VESMC
94	2	40.0	18	1	AHD2_TETPY
95	2	40.0	18	1	AL13_CARMA
96	2	40.0	18	1	D7A1_ACASC
97	2	40.0	18	1	DRPH_UCAPU
98	2	40.0	18	1	LCTN_LAMLA
99	2	40.0	19	1	ATPB_CANFA
100	2	40.0	19	1	FIBB_PIG

RESULT 1

## ALIGNMENTS

P30423 bothrops in  
P30424 bothrops in  
P1021 agkistrodon  
P04562 agkistrodon  
P12797 megascalia  
P81018 oncorhynchu  
P08163 homo sapien  
P08166 upoleleia r  
P01290 equus cabal  
P83322 penaeus mon  
P83349 sarcophaga  
P08613 kassina mac  
P08614 kassina mac  
P29611 kassina sen  
P29626 prunus sero  
P1020 bothrops ja  
P42172 parapolysia  
P81532 microplitis  
P81668 pinus pinas  
Q44592 ash yellow  
P83305 rana japoni  
Q04303 bacillus li  
P29263 prunus sero  
P12509 human immu  
P12511 human immu  
P83141 malva parvi  
P29260 prunus sero  
P21225 pisum sativ  
P58763 triticum ae  
P5640 conus aulic  
P19917 pseudomonas  
P18651 canis fami  
P03057 escherichia  
P80408 palomona pr  
P80731 solanum tub  
P29265 prunus sero  
P80657 physcomitre  
P80732 streptomyc  
P80612 zea mays (m  
P80625 zea mays (m  
P80631 zea mays (m  
P34938 hordeum vul  
P83440 metarhizium  
P83140 malva parvi  
P83142 malva parvi  
P29259 prunus sero  
P56539 conus aulic  
P56641 conus aulic  
P50984 conus penna  
P50985 conus penna  
P18638 coturnix co  
P80501 solanum tub  
P29264 prunus sero  
P81071 felis silve  
P80069 mycobacteri  
P81087 pinus pinas  
P81904 ictalurus p  
P36396 ursus arcto  
P81733 leucophaea  
P57672 vespula mac  
P35430 tetrathymena  
P81816 carcinus ma  
P83402 acanthopagr  
P08871 uca pugilat  
P83315 lama glam  
P99504 canis fami  
P14477 sus scrofa





CC -!- SIMILARITY: Contains 1 IGFBP domain.  
 CC -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.  
 DR PIR; JH0517;  
 DR InterPro; IPR000867; Insl\_gro\_fac\_dr.  
 DR InterPro; IPR000716; Thyroglobulin\_1.  
 DR PROSITE; PS00222; IGF\_BINDING; PARTIAL.  
 DR PROSITE; PS00484; THYROGLOBULIN\_1; PARTIAL.  
 KW Growth factor binding.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
 DB 7 PPP 9

## RESULT 5

APID\_BOMPA STANDARD; PRT; 17 AA.  
 AC P81464;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Apidaecin.  
 OS Bombus pascuorum (Brown bumble bee).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
 OC Apidae; Bombus.  
 OX NCBI\_TaxID=65598;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Hemolymph;  
 RX MEDLINE=97362903; PubMed=9219367;  
 RA Rees J.A., Monlatte M., Bulet P.;  
 RT "Novel antibacterial peptides isolated from a European bumblebee,  
 RT Bombus pascuorum (Hymenoptera, Apoidea).";  
 RL Insect Biochem. Mol. Biol. 27:413-422(1997).  
 CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE BACTERIA.

CC -!- INDUCTION: By bacterial infection.  
 CC InterPro; IPR004828; Apidaecin.  
 DR Pfam; PF00807; Apidaecin; 1.  
 KW Insect immunity; Antibiotic; Hemolymph.  
 SQ SEQUENCE 17 AA; 1963 MW; CDD0D02CBBC23D1 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
 DB 8 PPP 10

## RESULT 6

PSAE\_CUCSA STANDARD; PRT; 19 AA.  
 AC P42047;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Photosystem I reaction center subunit IV (PSI-E) (Photosystem I 19.5 kDa protein) (PS I subunit 6) (Fragment).  
 GN PSAB.  
 OS Cucumis sativus (Cucumber).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
 OX NCBI\_TaxID=3659;

RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cotyledon;  
 RX MEDLINE=91355209; PubMed=1883835;  
 RA Iwaseaki Y., Ishikawa H., Hibino T., Takabe T.;  
 RT "Characterization of genes that encode subunits of cucumber PS I complex by N-terminal sequencing.";  
 RL Biochim. Biophys. Acta 1059:141-148(1991).  
 CC -!- FUNCTION: Stabilizes the interaction between psac and the PSI core, assists the docking of the ferredoxin to PSI and interacts with ferredoxin-NADP oxidoreductase (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.  
 CC -!- SIMILARITY: BELONGS TO THE PSAE FAMILY.  
 CC PIR; G56819; G56819.  
 DR Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 1810 MW; A93E8BDD089F8738 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
 DB 6 PPP 8

## RESULT 7

PSAF\_MAIZE STANDARD; PRT; 20 AA.  
 ID PSFAF\_MAIZE  
 AC P13193;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Photosystem I reaction centre subunit III (Light-harvesting complex I 17 kDa protein) (PSI-F) (Fragment).  
 GN PSFAF.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.

RC STRAIN=CV, N273;  
 RX MEDLINE=90033290; PubMed=2680596;  
 RA Anandan S., Vainstein A., Thorner J.P.;  
 RT "Correlation of some published amino acid sequences for photosystem I polypeptides to a 17 kDa LHCI pigment-protein and to subunits III and IV of the core complex.";  
 RL FEBS Lett. 256:150-154(1989).  
 CC -!- FUNCTION: PROBABLY PARTICIPATES IN EFFICIENCY OF ELECTRON TRANSFER FROM PLASTOCYANIN TO P700 (OR CYTOCHROME C553 IN ALGAE AND CYANOBACTERIA). THIS PLASTOCYANIN-DOCKING PROTEIN CONTRIBUTES TO THE SPECIFIC ASSOCIATION OF PLASTOCYANIN TO PS I.

CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH LUMENAL SIDE OF THE THYLAKOID MEMBRANE.  
 CC -!- SIMILARITY: BELONGS TO THE PSAF FAMILY.  
 CC PIR; S06150; S06150.  
 DR MaizeDB; 69542; -.  
 KW Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2110 MW; F0499F98F6188997 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
 DB 7 PPP 9

```

RESULT 8
PAP2_PARMA
ID_PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moses sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE..
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P.; Primor N.; Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -|- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -|- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON TER 5 5 7769C9C8100000 CRC64;
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2
DB 4 FP 5

RESULT 9
TPFY_PACDA
ID_TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Trypophyllin-1 (pdt-1).
OS Pachymedusa dactinolor (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B.; Orr D.F.; Shaw C.;
RT "Pachymedusa dactinolor tryptophyllin-1 (pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -|- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
MOD_RES 3 3 HYDROXYLATION.

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FT MOD_RES 7 7 7772D37DC776350 CRC64;
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 2 PP 3

RESULT 10
UF04_MOUSE
ID_UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE..
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A.; Patterson R.M.; Wichter L.L.; He C.; Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON TER 7 7 68640AB77632700 CRC64;
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5
DB 1 PK 2

RESULT 11
ALL5_CALVO
ID_ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE..
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H.; Johnsen A.H.; Scott A.G.; Yu C.G.; Yagi K.J.; Tobe S.S.;
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H.; Johnsen A.H.; Scott A.G.; East P.; Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of

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RT a novel neuropeptide from the blowfly *Calliphora vomitoria*.";  
 RL J. Biol. Chem. 269:21059-21066(1994).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY  
 CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
 CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
 CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
 CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
 CC -1- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.  
 CC PIR; E47393; E47393.  
 DR PIR; E47393; E47393.  
 KW Neuropeptide; Amidation; Hydroxylation.  
 FT MOD\_RES 3 3 HYDROXYLATION (20%).  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 Db 2 PP 3  
 RESULT 12  
 PPK2\_PERAM STANDARD; PRT; 8 AA.  
 ID PPK2\_PERAM  
 AC P8262;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyroklinin-2 (Pea-PK-2) (FXPRL-amide).  
 OS Periplaneta americana (American cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 CC Blattidae; Periplaneta.  
 CC NCBI\_TaxID=6978;  
 RN [1]  
 RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RP TISSUE=Corpora cardiaca;  
 RX MEDLINE=97333923; PubMed=9210163;  
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of two pyroklinins from the  
 RL retrocerebral complex of the American cockroach.";  
 RL Peptides 18:473-478(1997).  
 RN [2]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.  
 CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro: IPR001484; Pyroklinin.  
 DR PROSITE: PS00539; PYROKININ; FALSE\_NEG.  
 KW Neuropeptide; Amidation; Pyroklinin.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 Db 2 PP 3  
 RESULT 13

RS7\_MYCIT STANDARD; PRT; 8 AA.  
 ID RS7\_MYCIT  
 AC P33564;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 30S ribosomal protein S7 (Fragment).  
 GN RPSG.  
 OS Mycobacterium intracellulare.  
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 CC NCBI\_TaxID=1767;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=93197130; PubMed=84511173;  
 RA Nair J., Rouse D.A., Morris S.L.;  
 RT "Nucleotide sequence analysis of the ribosomal S12 gene of  
 RT Mycobacterium intracellulare.";  
 RL Nucleic Acids Res. 21:1039-1039(1993).  
 CC -1- FUNCTION: One of the primary rRNA binding proteins, it binds  
 CC directly to 16S rRNA where it nucleates assembly of the head  
 CC domain of the 30S subunit. Is located at the subunit interface  
 CC close to the decoding center, probably blocks exit of the E-site  
 CC tRNA (By similarity).  
 CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9  
 CC and S11 (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.  
 CC  
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 CC  
 CC EMBL; L08171; AAA25376.1; -.  
 DR PIR; S35538; S35538.  
 DR HAMAP; MF 00480; -; 1.  
 DR InterPro: IPR000235; Ribosomal\_S7.  
 DR PROSITE: PS00052; RIBOSOMAL\_S7; PARTIAL.  
 KW Ribosomal protein; rRNA-binding; tRNA-binding.  
 FT INIT MET 0 0 BY SIMILARITY.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PK 5  
 Db 7 PK 8  
 RESULT 14  
 CONO\_CONGE STANDARD; PRT; 9 AA.  
 ID CONO\_CONGE  
 AC P05486;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lys-conopressin G.  
 OS Conus geographus (Geography cone).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 CC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 CC Neogastropoda; Conoidea; Conidae; Conus.  
 CC NCBI\_TaxID=6491;  
 RN [1]  
 RN SEQUENCE.  
 RP MEDLINE=88058932; PubMed=3680228;  
 RX Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
 RA Gray W.R., Olivera B.M.;

RT "Invertebrate vasopressin/oxytocin homologs. Characterization of  
RT peptides from *Conus geographus* and *Conus straitus* venoms.";  
RL J. Biol. Chem. 262:15821-15824 (1987).  
RN [2]

RP REVIEW.  
RX MEDLINE=89024586; PubMed=3052286;  
RT Gray W.R., Olivera B.M., Cruz L.J.;  
RT "Peptide toxins from venomous *Conus* snails.";  
RL Annu. Rev. Biochem. 57:665-700 (1988).  
CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR InterPro; IPR000981; Neutryp\_horm.

DR Pfam; PF00220; hormone4; 1.

DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.

KW Hormone; Amidation.

FT MOD RES 1 6 AMIDATION.

FT MOD RES 9 9

SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5

DB 7 PK 8

#### RESULT 15

KNL3 BOMVA

ID\_KNL3\_BOMVA STANDARD; PRT; 9 AA.

AC P83058;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE [Thr6]bradykinin.

OS Bombina variegata (Yellow-bellied toad).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.

ON NCBI\_TaxID=8348;

RN [1]

SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

CC TISSUE=Skin secretion.

CC Chen T.B., Orr D.F., Bjorson A.J., McClean S., Rao P.F., Shaw C.;

RT "Cloning and post-translational processing of frog skin kininogens.";

RL Submitted (JUL-2001) to the SWISS-PROT data bank.

CC -1- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat

arterial smooth muscle and constriction of intestinal smooth

muscle.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Skin.

CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.

KW Amphibian defense peptide; Vasodilator; Bradykinin.

SQ SEQUENCE 9 AA; 1074 MW; 3393D71A9C86777 CRC64;

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0.0%; Score 2; DB 1; Length 9;

100.0%; Pred. No. 1.3e+05;

2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

#### RESULT 16

SAMP MUSCA

ID\_SAMP\_MUSCA STANDARD; PRT; 9 AA.

AC P19055;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serum amyloid P-component (SAP) (Fragment).

RESULT 18  
 YBFR\_AZOV1 STANDARD; PRT; 9 AA.  
 AC P25875;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein in bfr 3'region (Fragment).  
 OS Azotobacter vinelandii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Azotobacter.  
 OX NCBI\_TaxID=354;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92196129; PubMed=1549605;  
 RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,  
 RA Stiefel E.I.;  
 RT "Unification of the ferritin family of proteins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).  
 CC -----  
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 CC -----  
 DR EMBL; M83692; AAA22122.1; --  
 DR PIR; B41983; B41983.  
 KW Hypothetical protein.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 DB 3 PP 4

RESULT 19  
 AH3\_PRUSE STANDARD; PRT; 10 AA.  
 AC P29261;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase  
 DE isozyme II) (AH II) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosidia I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -1- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-  
 CC glucose.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 CC EMBRYONAL TISSUES.  
 CC -1- PTM: GLYCOSYLATED.  
 KW Glycosidase; Hydrolase; Multigene family.  
 FT NON TER 10

SQL SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 DB 3 PP 4

RESULT 20  
 BPP2\_BOTIN STANDARD; PRT; 10 AA.  
 AC P30422;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -1- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; B37196; B37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1  
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 DB 9 PP 10

RESULT 21  
 BPP2\_BOTJA STANDARD; PRT; 10 AA.  
 AC P01022;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme  
 DE inhibitor V-6-II).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=72118526; PubMed=4334402;  
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,  
 RA Kocy O.;  
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops  
 RT jararaca. Isolation, elucidation of structure, and synthesis.";

RL Biochemistry 10:4033-4039(1971).  
 CC -I- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A01255; XAVI6B.  
 DR Hypotensive agent; Pyrrolidone carboxylic acid.  
 KW MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 1 1  
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 Db 9 PP 10

RESULT 22  
 BPP8\_BOTIN STANDARD; PRT; 10 AA.  
 ID BPP8\_BOTIN  
 AC P30426;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Iceland jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -I- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; H37196; H37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 1 1  
 SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 Db 9 PP 10

RESULT 23  
 BPP\_VIPAS STANDARD; PRT; 10 AA.  
 ID BPP\_VIPAS  
 AC P31351;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Vipera aspis (Aspic viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Vipera.  
 OX NCBI\_TaxID=8706;

[1]  
 RN SEQUENCE.  
 RP TISSUE=Venom;  
 RX MEDLINE=90382616; PubMed=2169439;  
 RA Komori Y., Sugihara H.;  
 RT "Characterization of a new inhibitor for angiotensin converting  
 RT enzyme from the venom of Vipera aspis aspis.";  
 RL Int. J. Biochem. 22:767-771(1990).  
 CC -I- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A60377; XASNPC.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 1 1  
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 Db 9 PP 10

RESULT 24  
 BRK\_ONCMY STANDARD; PRT; 10 AA.  
 ID BRK\_ONCMY  
 AC Q9PRZ1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lysyl-bradykinin-like.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=94039817; PubMed=8224232;  
 RX Conlon J.M., Olson K.R.;  
 RT "Purification of a vasoactive peptide related to lysyl-bradykinin from  
 RT trout plasma.";  
 RL FEBS Lett. 334:75-78(1993).  
 CC -I- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR  
 CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- TISSUE SPECIFICITY: Plasma.  
 CC -I- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
 DR PIR; S39030; S39030.  
 KW Bradykinin; Vasodilator.  
 SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 Db 3 PP 4

RESULT 25  
 PNEU\_HUMAN STANDARD; PRT; 10 AA.  
 ID PNEU\_HUMAN  
 AC P22103;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pneumadin (PNM).  
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
[1]
RP SEQUENCE.
RC TISSUE=Lung; PubMed=2274681;
RX MEDLINE=91110910; Mir S.A., Kapoor R., Kumar M.A.;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
CC PIR; B33143; B33143.
DR GO; GO:0030103; P:vasopressin secretion; NAS.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5
DB 4 PK 5

RESULT 26
PNEU_RAT STANDARD; PRT; 10 AA.
AC P21956;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
[1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
CC PIR; A33143; A33143.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5
DB 4 PK 5

RESULT 27
PVK_LOCMI STANDARD; PRT; 10 AA.
AC P83382;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Periviscerokinin (Iom-PVK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OX Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OX Acridoidea; Acrididae; Oedipodinae; Locusta.
RN NCBI_TaxID=7004;
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RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=21896327; PubMed=11897380;
RA Predel R., Gaede G.;
RT "Identification of the abundant neuropeptide from abdominal
perisymphathetic organs of locusts.";
RL Peptides 23:621-627(2002).
CC -!- FUNCTION: Myotropic peptide; increases the frequency of
contraction of the heart and stimulates amplitude and tonus of the
foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2
DB 7 FP 8

RESULT 28
Q2OB_COMTE STANDARD; PRT; 10 AA.
AC P80465;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
RN NCBI_TaxID=285;
[1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisaka B., Fetzner S., Lingsen F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
dioxygenase from Comamonas testosteroni 63. The first two enzymes in
quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
1,2-DIHYDROQUINOLINE.
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first
step.
CC -!- SUBUNIT: HETEROXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
TWO GAMMA CHAINS (PROBABLE).
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1241 MW; C2E2C25DD9DC769 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2
DB 3 FP 4

RESULT 29
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```
RL16 ACHLA
ID RL16 ACHLA STANDARD; PRT; 10 AA.
AC P29221;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 50S ribosomal protein L16 (Fragment).
GN RPLP
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92210505; PubMed=1556079;
RA Lim P.O., Sears B.B.;
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like
RT organism and Acholeplasma laidlawii deduced from two ribosomal protein
RT gene sequences.";
RL J. Bacteriol. 174:2606-2611(1992).
CC -|- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
CC LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER
CC (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M74771; AAA21914.1; -.
DR PIR; F41839; F41839.
DR InterPro; IPR000114; Ribosomal L16.
DR PROSITE; PS00586; RIBOSOMAL_L16_1; PARTIAL.
DR PROSITE; PS00701; RIBOSOMAL_L16_2; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 10
FT SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5
DB 4 PK 5

RESULT 30
SLAP_BACTG
ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckeivich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL J. Bacteriol. 171:6556-6667(1989).
CC -|- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -|- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH OBLIQUE (p2) SYMMETRY.
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DR PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2
DB 5 FP 6

RESULT 31
UPA2_HUMAN
ID UPA2_HUMAN STANDARD; PRT; 10 AA.
AC P30088;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.4, ITS MW IS: 49 kDa.
DR SWISS-2DPAGE; P30088; HUMAN.
DT NON_TER 1
FT UNSURE 6
FT NON_TER 10
FT SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 5 PP 6

RESULT 32
UPA5_HUMAN
ID UPA5_HUMAN STANDARD; PRT; 10 AA.
AC P30051;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
```



CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.  
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF  
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT  
 CC PROTEIN  
 DR SWISS-2DPAGE; P30091; HUMAN.  
 FT NON\_TER 1 1  
 FT VARIANT 9 9 G -> Y.  
 FT /FTID=VAR\_000002.  
 FT NON\_TER 10 10  
 FT SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
 DB 4 PK 5

RESULT 33  
 URE3\_MORMO STANDARD; PRT; 10 AA.  
 AC P17339;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea  
 DE amidohydrolase) (Fragment).  
 GN UREA.  
 OS Morganella morganii (Proteus morganii).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Morganella.  
 OX NCB\_TaxID=582;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90264298; PubMed=2345135;  
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
 RT "Morganella morganii urease: purification, characterization, and  
 RT isolation of gene sequences.";  
 RL J. Bacteriol. 172:3073-3080(1990).  
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.  
 DR PIR; C35389; C35389.  
 KW Hydrolase.  
 FT NON\_TER 10 10  
 FT SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 DB 5 PP 6

RESULT 34  
 BPP3\_BOTIN STANDARD; PRT; 11 AA.  
 AC P30423;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCB\_TaxID=8723;

RN [1]  
 RP SEQUENCE.  
 RC TISUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; C37196; C37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 DB 4 PP 5

RESULT 35  
 BPP4\_BOTIN STANDARD; PRT; 11 AA.  
 AC P30424;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCB\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; D37196; D37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 DB 4 PP 5

RESULT 36  
 BPPB\_AKHA STANDARD; PRT; 11 AA.  
 ID BPPB\_AKHA  
 AC P01021;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydus blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii."
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.8e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 PP 3
DB 4 PP 5

RESULT 37
BPP AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydus.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RA "Structure-function studies on the bradykinin potentiating peptide
RA from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.8e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 PP 3
DB 4 PP 5

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RESULT 38
BRK MEGFL STANDARD; PRT; 11 AA.
ID P12797;
AC 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
DE peptide ([Thr6]bradykinin)].
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Scolioidea;
OC Scolidae; Megascolia.
OX NCBI_TaxID=7437;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088;
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT "Two kinins isolated from an extract of the venom reservoirs of the
RT solitary wasp Megascolia flavifrons."
RL Toxicon 25:527-535(1987).
RN [2]
RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yashuara T., Mantel P.;
RT "Two kinins isolated from the venom of Megascolia flavifrons."
RL Toxicon 26:34-34(1988).
CC -|- FUNCTION: Both proteins have bradykinin-like, although lower
CC activities (e.g. smooth muscle contraction).
CC -|- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -|- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; B26744; B26744.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.8e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 PP 3
DB 2 PP 3

RESULT 39
LADD ONCMY STANDARD; PRT; 11 AA.
ID P81018;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ladderlectin (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293418; PubMed=9149391;
RA Jensen L.E., Thiel S., Petersen T.E., Jensenius J.C.;
RT "A rainbow trout lectin with multimeric structure."
RL Comp. Biochem. Physiol. 116B:385-390(1997).
CC -|- FUNCTION: LECTIN THAT BINDS SEPHAROSE.
CC -|- COFACTOR: CALCIUM IS ESSENTIAL FOR SEPHAROSE BINDING.
CC -|- SUBUNIT: MULTIMERIC.
KW Lectin; Calcium.
FT NON TER 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

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Query Match 40.0%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 DB 9 PP 10

RESULT 40  
 MORN\_HUMAN STANDARD; PRT; 11 AA.  
 AC P01163;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Morphogenic neuroepitope (Head activator) (HA).  
 OS Homo sapiens (Human).  
 OS Rattus norvegicus (Rat).  
 OS Bos taurus (Bovine).  
 OS Anthopleura elegantissima (Sea anemone), and  
 OS Hydra attenuata (Hydra) (Hydra vulgaris).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Human, Rat, and Bovine;  
 RX MEDLINE=82035850; PubMed=7290191;  
 RA Bodenmuller H., Schaller H.C.;  
 RT "Conserved amino acid sequence of a neuroepitope, the head activator,  
 RT from coelenterates to humans.";  
 RL Nature 293:579-580(1981).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=A. elegantissima, and H. attenuata;  
 RA Schaller H.C., Bodenmuller H.;  
 RT "Isolation and amino acid sequence of a morphogenetic peptide from  
 RT hydra.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).  
 RN [3]  
 RP SYNTHESIS.  
 RX MEDLINE=82050803; PubMed=7297679;  
 RA Birt C., Zachmann B., Bodenmuller H., Schaller H.C.;  
 RT "Synthesis of a new neuroepitope, the head activator from hydra.";  
 RL FEBS Lett. 131:317-321(1981).  
 RN [4]  
 RP FUNCTION.  
 RX MEDLINE=90059923; PubMed=2583101;  
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;  
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells  
 RT in the G2/mitosis transition.";  
 RL EMBO J. 8:3311-3318(1989).  
 CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS  
 CC IN THE G2/MITOSIS TRANSITION.  
 CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA  
 CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED  
 CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS  
 CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.  
 DR PIR; A01427; YHRT.  
 DR PIR; A93900; VHXA.  
 DR PIR; B01427; YHHA.  
 DR PIR; B93900; YHJFHY.  
 DR PIR; C01427; YHBO.  
 DR GK; P01163; -.  
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 DB 9 PP 10

RESULT 40  
 MORN\_HUMAN STANDARD; PRT; 11 AA.  
 AC P01163;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Morphogenic neuroepitope (Head activator) (HA).  
 OS Homo sapiens (Human).  
 OS Rattus norvegicus (Rat).  
 OS Bos taurus (Bovine).  
 OS Anthopleura elegantissima (Sea anemone), and  
 OS Hydra attenuata (Hydra) (Hydra vulgaris).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Human, Rat, and Bovine;  
 RX MEDLINE=82035850; PubMed=7290191;  
 RA Bodenmuller H., Schaller H.C.;  
 RT "Conserved amino acid sequence of a neuroepitope, the head activator,  
 RT from coelenterates to humans.";  
 RL Nature 293:579-580(1981).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=A. elegantissima, and H. attenuata;  
 RA Schaller H.C., Bodenmuller H.;  
 RT "Isolation and amino acid sequence of a morphogenetic peptide from  
 RT hydra.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).  
 RN [3]  
 RP SYNTHESIS.  
 RX MEDLINE=82050803; PubMed=7297679;  
 RA Birt C., Zachmann B., Bodenmuller H., Schaller H.C.;  
 RT "Synthesis of a new neuroepitope, the head activator from hydra.";  
 RL FEBS Lett. 131:317-321(1981).  
 RN [4]  
 RP FUNCTION.  
 RX MEDLINE=90059923; PubMed=2583101;  
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;  
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells  
 RT in the G2/mitosis transition.";  
 RL EMBO J. 8:3311-3318(1989).  
 CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS  
 CC IN THE G2/MITOSIS TRANSITION.  
 CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA  
 CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED  
 CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS  
 CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.  
 DR PIR; A01427; YHRT.  
 DR PIR; A93900; VHXA.  
 DR PIR; B01427; YHHA.  
 DR PIR; B93900; YHJFHY.  
 DR PIR; C01427; YHBO.  
 DR GK; P01163; -.  
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

QY 2 PP 3  
 DB 2 PP 3

RESULT 41  
 TKN2\_UPERU STANDARD; PRT; 11 AA.  
 AC P08616;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Rugosaupolein II ((Ly85,Thr6]physalaemin).  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 NCBI\_TaxID=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=80223080; PubMed=7389029;  
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;  
 RT "Physalaemin- and bombesin-like peptides in the skin of the  
 RT Australian leptodactylid frog Uperoleia rugosa.";  
 RL Chem. Pharm. Bull. 28:689-695(1980).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR InterPro; IPR002040; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 11 11 AMIDATION.  
 FT SEQUENCE 11 AA; 1270 MW; 3293693B59D1A327 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
 DB 4 PK 5

RESULT 42  
 TKN2\_HORSE STANDARD; PRT; 11 AA.  
 AC P01230;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 GN TAC1 OR NK1A OR TAC2 OR NKA.  
 OS Equus caballus (Horse), and  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 NCBI\_TaxID=9796, 10141;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Horse;  
 RA Studer R.O., Trzeciak A., Lergier W.;  
 RT "Isolation and amino-acid sequence of substance P from horse  
 RT intestine.";  
 RL Helv. Chim. Acta 56:860-866(1973).

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RN [2]
RP SEQUENCE.
RC SPECIES=C porcellus;
RX MEDLINE=90044685; PubMed=2478925;
RA Murphy R.;
RT "Primary amino acid sequence of guinea-pig substance P.";
RL Neuropeptides 14:105-110(1989).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A01558; SPHO.
DR PIR; A06554; A60554.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1349 MW; 3E757E3C9D6C6C7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5
DB 2 PK 3

RESULT 43
FAR7_PENMO
ID FAR7_PENMO STANDARD; PRT; 12 AA.
AC P8332;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE FMRFamide-like neuropeptide FLP7 (GYRKPFPNGSIF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OC NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkarn C., Longyant S.,
RA Chaiwisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1381.4; METHOD=WALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1393 MW; 31209192EF49D777 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 5 PP 6

RESULT 44

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FIF1_SARBU
ID FIF1_SARBU STANDARD; PRT; 12 AA.
AC P8339;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-Firamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OC NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meeusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 2 PP 3

RESULT 45
TKN1_KASMA
ID TKN1_KASMA STANDARD; PRT; 12 AA.
AC P08613;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hylambates kassinin ((Glu2,Pro3,kassinin)).
OS Kassinina maculata (African thacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OC NCBI_TaxID=8414;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus.";
RL Biomed. Res. 2:613-617(1981).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S10059; S10059.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.

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KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03; 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 4 PK 5
DB 3 PK 4

RESULT 46
TKN2 KASMA
ID TKN2 KASMA STANDARD; PRT; 12 AA.
AC P08614;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hylambatin.
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8414;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Yasuhara T.; Nakajima T.; Erspamer G.F.; Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus.";
RL Biomed. Res. 2:613-617(1981).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07436; S07436.
DE InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03; 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 PP 3
DB 2 PP 3

RESULT 47
TKN KASSE
ID TKN KASSE STANDARD; PRT; 12 AA.
AC P08611;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin.
OS Kassina senegalensis (Senegal running frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8415;
RN [1]
RP SEQUENCE.

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RC TISSUE=Skin secretion;
RX MEDLINE=77246385; PubMed=891753;
RA Anastasi A.; Montecucchi P.C.; Erspamer V.; Visser J.;
RT "Amino acid composition and sequence of kassinin, a tachykinin
RT dodecapeptide from the skin of the African frog Kassina
RT senegalensis.";
RL Experientia 33:857-858(1977).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07206; S07206.
DR PDB; 1MYU; 16-OCT-02.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW 3D-structure.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1336 MW; 91757AB89DD6DAB5 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03; 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 4 PK 5
DB 3 PK 4

RESULT 48
AH4 PRUSE
ID AH4 PRUSE STANDARD; PRT; 13 AA.
AC P29262;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II' (EC 3.2.1.117) (Amygdalin hydrolase
DE Isozyme II') (AH II') (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P.; Swain E.; Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1417 MW; F7CC4FA321B9D051 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.3e+03; 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 PP 3
DB 3 PP 4

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RESULT 49
BPPI_BOTJA STANDARD; PRT; 13 AA.
ID BPPI_BOTJA
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3.1 (13A) (Angiotensin-converting
enzyme inhibitor V-9).
OS Bothrops jararaca (Jararaca), and
OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OC NCBI_TaxID=8724, 8723;
RN [1]
RP SEQUENCE.
RC SPECIES=B.jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT Jararaca. Isolation, elucidation of structure, and synthesis.",
RL Biochemistry 10:4033-4039(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=B.insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.",
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01253; XAVI9B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

-Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 12 PP 13

RESULT 50
BRK_PARID STANDARD; PRT; 13 AA.
ID BRK_PARID
AC P42717;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Waspkinin.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apoecrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Parapolybia.
OC NCBI_TaxID=31921;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Toki T., Yasuhara T., Nakajima T.;
RT "Isolation and sequential analysis of peptides on the venom sac of
RT Parapolybia indica.",
RL Eisei Dobutei 39:105-111(1988).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
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CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Bradykinin; Vasodilator; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1573 MW; 2673CB3D83ECC867 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 5 PP 6

RESULT 51
MPI_MICOC STANDARD; PRT; 13 AA.
ID MPI_MICOC
AC P81532;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE MPI protein (Fragments).
OS Microplitis ocellatae (Braconid wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;
OC Braconidae; Microgastrinae; Microplitis.
OC NCBI_TaxID=99573;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RA Takahashi M., Quicke D.L.J.;
RL Submitted (OCT-1998) to the SWISS-PROT data bank.
CC -1- TISSUE SPECIFICITY: SALIVARY GLANDS.
CC -1- DEVELOPMENTAL STAGE: LARVAL.
CC NON_CONS 10 11
FT SEQUENCE 13 AA; 1595 MW; 0C0786C9DD82777B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 7 PP 8

RESULT 52
PSBP_PINPS STANDARD; PRT; 13 AA.
ID PSBP_PINPS
AC P81668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OEE2) (23 kDa subunit of oxygen
DE evolving system of photosystem II) (Fragment).
DE PSBP.
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OC NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.",
RL Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF PHOTOSYSTEM II.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
CC WITH THE PHOTOSYSTEM II COMPLEX (BY SIMILARITY).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
```

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CC (SPOT N179) IS: 5.9, ITS MW IS: 22 kDa.
CC -!- SIMILARITY: BELONGS TO THE PSBP FAMILY.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
FT NON TER 13
SQ SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5
DB 12 PK 13

RESULT 53
RS19 ASHYP STANDARD; PRT; 13 AA.
AC Q4452;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS OR RPS19.
OS Ash yellow phycoplasm.
OC Bacteria; Firmicutes; Mollicutes; Achleoplasmatales;
OC Achleoplasmataceae; Phycoplasmata.
OX NCBI_TaxID=35780;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmata): a basis for
RT their classification."
RL J. Bacteriol. 176:5244-5254 (1994).
CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; L26999; AAA83936.1; -
DR HAMAP; MF_00531; -; 1.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON TER 1
SQ SEQUENCE 13 AA; 1433 MW; CECA010B84E6305D CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5
DB 11 PK 12

RESULT 54
JAPI_RANJA STANDARD; PRT; 14 AA.
AC P83305;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Japonicin-1.
OS Rana japonica (Japanese reddish frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=21826910; PubMed=11835990;
RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;
RT "Antimicrobial peptides with atypical structural features from the
RT skin of the Japanese brown frog Rana japonica."
RL Peptides 23:419-425 (2002).
CC -!- FUNCTION: Antibacterial activity against the Gram-negative
CC bacterium E.coli and the Gram-positive bacterium S.aureus.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=2715.4; METHOD=Electrospray.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 8 14 BY SIMILARITY.
SQ SEQUENCE 14 AA; 1650 MW; C278625186DBE0B9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FP 2
DB 2 FP 3

RESULT 55
LPER_BACLI STANDARD; PRT; 14 AA.
ID LPER_BACLI
AC Q04303;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Erythromycin resistance leader peptide (23S rRNA methylase leader
DE peptide).
OS Bacillus licheniformis, and
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402, 1392;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.licheniformis; PubMed=6429477;
RX MEDLINE=84245158; PubMed=6429477;
RA Gryczan T., Israeli-Reches M., del Bue M., Dubnau D.;
RT "DNA sequence and regulation of ermD, a macrolide-lincosamide-
RT streptogramin B resistance element from Bacillus licheniformis."
RL Mol. Gen. Genet. 194:349-356 (1984).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.licheniformis; STRAIN=EMR-1;
RX MEDLINE=91310580; PubMed=1713206;
RA Kwak J.-K., Choi E.-C., Weisblum B.;
RT "Transcriptional attenuation control of ermK, a
RT macrolide-lincosamide-streptogramin B resistance determinant from
RT Bacillus licheniformis."
RL J. Bacteriol. 173:4725-4735 (1991).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.anthraxis; STRAIN=590;
RX MEDLINE=9323276; PubMed=8473865;
RA Kim H.-S., Choi E.-C., Kim B.-K.;
RT "A macrolide-lincosamide-streptogramin B resistance determinant from
RT Bacillus anthracis 590: cloning and expression of ermJ."
RL J. Gen. Microbiol. 139:601-607 (1993).
CC -!- FUNCTION: THIS PEPTIDE IS INVOLVED IN THE CONTROL MECHANISM OF
CC THE SYNTHESIS OF THE MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B
CC RESISTANCE PROTEIN. IT ACTS AS A TRANSCRIPTIONAL ATTENUATOR.
CC
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DR EMBL; L08389; AAA22596.1; -

DR EMBL; M29832; AAA22598.1; -

DR FIR; A42473; A42473.

KW Antibiotic resistance; Leader peptide.

SQ SEQUENCE 14 AA; 1732 MW; 5D1138B59F32ED07 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 4.6e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FP 2

DB 9 FP 10

RESULT 56

ID PH1 PRUSE STANDARD; PRT; 14 AA.

AC P29263;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Prunasin beta-glucosidase I (EC 3.2.1.118) (Prunasin hydrolase

isozyme I) (pH I) (Fragment).

OS Prunus serotina (Black cherry).

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

CC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

OX NCBI\_TaxID=23207;

RN [1]

RP SEQUENCE.

RC TISSUE=Seed;

RA Li C.P., Swain E., Poulton J.E.;

RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.;"

RL Plant Physiol. 100:282-290(1992).

CC -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-

CC glucose.

CC -1- SUBUNIT: Monomer.

CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS

CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON

CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR

CC EMBRYONAL TISSUES.

CC -1- PTM: GLYCOSYLATED.

KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.

FT NON TER 14 "14

SQ SEQUENCE 14 AA; 1575 MW; FB3D7F4FB90CA9CA CRC64;

Query Match

Best Local Similarity 40.0%; Score 2; DB 1; Length 14;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PP 3

DB 3 PP 4

RESULT 57

TAT HV1W2

ID TAT HV1W2 STANDARD; PRT; 14 AA.

AC P12509;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE TAT protein (Transactivating regulatory protein) (Fragment).

GN TAT.

OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).

CC Viruses; Retrovirdae; Lentivirus.

OX NCBI\_TaxID=11705;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86235450; PubMed=3012778;

RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,

RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;

RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or

at risk for AIDS.;"

RL Science 232:1548-1553(1986).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND

CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

CC PROMOTER.

CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.

CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM

CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO

CC WAS PERINATALLY INFECTED BY HER MOTHER.

CC -----

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CC -----

CC EMBL; M12507; AAB12991.1; -

DR HIV; M12507; TAT5WMJ2.

KW Transcription regulation; Activator; RNA-binding; Nuclear protein;

KW AIDS.

FT NON TER 1

SQ SEQUENCE 14 AA; 1467 MW; 37CC737BFEF67AA8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 4.6e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PK 5

DB 12 PK 13

RESULT 58

TAT HV1Z8

ID TAT HV1Z8 STANDARD; PRT; 14 AA.

AC P12511;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE TAT protein (Transactivating regulatory protein) (Fragment).

GN TAT.

OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).

CC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11681;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88281278; PubMed=3395517;

RA Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,

RA Gallo R.C.;

RT "Nucleotide sequence analysis of the env gene of a new Zairian

isolate of HIV-1.;"

RL AIDS Res. Hum. Retroviruses 4:165-173(1988).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND

CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

CC PROMOTER.

CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.

CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD

CC ZAIREAN MALE.

CC -----

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CC -----  
 DR EMBL; J03653; AAA44685.1; -  
 DR HIV; J03653; TAT5JY1.  
 KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
 KW AIDS.  
 FT NON TER 1 1  
 SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5  
 DB 12 PK 13

RESULT 59  
 AFIL\_MALPA STANDARD; PRT; 15 AA.  
 AC P83141;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antifungal protein 1 large subunit (CW-1) (Fragment).  
 OS Malva parviflora (little mallow) (Cheeseweed).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.  
 OC NCBI\_TaxID=145753;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Seed;  
 RX MEDLINE=20568734; PubMed=11118343;  
 RA Wang X., Bunkers G.J.;  
 RT "Potent heterologous antifungal proteins from cheeseweed (Malva  
 RL parviflora).";  
 RL Biochem. Biophys. Res. Commun. 279:669-673(2000).  
 CC -!- FUNCTION: Possesses antifungal activity against P.infestans but  
 CC not F-graminearum.  
 CC -!- SUBUNIT: Heterodimer of a large and a small subunit.  
 CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
 CC concentration.  
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.  
 KW Fungicide; Antibiotic.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1793 MW; 2CB3079F53CC70F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 DB 8 PP 9

RESULT 60  
 AH2\_PRUSE STANDARD; PRT; 15 AA.  
 AC P29260;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Amygdalin beta-glucosidase I' (EC 3.2.1.117) (Amygdalin hydrolase  
 DE isozyme I') (AH 1') (Fragment).  
 OS Prunus serotina (black cherry).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-  
 CC glucose.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 CC EMBRYONAL TISSUES.  
 CC -!- PTM: GLYCOSYLATED.  
 KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1650 MW; F7CC4FA321E12EC4 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 DB 5 PP 6

RESULT 61  
 CH11\_PEA STANDARD; PRT; 15 AA.  
 ID CH11\_PEA  
 AC P21225;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endochitinase A1 (EC 3.2.1.14) (Fragment).  
 OS Pisum sativum (Garden pea).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 OC NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Birte; TISSUE=Leaf;  
 RA Vad K., Mikkelsen J.D., Collinge D.B.;  
 RT "Induction, purification and characterization of chitinase isolated  
 RT from pea leaves inoculated with Ascochyta pisi.";  
 RL Planta 184:24-29(1991).  
 CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN  
 CC CONTAINING FUNGAL PATHOGENS.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-  
 CC acetyl-D-glucosamine polymers of chitin.  
 CC -!- INDUCTION: By infection with the fungal pathogen Ascochyta pisi.  
 CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO  
 CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL  
 CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL  
 CC HYDROLASES).  
 CC InterPro; IPR001002; Chitin binding 1.  
 DR InterPro; IPR000726; Glyco\_Hydro\_19\_  
 DR PROSITE; PS00026; CHITIN\_BINDING; PARTIAL.  
 DR PROSITE; PS00773; CHITINASE\_19\_1; PARTIAL.  
 DR PROSITE; PS00774; CHITINASE\_19\_2; PARTIAL.  
 KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding;  
 KW Multigene family.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1438 MW; 23355ED6B11E869 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 PP 3
Db      12 PP 13

RESULT 62
CKX_WHEAT
ID_CKX_WHEAT STANDARD; PRT; 15 AA.
AC P58763;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytokinin oxidase (EC 1.4.3.-) (CKO) (CKX) (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=cv. Samantha;
RX MEDLINE=21099312; PubMed=11168382;
RA Galuszka P., Frebort I., Sebel M., Sauer P., Jacobsen S., Pec P.;
RT "Cytokinin oxidase or dehydrogenase? Mechanism of cytokinin
degradation in cereals.";
RL Eur. J. Biochem. 268:450-461(2001).
CC -1- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-
substituted adenine derivatives that are plant hormones, where the
substituent is an isopentenyl group. Substrate preference is 2-(2-
hydroxyethylamino)-9-methyl-N(6)-isopentenyladenine >>
isopentenyladenine > cis-zeatin = isopentenyladenosine = zeatin >>
zeatin riboside.
CC -1- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-enyl)adenine + H(2)O +
O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).
CC -1- COFACTOR: FAD.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC -1- MISCELLANEOUS: Optimal pH is 6.5.
CC -1- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
oxidoreductase family.
KW Oxidoreductase; Flavoprotein; FAD.
FT UNSURE 1 1
FT NON TER 13 15
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1709 MW; 85B589BD53FCEDEF CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PK 5
Db      3 PK 4

RESULT 63
CKX2_CONAL
ID_CKX2_CONAL STANDARD; PRT; 15 AA.
AC P56640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-conotoxin AuiB.
OS Conus aulicus (Coutt cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99003392; PubMed=9786965;

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RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
RA Olivera B.M., McIntosh J.M.;
RT "Alpha-conotoxin AuiB selectively blocks alpha3 beta4 nicotinic
acetylcholine receptors and nicotine-evoked norepinephrine release.";
RL J. Neurosci. 18:8571-8579(1998).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=20187585; PubMed=10722709;
RA Cho J.H., Mok K.H., Olivera B.M., McIntosh J.M., Park K.H., Han K.H.;
RT "Nuclear magnetic resonance solution conformation of alpha-conotoxin
AuiB, an alpha(3)beta(4) subtype-selective neuronal nicotinic
acetylcholine receptor antagonist.";
RL J. Biol. Chem. 275:8680-8685(2000).
CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAChR) and thus
inhibit them. This peptide blocks mammalian nicotinic
acetylcholine receptors composed of alpha-3/beta-4 subunits.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1572.5; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
FAMILY.
CC PDB; 1DG2; 25-FEB-00.
DR PDB; 1MXN; 30-DEC-02.
DR PDB; 1MXP; 30-DEC-02.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 15
FT MOD RES 15 15
SQ SEQUENCE 15 AA; 1578 MW; 84EFE95FDC700155 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PP 3
Db      6 PP 7

RESULT 64
CKWM_PSECH
ID_CKWM_PSECH STANDARD; PRT; 15 AA.
AC P19917;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase medium'chain (EC 1.2.99.2) (CO
dehydrogenase subunit M) (CO-DH M) (Fragment).
GN CUTM.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
dioxide.
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
acceptor.
CC -1- COFACTOR: FAD.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
SMALL.
DR PIR; P0143; P0143.
KW Oxidoreductase; Flavoprotein; FAD.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1815 MW; 90508CF93E739D63 CRC64;

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Query Match      40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PK 5
DB      12 PK 13

RESULT 65
FGF1_CANPA
ID_FGF1_CANPA  STANDARD;          PRT;      15 AA.
AC  P18651;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Heparin-binding growth factor 1 (HBGF-1) (Acidic fibroblast growth
DE  factor) (AFGF) (Alpha-endothelial cell growth factor) (fragment).
GN  FGF1 OR FGF-1.
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX  NCBI_TaxID=9615;
RN  [1]
RX  MEDLINE=89231704; PubMed=2714282;
RA  Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethe N.,
RA  Sharma H.S., Schaper W.;
RT  "Isolation of heparin-binding growth factors from bovine, porcine and
RT  canine hearts.";
RL  Eur. J. Biochem. 181:67-73(1989).
CC  -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
CC  IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
CC  VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CC  CONCENTRATION OF THESE 2 GROWTH FACTORS.
CC  -!- SUBUNIT: Monomer.
CC  -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
CC  THAN DOES BFGF.
CC  -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
DR  PIR; S03955; S03955.
DR  InterPro; IPR002348; IL1_HBGF.
DR  PROSITE; PS00247; HBGF_FGF; PARTIAL.
KW  Growth factor; Mitogen; Angiogenesis; Heparin-binding.
FT  NON TER      15
SQ  SEQUENCE 15 AA; 1732 MW; 53CC9A3CADDDDAA1 CRC64;

Query Match      40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PK 5
DB      5 PK 6

RESULT 66
LFP_ECOLI
ID_LFP_ECOLI  STANDARD;          PRT;      15 AA.
AC  P03057;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  The leader peptide (Attenuator peptide).
DE  PHEL OR PHEAE OR B2598 OR SF2658.
GN  Escherichia coli, and
OS  Shigella flexneri.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Escherichia.
OX  NCBI_TaxID=562, 623;
RN  [1]
RX  SEQUENCE FROM N.A.
SPECIES=E.coli;

Query Match      40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FP 2
DB      14 FP 15

Query Match      40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FP 2
DB      14 FP 15

RESULT 67
MKI_PALPR
ID_MKI_PALPR  STANDARD;          PRT;      15 AA.
AC  P80408;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Metalnikowin I.
OS  Palomona prasina (Green shield bug).

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RX  MEDLINE=79033820; PubMed=360214;
RA  Zurawski G., Brown K., Killingly D., Yanofsky C.;
RT  "Nucleotide sequence of the leader region of the phenylalanine operon
RT  of Escherichia coli.";
RN  Proc. Natl. Acad. Sci. U.S.A. 75:4271-4275(1978).
RL  [2]
RP  SEQUENCE FROM N.A.
RC  SPECIES=E.coli;
RX  MEDLINE=91072346; PubMed=2254312;
RA  Gavini N., Davidson B.E.;
RT  "pheA mutants of Escherichia coli have a defective pheA attenuator.";
RL  J. Biol. Chem. 265:21532-21535(1990).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  SPECIES=E.coli; STRAIN=K12 / MG1655;
RX  MEDLINE=97426617; PubMed=9278503;
RA  Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA  Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA  Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA  Mau B., Shao Y.;
RT  "The complete genome sequence of Escherichia coli K-12.";
RL  Science 277:1453-1474(1997).
RN  [4]
RP  SEQUENCE FROM N.A.
RC  SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX  MEDLINE=22272406; PubMed=12384590;
RA  Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA  Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA  Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA  Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA  Yu J.;
RT  "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT  through comparison with genomes of Escherichia coli K12 and O157.";
RL  Nucleic Acids Res. 30:4432-4441(2002).
CC  -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC  OF PHENYLALANINE.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; V00314; CAA23600.1; -.
DR  EMBL; M10431; AAA24329.1; -.
DR  EMBL; M58024; AAA62783.1; -.
DR  EMBL; AE000346; AAC75647.1; -.
DR  EMBL; AE015281; AAN44154.1; -.
DR  PIR; A03593; LFECP.
DR  EcoGene; EG11271; pheJ.
KW  Leader peptide; Complete proteome.
SQ  SEQUENCE 15 AA; 1924 MW; CFE14AE3BFF935E0 CRC64;

Query Match      40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FP 2
DB      14 FP 15

Query Match      40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FP 2
DB      14 FP 15

RESULT 67
MKI_PALPR
ID_MKI_PALPR  STANDARD;          PRT;      15 AA.
AC  P80408;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Metalnikowin I.
OS  Palomona prasina (Green shield bug).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 OC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;  
 OC Palomena.  
 OX NCBI\_TaxID=55431;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
 RT "The inducible antibacterial peptides of the hemipteran insect  
 RT Palomena prasina: identification of a unique family of proline-rich  
 RT peptides and of a novel insect defensin.";  
 RL J. Insect Physiol. 42:81-89(1996).  
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE  
 CC BACTERIA.  
 CC -1- INDUCTION: By bacterial infection.  
 CC Antibiotic; Insect immunity.  
 KW SEQUENCE 15 AA; 1838 MW; 21407B663CE46299 CRC64;  
 SQ  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 DB 12 PP 13  
 RESULT 68  
 NU08\_SOLTU STANDARD; PRT; 15 AA.  
 ID NU08\_SOLTU STANDARD; PRT; 15 AA.  
 AC P80731;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 12 kDa subunit (EC 1.6.5.3)  
 DE (EC 1.6.99.3) (Complex I-12KD) (CI-12KD) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Bintje; TISSUE=Tuber;  
 RA Herz U., Grohmann L.;  
 RL Submitted (DEC-1996) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
 CC TO BE UBIQUINONE.  
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -1- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
 CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER  
 CC MEMBRANE.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1668 MW; EDC87B30AD155854 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 DB 10 PP 11  
 RESULT 69  
 PH3\_PRUSE STANDARD; PRT; 15 AA.  
 ID PH3\_PRUSE STANDARD; PRT; 15 AA.  
 AC CP29265;  
 DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase  
 DE Isozyme IIB) (PH IIB) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eursidae I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-  
 CC glucose.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 CC EMBRYONAL TISSUES.  
 CC -1- PTM: GLYCOSYLATED.  
 KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1635 MW; 4F3D7F4FB90CFE4C CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 DB 4 PP 5  
 RESULT 70  
 RBS\_PHYPA STANDARD; PRT; 15 AA.  
 ID RBS\_PHYPA STANDARD; PRT; 15 AA.  
 AC P80657;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ribulose biphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO  
 DE small subunit) (Fragment).  
 DE RBCS.  
 GN RBCS.  
 OS Physcomitrella patens (Moss).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.  
 OX NCBI\_TaxID=3218;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Protonema;  
 RX MEDLINE=97275459; PubMed=9129336;  
 RA Kasten B., Buck F., Nuske J., Reski R.;  
 RT "Cytokinin affects nuclear- and plastome-encoded energy-converting  
 RT plastid enzymes.";  
 RL Planta 201:261-272(1997).  
 CC -1- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-  
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic  
 CC carbon dioxide fixation, as well as the oxidative fragmentation of  
 CC the pentose substrate in the photorespiration process. Both  
 CC reactions occur simultaneously and in competition at the same  
 CC active site.  
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) = 2 3-  
 CC phospho-D-glycerate.  
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) =  
 CC 3-phospho-D-glycerate + 2-phosphoglycolate.  
 CC -1- SUBUNIT: 8 large chains + 8 small chains.  
 CC -1- SUBUNIT: 8 large chains + 8 small chains.  
 CC -1- SUBCELLULAR LOCATION: Chloroplast.  
 CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.  
 KW Photosynthesis; Carbon dioxide fixation; Photorespiration;  
 KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast.

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FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1801 MW; 28B9E7AC4AED6CE0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 5
DB 10 PK 11

RESULT 71
SODM_STRGR STANDARD; PRT; 15 AA.
ID SODM_STRGR 15 AA.
AC P80733;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).
GN SOD2.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE.
RC STRAIN=KCTC 9006; PubMed=8900409;
RX MEDLINE=97056064;
RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
Kang S.-O.;
RT "Unique isozymes of superoxide dismutase in Streptomyces griseus.";
RL Arch. Biochem. Biophys. 334:341-348 (1996).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Iron and zinc.
CC -1- SUBUNIT: Tetramer.
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
DR PROSITE: PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Iron; Zinc.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 8 PP 9

RESULT 72
UC06_MAIZE STANDARD; PRT; 15 AA.
ID UC06_MAIZE 15 AA.
AC P80612;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 1131)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;

us-09-641-801-12.oligo.rsp

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RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.8, ITS MW IS: 71.0 kDa.
DR Maize-2DPAGE; P80612; COLEOPTILE.
DR MaizeDB; 123930; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1390 MW; 7005E22830F23D61 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 5 PP 6

RESULT 73
UC19_MAIZE STANDARD; PRT; 15 AA.
ID UC19_MAIZE 15 AA.
AC P80625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 406)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.6, ITS MW IS: 18.4 kDa.
DR Maize-2DPAGE; P80625; COLEOPTILE.
DR MaizeDB; 123951; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1672 MW; 1CF69D4DA8737F9D CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 12 PP 13

RESULT 74
UC25_MAIZE STANDARD; PRT; 15 AA.
ID UC25_MAIZE 15 AA.
AC P80631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```

OC PACCAD clade: Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE..  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9, ITS MW IS: 31.6 kDa.  
 DR Maize-2DPAGE; P80631, COLEOPTILE.  
 DR MaizeDB; 123957; ..  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1580 MW; 83C54CF0CE1614D0 CRC64;  
  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 FP 2  
 Db ||  
 9 FP 10  
  
 RESULT 75  
 UE15\_HORVU  
 ID UE15\_HORVU STANDARD; PRT; 15 AA.  
 AC P34978;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown endosperm protein E-15/E-16/E-17 (fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE..  
 RC STRAIN=CV, H354-295-2-5; TISSUE=Starchy endosperm;  
 RX MEDLINE=94170739; PubMed=8125056;  
 RA Flengrød R.;  
 RT "Separation of acidic barley endosperm proteins by two-dimensional  
 RT electrophoresis.";  
 RL Electrophoresis 14:1060-1066(1993).  
 CC -!- TISSUE SPECIFICITY: STARCHY ENDOSPERM.  
 CC -!- DEVELOPMENTAL STAGE: GERMINATION.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1735 MW; 2669969DDEAFD97F CRC64;  
  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 PP 3  
 Db ||  
 7 PP 8

Search completed: November 25, 2003, 18:17:32  
 Job time : 3.42021 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 12.0479 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-12

Perfect score: 5

Sequence: 1 FPPPK 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL 23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	80.0	10	12	Q9Q0W9
2	4	80.0	10	12	Q8JV70
3	4	80.0	10	12	Q9Q0W1
4	4	80.0	10	12	Q8JV68
5	4	80.0	10	12	Q9Q0V9
6	4	80.0	10	12	Q9Q0W7
7	4	80.0	10	12	Q8JV66
8	4	80.0	10	12	Q9Q0V7
9	4	80.0	10	12	Q8JV82
10	4	80.0	10	12	Q8JV76
11	4	80.0	10	12	Q8JV74
12	4	80.0	10	12	Q9Q0W5
13	4	80.0	10	12	Q9Q0X3
14	4	80.0	10	12	Q9Q0X5
15	4	80.0	10	12	Q9Q0W3
16	4	80.0	10	12	Q8JV80

Q9Q0X1	polyomaviru	10	12	Q9Q0X1
Q9Q0X9	polyomaviru	10	12	Q9Q0X9
Q8V72	polyomaviru	10	12	Q8V72
P82439	nicotiana t	15	10	P82439
Q9T87	bos taurus	20	6	Q9T87
P92214	amblyopyrum	7	8	P92214
P92393	hordeum vul	7	8	P92393
P92403	lophopyrum	7	8	P92403
P92427	peridictyon	7	8	P92427
P92430	aequilops ta	7	8	P92430
P92221	bromus iner	7	8	P92221
P92425	pseudoroegn	7	8	P92425
P92381	hordeum bra	7	8	P92381
P92387	hentardia p	7	8	P92387
P92210	agropyron c	7	8	P92210
P92440	thincopyrum	7	8	P92440
P92218	australopyr	7	8	P92218
P92390	heteranthel	7	8	P92390
P92372	haynaldia v	7	8	P92372
P92442	taeniatheru	7	8	P92442
P92226	crithopsis	7	8	P92226
P92385	hordeum mar	7	8	P92385
P92421	psathyrosta	7	8	P92421
P81898	prunus dulc	10	10	P81898
Q8JV84	polyomaviru	10	12	Q8JV84
Q8JV78	polyomaviru	10	12	Q8JV78
Q60761	homo sapien	11	4	Q60761
Q26092	pisaster oc	11	5	Q26092
P82436	nicotiana t	11	10	P82436
Q9B249	homo sapien	12	4	Q9B249
O61574	ostertagia	12	5	O61574
Q93X21	zea mays (m	12	10	Q93X21
Q945C1	crypthecodi	13	10	Q945C1
Q8V3U6	tomato yell	14	12	Q8V3U6
Q15344	homo sapien	15	4	Q15344
Q9T45	bos taurus	15	6	Q9T45
Q9T14	bos taurus	15	6	Q9T14
Q9BGG8	sorex arane	16	6	Q9BGG8
Q9TQZ7	bos taurus	16	6	Q9TQZ7
Q9TRD1	bos taurus	16	6	Q9TRD1
Q9TR22	bos taurus	17	6	Q9TR22
Q49225	glycine max	17	10	Q49225
Q41400	sebania ro	17	10	Q41400
Q9UCT9	homo sapien	18	4	Q9UCT9
Q8NFB4	homo sapien	18	4	Q8NFB4
Q8SKY0	cuscuta ref	18	8	Q8SKY0
Q8FT3	gallus gall	18	13	Q8FT3
P82110	rana pipien	18	13	P82110
Q9UCL3	homo sapien	19	4	Q9UCL3
O63058	lathraea cl	19	8	O63058
P82941	hordeum vul	19	10	P82941
Q85B2	mus musculu	19	11	Q85B2
Q78351	human immun	19	15	Q78351
Q905G4	human immun	19	15	Q905G4
Q90514	human immun	19	15	Q90514
Q9R509	bacillus al	20	2	Q9R509
Q9R4D7	escherichia	20	2	Q9R4D7
Q9TNG4	homo sapien	20	7	Q9TNG4
Q9E8R2	solanum tub	20	10	Q9E8R2
Q912B4	human eryth	20	12	Q912B4
Q9Z1E9	neisseria m	8	2	Q9Z1E9
O19957	gossypium h	8	8	O19957
O19961	gossypium d	8	8	O19961
O19958	gossypium b	8	8	O19958
O19960	gossypium m	8	8	O19960
O19959	gossypium t	8	8	O19959
O19956	gossypium a	8	8	O19956
Q42507	tritium ae	8	10	Q42507
Q91205	hepatitis c	8	12	Q91205
Q99193	pseudomonas	9	2	Q99193
Q9UCS8	homo sapien	9	4	Q9UCS8
Q16605	homo sapien	9	4	Q16605
Q9TWW0	anthopleura	9	5	Q9TWW0

Q28121 bos taurus  
 Q95ds5 magnolia sa  
 Q95ds0 manglietia  
 Q9tnf0 magnolia tr  
 Q95ds1 manglietia  
 Q9tnes9 magnolia co  
 Q9tnf4 magnolia sc  
 Q9tbl7 magnolia si  
 Q9tnes0 michelia co  
 Q9tnes4 magnolia sa  
 Q95ds6 magnolia w1

90 2 40.0 9 6 Q28121  
 91 2 40.0 9 8 Q95DS5  
 92 2 40.0 9 8 Q95DS0  
 93 2 40.0 9 8 Q9TNF0  
 94 2 40.0 9 8 Q95DS1  
 95 2 40.0 9 8 Q9TNES9  
 96 2 40.0 9 8 Q9TNF4  
 97 2 40.0 9 8 Q9THL7  
 98 2 40.0 9 8 Q9TNE0  
 99 2 40.0 9 8 Q9TNE4  
 100 2 40.0 9 8 Q95DS6

## ALIGNMENTS

RESULT 1  
 Q9Q0W9 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0W9;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UMEA3;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245 (2000).  
 DR EMBL; AF119350; AAF24106.1; --  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 Db 7 PPPK 10

RESULT 2  
 Q8JV70 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV70;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA 5;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA."  
 RL J. Virol. 75:10290-10299 (2001).  
 DR EMBL; AF304367; AAM97804.1; --  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPPK 5  
 Db 7 PPPK 10

RESULT 3  
 Q9Q0W1 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0W1;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CSFB;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245 (2000).  
 DR EMBL; AF119354; AAF24114.1; --  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 Db 7 PPPK 10

RESULT 4  
 Q8JV68 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV68;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA 6;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA."  
 RL J. Virol. 75:10290-10299 (2001).  
 DR EMBL; AF304388; AAM97806.1; --  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 Db 7 PPPK 10



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RESULT 5
Q9QOV9 PRELIMINARY; PRT; 10 AA.
AC Q9QOV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFE;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119355; AAF24116.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 7 PPPK 10

RESULT 6
Q9QOW7 PRELIMINARY; PRT; 10 AA.
AC Q9QOW7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NANCY2;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119351; AAF24108.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 7 PPPK 10

RESULT 7
Q8JV66 PRELIMINARY; PRT; 10 AA.
AC Q8JV66;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.

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OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSF K;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to vitions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304389; AAW97808.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 7 PPPK 10

RESULT 8
Q9QOV7 PRELIMINARY; PRT; 10 AA.
AC Q9QOV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFJ;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119356; AAF24118.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 7 PPPK 10

RESULT 9
Q8JV82 PRELIMINARY; PRT; 10 AA.
AC Q8JV82;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;

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RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF303944; AAM97792.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 DB 7 PPPK 10

## RESULT 10

Q8JV76 ID Q8JV76 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV76;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA2;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF303947; AAM97798.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 DB 7 PPPK 10

## RESULT 11

Q8JV74 ID Q8JV74 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV74;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA3;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF303948; AAM97800.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 DB 7 PPPK 10

## RESULT 12

Q9QW5 ID Q9QW5 PRELIMINARY; PRT; 10 AA.  
 AC Q9QW5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RETORIA3;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage.";  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119352; AAF24110.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 DB 7 PPPK 10

## RESULT 13

Q9QX3 ID Q9QX3 PRELIMINARY; PRT; 10 AA.  
 AC Q9QX3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCN8;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage.";  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119348; AAF24102.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 DB 7 PPPK 10

```

RESULT 14
Q900X5 ID Q900X5 PRELIMINARY; PRT; 10 AA.
AC Q900X5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
population by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119347; AAF24100.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 7 PPPK 10

RESULT 15
Q900W3 ID Q900W3 PRELIMINARY; PRT; 10 AA.
AC Q900W3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIA1;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
population by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119353; AAF24112.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 7 PPPK 10

RESULT 16
Q8JV80 ID Q8JV80 PRELIMINARY; PRT; 10 AA.
AC Q8JV80;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.

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OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303945; AAM97794.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 7 PPPK 10

RESULT 17
Q900X1 ID Q900X1 PRELIMINARY; PRT; 10 AA.
AC Q900X1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN15;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
population by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119349; AAF24104.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 7 PPPK 10

RESULT 18
Q900X9 ID Q900X9 PRELIMINARY; PRT; 10 AA.
AC Q900X9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN0;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human

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RT populations by studying their presence in urban sewage.";  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR ENBL; AF119345; AAF24096.1; -.  
 FT NON\_TER 1 1

SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5  
 DB 7 PPK 10

## RESULT 19

Q8JUV72 PRELIMINARY; PRT; 10 AA.

AC Q8JUV72; DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP - SEQUENCE FROM N.A.  
 RC STRAIN=USA 4;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR ENBL; AF304386; AAM97802.1; -.  
 FT NON\_TER 1 1

SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 80.0%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5  
 DB 7 PPK 10

## RESULT 20

P82439 PRELIMINARY; PRT; 15 AA.

AC P82439; DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 200 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.";  
 RL Planta 200:0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -4- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall; Hydroxylation.  
 FT MOD\_RES 6 6 HYDROXYLATION.

FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1870 MW; 3E1E05A20A3C5681 CRC64;

Query Match 80.0%; Score 4; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5  
 DB 8 PPK 11

## RESULT 21

Q9TR87 PRELIMINARY; PRT; 20 AA.

AC Q9TR87; DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE PA28 protein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=55081084; PubMed=7989312;  
 RA Mott J.D., Pramanik B.C., Moomaw C.R., Afendis S.J., DeMartino G.N.,  
 RA Slaughter C.A.;  
 RT "PA28, an activator of the 20 S proteasome, is composed of two  
 RT nonidentical but homologous subunits.";  
 RL J. Biol. Chem. 269:31466-31471(1994).  
 SQ SEQUENCE 20 AA; 2205 MW; 15DA3F0E8D20C2E9 CRC64;

Query Match 80.0%; Score 4; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5  
 DB 10 PPK 13

## RESULT 22

P92214 PRELIMINARY; PRT; 7 AA.

AC P92214; DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein L1 (Fragment).  
 GN RPS11.  
 OS Amblyopyrum muticum.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Amblyopyrum.  
 OX NCBI\_TaxID=4595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5572; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR ENBL; Z77756; CAB01346.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;

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Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
   |||
Db 1 PPK 3

RESULT 23
P92393 ID P92393 PRELIMINARY; PRT; 7 AA.
AC P92393;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11..
OS Hordeum vulgare (Barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H3139; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77764; CAB01370.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
   |||
Db 1 PPK 3

RESULT 24
P92403 ID P92403 PRELIMINARY; PRT; 7 AA.
AC P92403;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Lophopyrum.
OX NCBI_TaxID=4588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6692; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77743; CAB01307.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Best Local Similarity 100.0%; Score 3; DB 8; Length 7;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
   |||
Db 1 PPK 3

RESULT 25
P92427 ID P92427 PRELIMINARY; PRT; 7 AA.
AC P92427;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein (Fragment).
GN RPS11.
OS Peridictyon sanctum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Peridictyon.
OX NCBI_TaxID=37683;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5575; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77749; CAB01325.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
   |||
Db 1 PPK 3

RESULT 26
P92430 ID P92430 PRELIMINARY; PRT; 7 AA.
AC P92430;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Aegilops tauschii (Aegilops squarrosa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6668; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77758; CAB01352.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

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SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;
Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
Db 1 PPK 3

RESULT 27
P92221 PRELIMINARY; PRT; 7 AA.
AC P92221;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Bromus inermis (Smooth brome grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Bromae; Bromus.
OC NCBI_TaxID=15371;
OX [1]_TaxID=15371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OSA414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01355.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
Db 1 PPK 3

RESULT 28
P92425 PRELIMINARY; PRT; 7 AA.
AC P92425;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Pseudoroegneria.
OX NCBI_TaxID=4604;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H9082; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77744; CAB01310.1; -.
KW Chloroplast.
FT NON TER

SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
Db 1 PPK 3

RESULT 29
P92381 PRELIMINARY; PRT; 7 AA.
AC P92381;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum brachyantherum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=52712;
RN [1]_TaxID=52712;
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77761; CAB01361.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
Db 1 PPK 3

RESULT 30
P92387 PRELIMINARY; PRT; 7 AA.
AC P92387;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Henrardia persica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Henrardia.
OX NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01322.1; -.
KW Chloroplast.

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FT  NON_TER      1      1
SQ  SEQUENCE     7 AA; 894 MW; 6734140333277700 CRC64;

Query Match      60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PPK 5
    |||
Db  1 PPK 3

RESULT 31
P92210
ID  P92210      PRELIMINARY;      PRT;      7 AA.
AC  P92210;
DT  01-MAY-1997 (TrEMBLrel. 03, Created)
DT  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Ribosomal protein 11 (Fragment).
GN  RPS11.
OS  Agropyron cristatum.
OG  Chloroplast.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC  Triticeae; Agropyron.
OX  NCBI_TaxID=4593;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=H4349; TISSUE=Leaf;
RX  MEDLINE=97271648; PubMed=9126564;
RA  Petersen G., Seberg O.;
RT  "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL  Mol. Phylogenet. Evol. 7:217-230(1997).
DR  EMBL; Z77771; CAB01391.1; -.
KW  Chloroplast.
FT  NON_TER      1
SQ  SEQUENCE     7 AA; 894 MW; 6734140333277700 CRC64;

Query Match      60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PPK 5
    |||
Db  1 PPK 3

RESULT 32
P92440
ID  P92440      PRELIMINARY;      PRT;      7 AA.
AC  P92440;
DT  01-MAY-1997 (TrEMBLrel. 03, Created)
DT  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Ribosomal protein 11 (Fragment).
GN  RPS11.
OS  Thinopyrum bessarabicum.
OG  Chloroplast.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC  Triticeae; Thinopyrum.
OX  NCBI_TaxID=4601;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=H6725; TISSUE=Leaf;
RX  MEDLINE=97271648; PubMed=9126564;
RA  Petersen G., Seberg O.;
RT  "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL  Mol. Phylogenet. Evol. 7:217-230(1997).
DR  EMBL; Z77769; CAB01385.1; -.

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KW  Chloroplast.
FT  NON_TER      1
SQ  SEQUENCE     7 AA; 894 MW; 6734140333277700 CRC64;

Query Match      60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PPK 5
    |||
Db  1 PPK 3

RESULT 33
P92218
ID  P92218      PRELIMINARY;      PRT;      7 AA.
AC  P92218;
DT  01-MAY-1997 (TrEMBLrel. 03, Created)
DT  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Ribosomal protein 11 (Fragment).
GN  RPS11.
OS  Australopyrum retrofractum.
OG  Chloroplast.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC  Triticeae; Australopyrum.
OX  NCBI_TaxID=4597;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=H6723; TISSUE=Leaf;
RX  MEDLINE=97271648; PubMed=9126564;
RA  Petersen G., Seberg O.;
RT  "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL  Mol. Phylogenet. Evol. 7:217-230(1997).
DR  EMBL; Z77767; CAB01379.1; -.
KW  Chloroplast.
FT  NON_TER      1
SQ  SEQUENCE     7 AA; 894 MW; 6734140333277700 CRC64;

Query Match      60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PPK 5
    |||
Db  1 PPK 3

RESULT 34
P92390
ID  P92390      PRELIMINARY;      PRT;      7 AA.
AC  P92390;
DT  01-MAY-1997 (TrEMBLrel. 03, Created)
DT  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Ribosomal protein 11 (Fragment).
GN  RPS11.
OS  Heterantheium piliferum.
OG  Chloroplast.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC  Triticeae; Heterantheium.
OX  NCBI_TaxID=37679;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=H5557; TISSUE=Leaf;
RX  MEDLINE=97271648; PubMed=9126564;
RA  Petersen G., Seberg O.;
RT  "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RL  Mol. Phylogenet. Evol. 7:217-230(1997).

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DR EMBL; Z77750; CAB01328.1; -.
KW Chloroplast. 1 1
FT NON_TER 7 AA; 894 MW; 6734140333277700 CRC64;
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
Db |||
1 PPK 3

RESULT 35
P92372 PRELIMINARY; PRT; 7 AA.
AC P92372;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein l1 (Fragment).
GN RPS11.
OS Haynaldia villosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Haynaldia.
OX NCBI_TaxID=40247;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5561; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77741; CAB01301.1; -.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
Db |||
1 PPK 3

RESULT 36
P92442 PRELIMINARY; PRT; 7 AA.
AC P92442;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein l1 (Fragment).
GN RPS11.
OS Taeniatherum caput-medusae (Medusahead).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Taeniatherum.
OX NCBI_TaxID=37687;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H10254; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
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RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77760; CAB01358.1; -.
KW Chloroplast. 1 1
FT NON_TER 7 AA; 894 MW; 6734140333277700 CRC64;
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
Db |||
1 PPK 3

RESULT 37
P92226 PRELIMINARY; PRT; 7 AA.
AC P92226;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein l1 (Fragment).
GN RPS11.
OS Crithopsis delileana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Crithopsis.
OX NCBI_TaxID=37674;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5558; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77751; CAB01331.1; -.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
Db |||
1 PPK 3

RESULT 38
P92385 PRELIMINARY; PRT; 7 AA.
AC P92385;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ribosomal protein l1 (Fragment).
GN RPS11.
OS Hordeum marinum (Seaside barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H299, and H801; TISSUE=Leaf;
RX Petersen G., Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z77763; CAB01367.1; -.
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DR EMBL; Z77762; CAB01364.1; -.
KW Chloroplast; Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
   |||
Db 1 PPK 3

RESULT 39
P92421 PRELIMINARY; PRT; 7 AA.
AC P92421; P92419;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Peathyrostachys fragilis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Psathyrostachys.
OX NCBI_TaxID=37729;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4372, and H917; TISSUE=Leaf;
RA Petersen G., Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z77753; CAB01337.1; -.
DR EMBL; Z77752; CAB01334.1; -.
KW Chloroplast; Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
   |||
Db 1 PPK 3

RESULT 40
P81898 PRELIMINARY; PRT; 10 AA.
AC P81898;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, small
chain (Subunit B) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-
glycosidase) (N-glycanase) (Fragment).
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Euphorbia; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RX PubMed=9523720;
RA Altmann F., Paschinger K., Dalik T., Voraue K.;
RT "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine
amidase A and its N-glycans.";
RL Eur. J. Biochem. 252:118-123 (1998).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4- (ACETYL-BETA-D-
GLUCOSAMINYL) ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
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CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
CC CONTAINING AN ASPARTIC RESIDUE.
CC -!- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
CC -!- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
CC DEGLYCOSYLATION.
CC -!- MASS SPECTROMETRY: MW=21247; METHOD=MALDI.
KW Hydrolase; Glycoprotein.
FT NON TER 10
SQ SEQUENCE 10 AA; 1149 MW; 863278CAA1E73771 CRC64;

Query Match 60.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPK 3
   |||
Db 8 PPK 10

RESULT 41
Q8JV84 PRELIMINARY; PRT; 10 AA.
AC Q8JV84;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GL;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Was S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303943; AAM97790.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1180 MW; 4CD6A97AF1A32763 CRC64;

Query Match 60.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
   |||
Db 8 PPK 10

RESULT 42
Q8JV78 PRELIMINARY; PRT; 10 AA.
AC Q8JV78;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USAI;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Was S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
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DR EMBL; AF303946; AAM97796.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1183 MW; 4CD6A96731A32763 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 12; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
DB 8 PPK 10

RESULT 43
O60761 PRELIMINARY; PRT; 11 AA.
AC O60761;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NPT-1 protein (Fragment).
DE NPT-1.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98207118; PubMed=9545579;
RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,
RA Tatum S., Morita K., Takeda E.;
RT "Characterization of the 5' flanking region of the human NPT-1
RT Na+/phosphate cotransporter gene.";
RL Biochim. Biophys. Acta 1396:267-272(1998).
DR EMBL; D83236; JBA25645.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 4; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
DB 8 PPK 10

RESULT 44
Q26092 PRELIMINARY; PRT; 11 AA.
AC Q26092;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Sea Star histone H2B gene 5' region (Fragment).
DE Pisaster ochraceus (Sea star).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asterozoa; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OX NCBI_TaxID=7612;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Sperm;
RC Howell A.M., Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;
RA "Organization and Unusual Expression of Histone Genes in the Sea Star
RT Pisaster ochraceus.";
RL J. Mol. Evol. 25:29-36(1987).
DR EMBL; X05619; CAA29106.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1128 MW; 5173974A3865BDD3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 5; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 PPK 5
DB 2 PPK 4

RESULT 45
P82436 PRELIMINARY; PRT; 11 AA.
AC P82436;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 65 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
[1]
RN SEQUENCE.
RP STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000);
CC -!- SUBCELLULAR LOCATION: CELL WALL.
KW Cell wall.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1068 MW; 34FD25CCB325B867 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 10; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 4
DB 2 PPK 4

RESULT 46
Q9BZ49 PRELIMINARY; PRT; 12 AA.
AC Q9BZ49;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Glycophorin C (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,
RA Zimmerman P.A.;
RT "The association of the glycoporphin C exon 3 deletion with
RT ovalocytosis and malaria susceptibility in the Wosera, Papua New
RT Guinea.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342984; AAK01459.1; -.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 4; Length 12;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 4
DB 2 PPK 4

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Db 9 PPP 11

## RESULT 47

O61574 PRELIMINARY; PRT; 12 AA.

AC O61574; (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hypothetical 1.4 kDa protein (Fragment).

OS Ostertagia ostertagi.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;

OC Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.

OC NCBI\_TaxID=6317;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20233682; PubMed=10769181;

RA Moore J., Tetley L., Devaney E.;

RT "Identification of abundant mRNAs from the third stage larvae of the

RT parasitic nematode, *Ostertagia ostertagi*."

RL Biochem. J. 347:763-770(2000).

DR EMBL; AF052049; AAC06297.1; --

KW Hypothetical protein.

FT NON\_TER 12 12

SQ SEQUENCE 12 AA; 1369 MW; C6FF867C1CA776C6 CRC64;

Query Match 60.0%; Score 3; DB 5; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5

Db 2 PPK 4

## RESULT 48

Q93X21 PRELIMINARY; PRT; 12 AA.

AC Q93X21; (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Polyubiquitin homolog (Fragment).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OC NCBI\_TaxID=4577;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. INRA 258; TISSUE=Leaf;

RX MEDLINE=96236829; PubMed=8680303;

RA Diderjean L., Frendo P., Nasser W., Genot G., Marivet J., Burkard G.;

RT "Heavy-metal-responsive genes in maize: identification and comparison

RT of their expression upon various forms of abiotic stress."

RL Planta 199:1-8(1996).

DR EMBL; S82313; AAB47175.1; --

FT NON\_TER 1 1

SQ SEQUENCE 12 AA; 1277 MW; 250D2D2F6F340DD8 CRC64;

Query Match 60.0%; Score 3; DB 10; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

Db 2 PPP 4

## RESULT 49

Q945C1 PRELIMINARY; PRT; 13 AA.

ID Q945C1

AC Q945C1;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Dip5 protein (Fragment).

OS Cryptocodinium cohnii (Dinoflagellate).

OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptecodiniaceae;

OC Cryptocodinium.

OC NCBI\_TaxID=2866;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21428164; PubMed=11545436;

RA Guillebaud D., Berelle E., Bhaud Y., Moreau H.;

RT "Role of nuclear WW domains and proline-rich proteins in

RT dinoflagellate transcription."

RL Protist 152:127-138(2001).

DR EMBL; AF417570; AALJ5908.1; --

FT NON\_TER 13 13

SQ SEQUENCE 13 AA; 1225 MW; 322FA05EE70CB327 CRC64;

Query Match 60.0%; Score 3; DB 10; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5

Db 5 PPK 7

## RESULT 50

Q8V3U6 PRELIMINARY; PRT; 14 AA.

AC Q8V3U6;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Tomato yellow leaf curl virus TYLCV/TYLCV recombinant isolate Spain

DE ES42199 C1 (Fragment).

OS Tomato yellow leaf curl virus (TYLCV).

OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OC NCBI\_TaxID=10832;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TYLCV/TYLCV recombinant isolate Spain ES42199;

RA Monci F., Navas-Castillo J., Moriones E.;

RT "Evidence of the occurrence of a natural recombinant between Tomato

RT yellow leaf curl virus."

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF401478; AAL59158.1; --

FT NON\_TER 14 14

SQ SEQUENCE 14 AA; 1710 MW; D296A16BF41A7FD9 CRC64;

Query Match 60.0%; Score 3; DB 12; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5

Db 3 PPK 5

## RESULT 51

Q15344 PRELIMINARY; PRT; 15 AA.

ID Q15344

AC Q15344;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

DE Aml1 protein (Fragment).

GN AML1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96226397; PubMed=8634147;
RA Levanon D., Bernstein Y., Negreanu V., Ghozi M.C., Bar-Am I.,
RA Aloya R., Goldenberg D., Lotem J., Groner Y.;
RT "A large variety of alternatively spliced and differentially expressed
RT mRNAs are encoded by the human acute myeloid leukemia gene AML1.";
RL DNA Cell Biol. 15:175-185(1996).
DR EMBL; X90980; CAA62467.2; -.
FT NON TER 1
FT NON TER 15
SQ SEQUENCE 15 AA; 1931 MW; 228A48EBEB675423 CRC64;

Query Match 60.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPP 3
Db 7 FPP 9

RESULT 52
Q9TR45 PRELIMINARY; PRT; 15 AA.
AC Q9TR45;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Amphoterin homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RX MEDLINE=96029671; PubMed=7592757;
RA Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,
RA Nagashima M., Lundh E.R., Vijay S., Nitecki D.;
RT "The receptor for advanced glycation end products (RAGE) is a cellular
RT binding site for amphoterin. Mediation of neurite outgrowth and co-
RT expression of rage and amphoterin in the developing nervous system.";
RL J. Biol. Chem. 270:25752-25761(1995).
SQ SEQUENCE 15 AA; 1757 MW; 390B9679501CE020 CRC64;

Query Match 60.0%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
Db 5 PPK 7

RESULT 53
Q9TR14 PRELIMINARY; PRT; 15 AA.
AC Q9TR14;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE..
RX MEDLINE=96187584; PubMed=8611748;

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RA Nakai Y., Nishimura T., Shimizu M., Arai S.;
RT "Effects of freezing on the proteolysis of beef during storage at 4
RT degrees C.";
RL Biosci. Biotechnol. Biochem. 59:2255-2258(1995).
SQ SEQUENCE 15 AA; 1597 MW; C98A5B44A79E4777 CRC64;

Query Match 60.0%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
Db 2 PPP 4

RESULT 54
Q9BGG8 PRELIMINARY; PRT; 16 AA.
AC Q9BGG8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Thyroid hormone receptor alpha (Fragment).
GN THRA1.
OS Sorex araneus (Eurasian common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
OX NCBI_TaxID=42254;
RN [1]
RP SEQUENCE FROM N.A.
RA Larkin D., Serov O., Zhdanova N.;
RT "Mapping of five genes from human chromosome 17 to chromosome 17 of
RT the common shrew (Sorex araneus).";
RL Acta Theriol. (Warsz) 45:143-146(2000).
DR EMBL; AF314827; AAK13419.1; -.
KW Receptor.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 16 AA; 1951 MW; 775186E3FE5F52E2 CRC64;

Query Match 60.0%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPP 3
Db 3 FPP 5

RESULT 55
Q9TQZ7 PRELIMINARY; PRT; 16 AA.
AC Q9TQZ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Factor H (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RX MEDLINE=96202005; PubMed=8615824;
RA Soames C.J., Day A.J., Sim R.B.;
RT "Prediction from sequence comparisons of residues of factor H involved
RT in the interaction with complement component C3b.";
RL Biochem. J. 315:523-531(1996).
SQ SEQUENCE 16 AA; 1871 MW; 7052751E485EC825 CRC64;

Query Match 60.0%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 PPP 4
DB      6 PPP 8

RESULT 56
Q9TRD1  PRELIMINARY;      PRT;      16 AA.
AC Q9TRD1;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Basic fibroblast growth factor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=94106247; PubMed=7506473;
RA Bechtner G., Rieder B., Linsenmaier U., Kellermann J., Greil W.,
RA Gartner R.;
RT "Isolation and partial molecular characterization of basic fibroblast
RT growth factor from isolated porcine thyroid follicles and entire
RT porcine thyroid glands.";
RL Acta Endocrinol. 129:458-466(1993).
DR HSP; P09038; IBLA.
SQ SEQUENCE 16 AA; 1649 MW; 9A87A8763D83F595 CRC64;

Query Match      60.0%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FPP 3
DB     12 FPP 14

RESULT 57
Q9TR22  PRELIMINARY;      PRT;      17 AA.
AC Q9TR22;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)
DE NONAMELOGENIN glycoprotein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96126798; PubMed=8564801;
RA Punzi J.S., DenBesten P.K.;
RA "Purification of nonamelogenin proteins from bovine secretory
RT enamel.";
RL Calif. Tissue Int. 57:379-384(1995).
SQ SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;

Query Match      60.0%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPP 4
DB      8 PPP 10

RESULT 58
O49225  PRELIMINARY;      PRT;      17 AA.
ID O49225

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AC O49225;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Hydroxyproline-rich glycoprotein (Fragment)..
GN HRGP.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Essex; TISSUE=Root;
RX MEDLINE=94211912; PubMed=8159793;
RA Hong J.C., Cheong Y.H., Nagao R.T., Bahk J.D., Cho M.J., Key J.L.;
RT "Isolation and characterization of three soybean extensin cDNAs.";
RL Plant Physiol. 104:793-796(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Essex; TISSUE=Root;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047052; AAC03558.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;

Query Match      60.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPP 4
DB     11 PPP 13

RESULT 59
Q41400  PRELIMINARY;      PRT;      17 AA.
ID Q41400;
AC Q41400;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
DE Hydroxyproline-rich protein (Fragment).
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
OX NCBI_TaxID=3895;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sesbania rostrata;
RC TISSUE=Bacterial infected stem located root primordia;
RX MEDLINE=96112737; PubMed=8664492;
RA Gookmarchig S., Valerio-Lepiniec M., Szczyglowski K., Van Montagu M.,
RA Holsters M., De Bruijn F.;
RT "Use of differential display to identify novel Sesbania rostrata genes
RT enhanced by Acetorhizobium caulinodans infection.";
RL Mol. Plant Microbe Interact. 8:816-824(1995).
DR EMBL; Z48673; CAA88592.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match      60.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPP 4
DB     10 PPP 12

RESULT 60

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Q9UCT9 ID Q9UCT9 PRELIMINARY; PRT; 18 AA.  
AC Q9UCT9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE PRG=PROLINE-rich glycoprotein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=9137355; PubMed=1894623;  
RA Gillice-Castro B.L., Prakhophol A., Burlingame A.L., Leffler H.,  
RA Fisher S.J.;  
RT "Structure and bacterial receptor activity of a human salivary  
RT proline-rich glycoprotein.";  
RL J. Biol. Chem. 266:17358-17368 (1991).  
FT NON\_TER 1 1  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 1780 MW; 961F6FE0A83D2E40 CRC64;  
Query Match 60.0%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db |||  
4 PPP 6  
RESULT 61  
Q8NFB4 ID Q8NFB4 PRELIMINARY; PRT; 18 AA.  
AC Q8NFB4;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Mutant enamelin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kida M., Ariga T.;  
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused  
RT by an enamelin gene mutation at exon-intron boundary.";  
RL J. Dent. Res. 81:0-0 (2002).  
DR EMBL; AF530444; AM97323.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 1893 MW; 492D2B2E3B8B512 CRC64;  
Query Match 60.0%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db |||  
3 PPP 5  
RESULT 62  
Q8SKY0 ID Q8SKY0 PRELIMINARY; PRT; 18 AA.  
AC Q8SKY0;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Ribosomal protein S11 (Fragment).  
OS Rps11.

OS Cuscuta reflexa (Southern Asian dodder).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Convolvulaceae; Cuscuta.  
OX NCBI\_TaxID=4129;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Berg S.;  
RT "Sequence analysis and coding potential of the holoparasitic flowering  
RT plant genus Cuscuta.";  
RL Thesis (2002), Department of Institute of Botany, .  
DR EMBL; AJ439611; CAD28796.1; -.  
DR InterPro: IPR001971; Ribosomal\_S11.  
DR Pfam: PF00411; Ribosomal\_S11; I.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 2088 MW; 130D427BFE680B24 CRC64;  
Query Match 60.0%; Score 3; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PPK 5  
Db |||  
12 PPK 14  
RESULT 63  
Q8QFT3 ID Q8QFT3 PRELIMINARY; PRT; 18 AA.  
AC Q8QFT3;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Sterol regulatory element binding protein 1 (Fragment).  
GN SREBP-1.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Assaf S., Pitel F., Morisson M., Alizadeh M., Gondret F., Diot C.,  
RA Leclercq B., Vignat A., Douaire M., Lagarrigue S.;  
RT "Partial cloning, tissue expression, chromosomal localisation of  
RT chicken SREBP genes and relationships to fatness variability in  
RT genetically fat and lean chicken lines.";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ441122; CAD29619.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 1947 MW; 3206A67750EFD7EA CRC64;  
Query Match 60.0%; Score 3; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db |||  
15 PPP 17  
RESULT 64  
P82110 ID P82110 PRELIMINARY; PRT; 18 AA.  
AC P82110;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Peptide leucine arginine (PLR).  
OS Rana pipiens (Northern leopard frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
RN NCBI_TaxID=8404;
RP [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=SKIN;
RA Salmon A.L., Cross L.J.M., Irvine A.E., Leppin T.R.J., Canning P.,
RA Thim L., Gaida W., Bienen M., Shaw C.;
RT "Peptide leucine arginine, a potent immunomodulatory peptide, isolated
RT and structurally characterized from the skin of the Leopard frog,
RT Rana pipiens.";
RL J. Biol. Chem. 0:0-0(1999).
RN [2]
RN FUNCTION.
RA Boyer M., van Den Berg H.W., Shaw C., Lynch M., Johnston P.;
RT "Breat cancer cell lines express specific binding sites for plr, a
RT novel anti-proliferative peptide from frog skin venom.";
RL Br. J. Cancer 48:41-41(1998)
CC -1- FUNCTION: ANTIPROLIFERATIVE ACTIVITY AGAINST HUMAN BREAST AND
CC OVARIAN TUMOR CELL LINES IN VITRO. INHIBITS GRANULOPOIESIS IN
CC VITRO IN RAT AND CAUSES HISTAMINE RELEASE FROM RAT PERITONEAL
CC MAST CELLS IN VITRO.
KW Inflammatory response.
FT DISULFID 5 15
SQ SEQUENCE 18 AA; 2138 MW; 98060469E0FAFFAB CRC64;

Query Match 60.0%; Score 3; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
DB 11 PPK 13

RESULT 65
Q9UCU3 PRELIMINARY; PRT; 19 AA.
ID Q9UCU3
AC Q9UCU3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Insulin-like growth factor binding protein 34 kDa form (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93091816; PubMed=1726837;
RA Roghani M., Segovia B., Whitechurch O., Binoux M.;
RT "Purification from human cerebrospinal fluid of insulin-like growth
RT factor binding proteins (IGFBPs). Isolation of IGFBP-2, an altered form
RT of IGFBP-3 and a new IGFBP species.";
RL Growth Regul. 1:125-130(1991).
SQ SEQUENCE 19 AA; 2032 MW; A73497C418219088 CRC64;

Query Match 60.0%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 16 PPP 18

RESULT 66
O63058 PRELIMINARY; PRT; 19 AA.
ID O63058
AC O63058
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE

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DE Ribosomal protein S11 (Fragment).
GN RPS11.
OS Lathraea clandestina.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Lamiaceae; Orobanchaceae;
OC Orobanchaceae incertae sedis; Lathraea.
OX NCBI_TaxID=41911;
RN [1]
RP SEQUENCE FROM N.A.
RA Lussan M., Delavault P., Thelouarn P.;
RT "The rbcL gene from Lathraea (holoparasitic) is not transcribed by a
RT plastid-encoded RNA polymerase.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030983; AAC16521.1; -.
DR InterPro: IPR001971; Ribosomal_S11.
DR Pfam: PF00411; Ribosomal_S11; I.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 19 AA; 2245 MW; 130D2AB3FE680B24 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
DB 13 PPK 15

RESULT 67
P82941 PRELIMINARY; PRT; 19 AA.
ID P82941
AC P82941
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Unknown endosperm protein V (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. BOMI; TISSUE=Starchy endosperm;
RX MEDLINE=21088911; PubMed=11271488;
RA Kristoffersen H.E., Flengsrud R.;
RT "Separation and characterization of basic barley seed proteins.";
RL Electrophoresis 21:3693-3700(2000).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.0, ITS MW IS: 19.9 KDA.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2026 MW; 053B874BAD6C02E0 CRC64;

Query Match 60.0%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 2 PPP 4

RESULT 68
Q8R5B2 PRELIMINARY; PRT; 19 AA.
ID Q8R5B2
AC Q8R5B2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 2.1 kDa protein (Fragment).

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OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC023093; AA23093.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 FT 1  
 SQ SEQUENCE 19 AA; 2108 MW; 6DD09F5D5252D7F2 CRC64;  
 Query Match 60.0%; Score 3; DB 11; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPP 3  
 Db 11 FPP 13  
 RESULT 69  
 Q78351 ID Q78351 PRELIMINARY; PRT; 19 AA.  
 AC Q78351;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Viral sample FLPBR4A (Florida patient B), partial env cds, V4 region (Fragment).  
 DE Human immunodeficiency virus 1.  
 OS Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang L.O., Leigh-Brown A.J.;  
 RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92271245; PubMed=1589796;  
 RX Ou C.-Y., Ciesielski C.A., Myers G., Bantea C.I., Luo C.C.,  
 RA Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,  
 RA Egononou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,  
 RA Jaffe H.W.;  
 RT "Molecular Epidemiology of HIV Transmission in a Dental Practice."  
 RL Science 256:1165-1171(1992).  
 DR EMBL; M92118; AAA44488.1; -.  
 FT NON\_TER 1  
 FT 1  
 SQ SEQUENCE 19 AA; 1985 MW; 5FFC8787D98CEA1C CRC64;  
 Query Match 60.0%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPP 3  
 Db 2 FPP 4  
 RESULT 70  
 Q905G4 ID Q905G4 PRELIMINARY; PRT; 19 AA.  
 AC Q905G4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 OS Human immunodeficiency virus 1.  
 OS Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=97CG284;  
 RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in Republic of Congo-Brazzaville."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF410448; AAL10258.1; -.  
 FT NON\_TER 1  
 FT 1  
 SQ SEQUENCE 19 AA; 2263 MW; 3B5E64FD66039636 CRC64;  
 Query Match 60.0%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPK 5  
 Db 6 PPK 8  
 RESULT 71  
 Q905I4 ID Q905I4 PRELIMINARY; PRT; 19 AA.  
 AC Q905I4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 OS Human immunodeficiency virus 1.  
 OS Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=96CG30;  
 RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in Republic of Congo-Brazzaville."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF410443; AAL10238.1; -.  
 FT NON\_TER 1  
 FT 1  
 SQ SEQUENCE 19 AA; 2151 MW; 2A91C2A4D1167636 CRC64;  
 Query Match 60.0%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPP 4  
 Db 6 PPP 8  
 RESULT 72  
 Q9R509 ID Q9R509 PRELIMINARY; PRT; 20 AA.  
 AC Q9R509;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Adenylate kinase (EC 2.7.4.3) (App-AMP transphosphorylase) (Fragment).  
 DE ADK.  
 GN ADK.  
 OS Bacillus alcalophilus.  
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1445;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94117390; PubMed=8288548;  
 RX Gilles A.M., Glaser P., Perrier V., Meier A., Longin R., Sebaid M.,



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RA Maignan L., Pistotnik E., Barzu O.;
RT "Zinc, a structural component of adenylate kinases from gram-positive
RT bacteria.";
RL J. Bacteriol. 176:520-523(1994).
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase_1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 20 AA; 2190 MW; 94D98FC289220254 CRC64;

Query Match 60.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
DB 8 PPK 10

RESULT 73
Q9R4D7 ID Q9R4D7 PRELIMINARY; PRT; 20 AA.
AC Q9R4D7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE 57 kDa outer membrane protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP MEDLINE=96355881; PubMed=8751919;
RA Yamamoto T., Wakisaka N., Nakae T., Kamano T., Serichantalergs O.,
RA Echeverria P.;
RT "Characterization of a novel hemagglutinin of diarrhea-associated
RT Escherichia coli that has characteristics of diffusely adhering E. coli
RT and enteroggregative E. coli.";
RL Infect. Immun. 64:3694-3702(1996).
SQ SEQUENCE 20 AA; 1988 MW; A7AB608E52F5458 CRC64;

Query Match 60.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 3 PPP 5

RESULT 74
Q9TN04 ID Q9TN04 PRELIMINARY; PRT; 20 AA.
AC Q9TN04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE HLA-DRI-associated LI peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94148715; PubMed=8106277;
RA Max H., Halder T., Kropshofer H., Kalbus M., Muller C.A.,
RA Kalbacher H.;

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RT "Characterization of peptides bound to extracellular and intracellular
RT HLA-DRI molecules.";
RL Hum. Immunol. 38:193-200(1993).
KW MHC.
SQ SEQUENCE 20 AA; 2264 MW; D802F7C2C0FAE534 CRC64;

Query Match 60.0%; Score 3; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5
DB 4 PPK 6

RESULT 75
Q9S8R2 ID Q9S8R2 PRELIMINARY; PRT; 20 AA.
AC Q9S8R2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Starch branching enzyme (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RX MEDLINE=94009663; PubMed=8405428;
RA Khoshnoodi J., Ek B., Raak L., Larsson H.;
RT "Characterization of the 97 and 103 kDa forms of starch branching
RT enzyme from potato tubers.";
RL FEBS Lett. 332:132-138(1993).
SQ SEQUENCE 20 AA; 2339 MW; 0C69903743FC686D CRC64;

Query Match 60.0%; Score 3; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 12 PPP 14

Search completed: November 25, 2003, 18:25:35
Job time : 15.0979 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 16.1968 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-12

Perfect score: 5

Sequence: 1 FPPPK 5

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size: 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database: A\_Geneseq\_19Jun03.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	22	Colostrinin derive
2	5	100.0	5	22	Colostrinin peptid
3	5	100.0	5	22	Colostrinin peptid
4	5	100.0	5	22	Ewe colostrinin pe
5	5	100.0	5	23	Colostrinin consti
6	5	100.0	5	23	Colostrinin consti
7	5	100.0	5	23	Neural cell regula
8	5	100.0	10	22	Ewe colostrinin pe
9	4	80.0	5	19	EVH1 ligand motif.

10	4	80.0	5	20	AAW98982	FAM- (Pro) 4-Lys (eps
11	4	80.0	5	22	AAW98982	Amino acid sequenc
12	4	80.0	5	22	AAU09140	Ena/VASP homology
13	4	80.0	5	23	AAO17762	Zyxine VASP bindin
14	4	80.0	6	19	AAW31441	Transcriptional ac
15	4	80.0	7	20	AAW42877	Vpr-binding peptid
16	4	80.0	7	20	AAW98983	FAM- (Pro) 6-Lys (eps
17	4	80.0	8	14	AAW43504	Sm B/B' epitope 83
18	4	80.0	8	22	AAW97318	U3 RNP epitope pep
19	4	80.0	9	20	AAW98979	FAM- (Pro) 8-Lys (eps
20	4	80.0	9	22	AAU09144	Ena/VASP homology
21	4	80.0	9	22	AAW76143	Tumour associated
22	4	80.0	9	22	AAW76144	Tumour associated
23	4	80.0	9	23	AAE17284	Human leukocyte an
24	4	80.0	9	24	ABJ20100	MHC binding peptid
25	4	80.0	9	24	ABP58250	Human pre-gastroki
26	4	80.0	9	24	AAE33297	Human pre-AMP-18 p
27	4	80.0	10	9	AAF80874	Hook region #5 con
28	4	80.0	10	22	AAU09138	Ena/VASP homology
29	4	80.0	10	22	AAW76191	Tumour associated
30	4	80.0	11	20	AAW98980	FAM- (Pro) 10-Lys (ep
31	4	80.0	11	21	AAW56001	Mucor hiemalis end
32	4	80.0	12	18	AAW32743	Human platelet gly
33	4	80.0	12	18	AAW23206	Terminal peptide e
34	4	80.0	12	18	AAW21083	Lipolytic enzyme o
35	4	80.0	12	21	AAW67258	PTP-PEST substrate
36	4	80.0	13	16	AAW74384	HTLV-1 p27(rex) pr
37	4	80.0	13	18	AAW38122	PPPY motif contain
38	4	80.0	13	18	AAW38064	Peptide recognitio
39	4	80.0	13	20	AAW98981	FAM- (Pro) 12-Lys (ep
40	4	80.0	14	11	AAW06249	Antigenic peptide
41	4	80.0	14	22	AAW79174	Peptide derived fr
42	4	80.0	14	24	ABP58245	Human pre-gastroki
43	4	80.0	14	24	AAE33291	Human pre-AMP-18 p
44	4	80.0	15	11	AAW02172	Peptide which bind
45	4	80.0	15	18	AAW38996	Peptide resembling
46	4	80.0	15	18	AAW38935	Synthetic antigen
47	4	80.0	15	22	AAW79166	Human vacuole prot
48	4	80.0	15	22	AAW64569	Colostrinin derive
49	4	80.0	15	22	AAW7252	Colostrinin peptid
50	4	80.0	15	22	AAW72506	Colostrinin peptid
51	4	80.0	15	22	AAW72538	Ewe colostrinin pe
52	4	80.0	15	22	AAW59312	Human ribosomal pr
53	4	80.0	15	23	ABG72860	Human ribonucleoti
54	4	80.0	15	23	ABP59535	Human ciliary roo
55	4	80.0	15	23	ABW81220	Colostrinin consti
56	4	80.0	15	23	AAE20234	Colostrinin consti
57	4	80.0	15	23	AAW51042	Neural cell regula
58	4	80.0	15	23	AAO14583	Human quinine redu
59	4	80.0	16	18	AAW39031	Peptide resembling
60	4	80.0	16	18	AAW38989	Peptide resembling
61	4	80.0	16	18	AAW38947	Peptide resembling
62	4	80.0	16	18	AAW38947	AAV-2 antigenic pe
63	4	80.0	16	21	AAW87908	Ewe colostrinin pe
64	4	80.0	16	22	AAW59343	Human papillomavir
65	4	80.0	16	23	AAO15252	Peptide resembling
66	4	80.0	17	18	AAW38983	Peptide resembling
67	4	80.0	17	18	AAW38939	Peptide resembling
68	4	80.0	17	19	AAW83513	LRP5 protein fragm
69	4	80.0	17	22	AAU01833	Wheat Gliadin pept
70	4	80.0	17	22	AAU01840	Wheat peptide anta
71	4	80.0	17	17	AAW05469	SH3-binding peptid
72	4	80.0	18	18	AAW37677	PPPY motif contain
73	4	80.0	18	18	AAW38909	Peptide resembling
74	4	80.0	18	19	AAW47567	Extendin agonist (1
75	4	80.0	18	19	AAW47569	Extendin agonist (2
76	4	80.0	18	19	AAW47571	Extendin agonist (2
77	4	80.0	18	19	AAW47577	Extendin agonist (2
78	4	80.0	18	19	AAW47562	Extendin agonist (1
79	4	80.0	18	19	AAW47564	Extendin agonist (1
80	4	80.0	18	19	AAW47550	Extendin agonist (1
81	4	80.0	18	19	AAW47552	Extendin agonist (3
82	4	80.0	18	20	AAW03721	Extendin agonist co

83 4 80.0 18 20 AAY03723 Extendin agonist co  
 84 4 80.0 18 20 AAY03733 Extendin agonist co  
 85 4 80.0 18 20 AAY03735 Extendin agonist co  
 86 4 80.0 18 20 AAY03738 Extendin agonist co  
 87 4 80.0 18 20 AAY03740 Extendin agonist co  
 88 4 80.0 18 20 AAY03742 Extendin agonist co  
 89 4 80.0 18 20 AAW97632 Systemin-like pept  
 90 4 80.0 18 20 AAW97633 Systemin-like pept  
 91 4 80.0 18 21 AAB30689 Amino acid sequenc  
 92 4 80.0 18 21 AAB30690 Amino acid sequenc  
 93 4 80.0 18 21 AAB52873 Extendin agonist c  
 94 4 80.0 18 21 AAB52876 Extendin agonist c  
 95 4 80.0 18 21 AAB52878 Extendin agonist c  
 96 4 80.0 18 21 AAB52880 Extendin agonist c  
 97 4 80.0 18 21 AAB52885 Extendin agonist c  
 98 4 80.0 18 21 AAB52886 Extendin agonist c  
 99 4 80.0 18 23 ABG96151 Cysteine-containing  
 100 4 80.0 18 24 ABP58246 Human pre-gastroki

## ALIGNMENTS

RESULT 1  
 AAB72257  
 ID AAB72257 standard; peptide; 5 AA.  
 AC AAB72257;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 12.  
 XX  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22818.  
 XX  
 PR 17-AUG-1999; 99US-0149311.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REG-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 DR WPI; 2001-202804/20.  
 XX  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrinum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX SQ Sequence 5 AA;  
 Query Match 100.0%; Score 5; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 FPPPK 5  
 DB 1 FPPPK 5  
 RESULT 2  
 AAB72510  
 ID AAB72510 standard; Peptide; 5 AA.  
 XX  
 AC AAB72510;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #11.  
 XX  
 KW Dermatological; oxidative stress regulator; colostrinin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22665.  
 XX  
 PR 17-AUG-1999; 99US-0149310.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2001-218342/22.  
 XX  
 XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 5 AA;  
 Query Match 100.0%; Score 5; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 FPPPK 5  
 DB 1 FPPPK 5  
 RESULT 3  
 AAB72542  
 ID AAB72542 standard; Peptide; 5 AA.  
 XX  
 AC AAB72542;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX

DE Colostrinin peptide #11.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 XX  
 PD 22-FEB-2001.  
 XX  
 XX  
 PF 17-AUG-2000; 2000WO-US22774.  
 XX  
 PR 17-AUG-1999; 99US-0149633.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 PI Boldogh I;  
 XX  
 XX  
 DR WPI; 2001-226545/23.  
 XX  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 5; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPPK 5  
 DB |||||  
 1 FPPPK 5  
 RESULT 4  
 AAB59320  
 ID AAB59320 standard; Peptide; 5 AA.  
 XX  
 AC AAB59320;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment B-5.  
 XX  
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 PN WO200075173-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 XX  
 PF 02-JUN-2000; 2000WO-GB02128.  
 XX  
 XX  
 PR 02-JUN-1999; 99GB-0012852.  
 XX  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 PA  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-071058/08.  
 XX  
 PT Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 XX characterized by amyloid plaques -  
 XX  
 PS Claim 7; Page 27; 63pp; English.  
 XX  
 CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 5; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPPK 5  
 DB |||||  
 1 FPPPK 5  
 RESULT 5  
 AAE20239  
 ID AAE20239 standard; peptide; 5 AA.  
 XX  
 AC AAE20239;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide #11.  
 XX  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnary.  
 XX  
 OS Unidentified.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 5  
 FT /note= "Optionally C-terminal amide"  
 XX  
 PN WO200213850-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22776.  
 XX  
 PR 17-AUG-2000; 2000WO-US22776.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 XX WPI; 2002-269151/31.  
 XX  
 PT Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 PS Claim 6; Page 25; 51pp; English.  
 XX  
 CC The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidizing species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPK 5  
 |||||  
 Db 1 FPPPK 5

#### RESULT 6

AAW51046  
 ID AAW51046 standard; Peptide; 5 AA.

XX AC AAW51046;

DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide.

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 XX KW blood cell regulator; cytokine inducer; beta-casein; human.  
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Modified-site 5 /note= "optional C-terminal amidation"

XX PN WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX DR WPI; 2002-269150/31.

XX PT Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue

XX PS Claim 1; Page 34; 54pp; English.

XX CC The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. The peptide is  
 CC classified as having a beta-casein homologue precursor. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patient. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPK 5  
 |||||  
 Db 1 FPPPK 5

#### RESULT 7

AAO14588  
 ID AAO14588 standard; peptide; 5 AA.

XX AC AAO14588;

DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 11.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers  
 FT Modified-site 5 /note= "Optional C-terminal amide"

XX PN WO200213851-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX DR WPI; 2002-269152/31.

XX PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog

XX PS Claim 7; Page 21; 37pp; English.

XX CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX  
SQ Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPK 5

|||||  
Db 1 FPPPK 5

RESULT 8

AAW59350

ID AAW59350 standard; Peptide; 10 AA.

XX

AC AAW59350;

DT 21-MAR-2001 (first entry)

XX Ewe colostrin peptide fragment derived sequence #10.

XX Sheep, colostrin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX Ovis sp.

XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB02128.

XX 02-JUN-1999; 99GB-0012852.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from  
PT colostrin for treating e.g. disorders of the central nervous system  
PT and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -

XX Claim 8; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.

XX Sequence 10 AA;

Query Match 100.0%; Score 5; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPK 5

|||||  
Db 2 FPPPK 6

RESULT 9

AAW37157

ID AAW37157 standard; Peptide; 5 AA.

XX

AC AAW37157;

XX 06-JUL-1998 (first entry)

XX EVH1 ligand motif.

XX Mena protein; mammalian Ena; Enabled; Evi protein; cytoskeleton;  
KW cell morphology; cell adhesion; cell differentiation; cell growth;  
KW cell motility; mouse; EVH1 ligand.

XX Synthetic.

XX WO9801755-A1.

XX 15-JAN-1998.

XX 03-JUL-1997; 97WO-US11669.

XX 05-JUL-1996; 96US-0675815.

XX (GBPB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.

XX Gertler FB, Niebuhr K, Soriano P, Wehland J;  
PI WPI; 1998-101197/09.

XX Detection of modulators of Mena and Ena-VASP-like genes and proteins  
PT - used in control of cytoskeletal dynamic events in normal and  
PT abnormal cell morphology, adhesion, motility, growth and  
PT differentiation

XX Example 7; Page 44; 77pp; English.

XX This peptide motif is found in zyxin, vinculin and other focal  
CC adhesion proteins containing an ActA-like motif. The N-terminal  
CC portion of novel murine Mena (mammalian Ena) protein (see AAW37148)  
CC contains an Ena-VASP homology domain (EVH1) that directs the proper  
CC localisation of Mena to focal contacts via directed protein-protein  
CC interactions with zyxin, vinculin etc. This suggests that the  
CC FPPPP motif may comprise the core recognition site in EVH1 ligands.  
CC Based on the disclosed Mena and Evi genes (see AAV02996-98) and  
CC proteins (see AAW37148-53), a variety of methods and compositions are  
CC provided for screening, isolating and characterising endogenous and  
CC exogenous factors, drugs and therapeutic agents useful to evaluate  
CC and/or control cytoskeletal dynamic events involved in normal and  
CC abnormal cell morphology, adhesion, motility, growth and/or  
CC differentiation.

XX SQ Sequence 5 AA;

Query Match 80.0%; Score 4; DB 19; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPP 4

|||||  
Db 1 FPPPP 4

RESULT 10

AAW98982

ID AAW98982 standard; peptide; 5 AA.

XX

AC AAW98982;

XX

DT 11-MAY-1999 (first entry)

XX FAM-(Pro)4-Lys(epsilon-TMR) peptide.

XX Energy transfer; DNA base sequencing; reporter; donor; acceptor;

XX terminator; chain terminator method.

XX

OS Synthetic.  
 PN WO9902544-A1.  
 XX  
 XX 21-JAN-1999.  
 PD  
 XX  
 XX 10-JUL-1998; 98WO-JP03093.  
 XX  
 XX 11-JUL-1997; 97JP-0186886.  
 PR  
 XX (RIKA ) INST PHYSICAL & CHEM RES.  
 PA (WAKP ) WAKO PURE CHEM IND LTD.  
 XX  
 XX Hayashizaki Y, Tanaka T;  
 PI  
 XX WPI; 1999-120768/10.  
 DR  
 XX  
 XX New nucleotide derivatives having energy transfer function - contain  
 PT reporters to serve as donor and acceptor, useful in chain  
 PT termination DNA base sequencing  
 PT  
 XX Example; Page 41; 75pp; Japanese.  
 PS  
 XX The present invention describes nucleotide compounds of formula (I):  
 CC Q-V-CO-R1(NH-W2)-NH(CO-CHR2-NR3)m-W1 (I) Q = mono or oligonucleotide;  
 CC V = C triple bond C-(CH2)nNH or CH-CH(CH2)n2NH; n1, n2, m = integer;  
 CC R1 = trivalent group; R2, R3 = H or hydrocarbyl; or CHR2NR3 = a ring;  
 CC W1, W2 = fluorescent group. Also described is the use of RNA polymerase  
 CC and a mono or oligonucleotide compound (I') as initiator in a chain  
 CC terminator method for DNA base sequencing. (I') has: (i) a 5'-phosphate  
 CC group; and (ii) two reporters capable of serving as a donor and an  
 CC acceptor in energy transfer. (I') including (I) have improved uptake  
 CC efficiency by RNA polymerases and can so be used with RNA polymerases  
 CC as terminators in DNA base sequencing methods. The present invention  
 CC represents a peptide used in an example from the present invention.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 80.0%; Score 4; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPPK 5  
 DB ||||  
 2 PPPK 5  
 RESULT 11  
 AAG79177  
 ID AAG79177 standard; peptide; 5 AA.  
 XX  
 AC AAG79177;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Amino acid sequence of a Fyb/SLAP complex inhibitor.  
 XX  
 KW Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;  
 KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;  
 KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;  
 KW infectious disease; cancer; autoimmune disease; inflammation;  
 KW platelet aggregation; wound healing; clotting.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200174858-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 03-APR-2001; 2001WO-US10753.  
 XX  
 XX 03-APR-2000; 2000US-194215P.  
 PR  
 XX

PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 PI Krause M, Sechi AS, Gertler FB, Wehland J;  
 XX WPI; 2001-616686/71.  
 DR  
 XX Modulating cytoskeletal rearrangement to regulate T cell and macrophage  
 PT activation for treating cancer, autoimmune disease, and infectious  
 PT disease, comprises contacting with a Fyb/SLAP complex modulator -  
 XX  
 XX Claim 4; Page 56; 79pp; English.  
 PS  
 XX The present sequence represents a Fyb/SLAP complex inhibitor. Fyb/SLAP  
 CC proteins are ligands for the EVH1 domains of  
 CC Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins. The  
 CC specification describes a method for modulating cytoskeletal  
 CC rearrangement in a cell, or T cell response to T cell receptor  
 CC stimulation. The method comprises contacting the cell or T cell with  
 CC a Fyb/SLAP complex modulator sufficient to modulate the formation  
 CC of a complex of an Ena/VASP protein and a Fyb/SLAP protein. The  
 CC method is useful for modulating cytoskeletal rearrangement in a cell  
 CC such as a lymphocyte, preferably a T cell, a macrophage or a cell  
 CC fragment such as a platelet and for modulating T cell response to a  
 CC T cell receptor stimulation. T cell response is increased in a subject  
 CC having or at risk of developing infectious disease or cancer and T cell  
 CC response is inhibited in a subject having or is at risk of developing an  
 CC autoimmune disease or a condition characterized by inflammation. A  
 CC composition comprising a Fyb/SLAP complex inhibitor is useful for  
 CC increasing platelet aggregation for promoting wound healing or  
 CC clotting.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 80.0%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 DB ||||  
 1 FPPP 4  
 RESULT 12  
 AAU09140  
 ID AAU09140 standard; peptide; 5 AA.  
 XX  
 AC AAU09140;  
 XX  
 DT 19-DEC-2001 (first entry)  
 XX  
 DE Ena/VASP homology (EVH) proline-rich motif #1.  
 XX  
 KW Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;  
 KW cell migration; Ena/VASP; wound healing; actin polymerisation;  
 KW neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;  
 KW Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;  
 KW Tourette's syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;  
 KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;  
 KW inflammatory disorder; arthritis; allergy; gout; organ transplant;  
 KW cancer; ischaemia.  
 XX  
 OS Listeria monocytogenes.  
 XX  
 PN WO200174853-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US10249.  
 XX  
 PR 03-APR-2000; 2000US-194564P.  
 XX



PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 PI Gertler FB, Bear JE, Wehland J, Loureiro JJ;  
 XX WPI; 2001-626380/72.  
 DR  
 XX  
 XX Regulating cell motility for promoting wound healing and tissue  
 PT regeneration, treating, neurodegenerative disease and metastasis, by  
 PT inducing or depleting a functional enabled/vasodilator-stimulated  
 PT phosphoprotein -  
 XX  
 XX Example 2; Page 60; 107pp; English.  
 PS  
 XX  
 XX The invention relates to a method of preventing mammalian cell migration,  
 CC comprising inducing a functional Ena(enabled)/vasodilator-stimulated  
 CC phosphoprotein (VASP) or promoting cell migration comprising depleting  
 CC functional Ena/VASP protein in the mammalian cell. The method is useful  
 CC for preventing or promoting mammalian cell migration, preferably tumour  
 CC cell migration in vitro or in vivo and to prevent tumour cell metastasis  
 CC in a subject. An Ena/VASP activator or inhibitor is useful for promoting  
 CC wound healing, preferably fibroblasts or nerve cells of a tissue type  
 CC with the inhibitor to promote actin polymerisation and tissue formation  
 CC on a scaffold. The inhibitor is also useful for preventing  
 CC neurodegeneration such as in Alzheimer's disease, Down Syndrome,  
 CC Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct  
 CC trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia  
 CC complex, progressive supranuclear palsy, progressive bulbar palsy,  
 CC spinomuscular atrophy, cerebral amyloidosis, Pick's atrophy, Retts  
 CC cerebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia,  
 CC Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP  
 CC inhibitor is further useful for enhancing learning and memory in a  
 CC subject having or at risk of developing a learning disorder such as  
 CC Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile  
 CC dementia, Korsakow's disorder and age-related memory loss. The inhibitor  
 CC is administered in an amount for inhibiting the activity of Mena in a  
 CC synapse. Ena/VASP activator is useful for disrupting learning and memory  
 CC and the activator is administered in an amount to promote Ena/VASP  
 CC protein-FE65 interaction. Inducing the activity of Ena/VASP protein  
 CC in immune or haematopoietic cells reduces the ability of the cells to  
 CC migrate and this is useful for treating and preventing inflammatory  
 CC disorders such as arthritis, allergy, gout, organ transplant,  
 CC ulcerative colitis and ischaemic diseases and also for treating cancer  
 CC metastasis. The present sequence represents the amino acid sequence  
 CC of Ena/VASP homology (EVH) proline-rich motif #1.  
 XX  
 XX Sequence 5 AA;  
 SQ

Query Match 80.0%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 DB 1 FPPP 4

RESULT 13  
 AAO17762  
 ID AAO17762 standard; peptide; 5 AA.  
 XX  
 XX AAO17762;  
 AC  
 XX 15-AUG-2002 (first entry)  
 DT  
 XX  
 DE Zyxine VASP binding motif.  
 XX  
 XX Zyxine; EVH-1; cardiovascular disease; inflammation; cancer;  
 KW Ena-vasodilator-stimulated phosphoprotein homologue; VASP homologue;  
 KW cardiant; antiinflammatory; cytostatic.  
 XX  
 OS Unidentified.  
 XX

PN WO200242777-A2.  
 XX  
 PD 30-MAY-2002.  
 XX  
 PF 22-NOV-2001; 2001WO-EP13592.  
 XX  
 PR 25-NOV-2000; 2000DE-1058596.  
 XX  
 XX (AVET ) AVENTIS PHARMA DEUT GMBH.  
 PA (VASO-) VASOPHARM BIOTECH GMBH.  
 XX  
 XX Jordan B, Drueckes P, Jarchau T, Walter U;  
 XX WPI; 2002-463650/49.  
 DR  
 XX  
 XX Identifying compounds that modulate Ena-vasodilator-stimulated  
 PT phosphoprotein homolog (EVH)-1 binding interactions, useful e.g. for  
 PT treating cardiovascular disease, comprises using antibodies -  
 XX  
 XX Example 4; Page 18; 34pp; German.  
 PS  
 XX The present invention relates to a method of identifying compounds which  
 CC modulate the interaction between an EVH-1 (Ena-vasodilator-stimulated  
 CC phosphoprotein (VASP) homologue) binding domain and an EVH-1 domain. Such  
 CC compounds can be used for treating cardiovascular diseases, inflammation  
 CC and neoplastic cell/tissue alterations such as cancer. The present  
 CC sequence is a VASP binding domain from zyxine described in the  
 CC exemplification of the invention.  
 XX  
 XX Sequence 5 AA;  
 SQ

Query Match 80.0%; Score 4; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 DB 1 FPPP 4

RESULT 14  
 AAW31441  
 ID AAW31441 standard; Protein; 6 AA.  
 XX  
 XX AAW31441;  
 AC  
 XX 04-AUG-1998 (first entry)  
 DT  
 XX  
 DE Transcriptional activator peptide fragment LS46.  
 XX  
 XX Activating sequence; Gal4; transcriptional activator; RNA polymerase;  
 KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;  
 KW Gal4; DNA binding domain.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9744447-A2.  
 PN  
 XX 27-NOV-1997.  
 PD  
 XX  
 PF 02-MAY-1997; 97WO-US07338.  
 XX  
 PR 01-MAY-1997; 97US-0017016.  
 PR 03-MAY-1996; 96US-0017016.  
 XX  
 XX (HARD ) HARVARD COLLEGE.  
 PA  
 XX Lu X, Ptashne M, Wu Y;  
 PI  
 XX WPI; 1998-018502/02.  
 DR N-PSDB; AAV02536.  
 XX  
 XX New transcriptional activator containing DNA binding domain bound to  
 PT

PT peptide - useful for controlling gene expression, especially in gene  
 PT therapy, and in protein-protein interaction assays, does not inhibit  
 PT other transcription activators  
 XX  
 PS Example 1; Page 24; 55pp; English.  
 XX  
 CC AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076  
 CC are fragments used in an assay to determine novel transcriptional  
 CC activators. The method involves the production of transcriptional  
 CC activators comprising of a DNA-binding group and a 6-25 amino acid  
 CC peptide that is covalently bonded to the DNA binding group and does not  
 CC represent a fragment of a natural transcription activator.  
 CC Protein-protein interactions are identified in the assay by fusing a  
 CC DNA-binding domain to a library of DNA fragments and introducing this and  
 CC a fusion of target protein and a polypeptide containing a region of Gal4  
 CC which interacts with Gal4p into a cell containing Gal4p and identifying  
 CC members of the library that interact with the target for activation of  
 CC transcription. Such constructs are used to activate transcription in a  
 CC cell, e.g. for controlling gene activity, particularly in gene therapy  
 CC (e.g. recognizing a site close to a selected therapeutic gene).  
 CC Transcription can be activated without blocking other transcriptional  
 CC activators. They probably act by interacting with a component of the RNA  
 CC polymerase II holoenzyme, Gal4, the strongest known yeast activator,  
 CC which provides a more sensitive assay allowing detection of even weak  
 CC protein-protein interactions. Such activators do not create toxicity  
 CC problems even when overexpressed.

XX SQ Sequence 6 AA;  
 Query Match 80.0%; Score 4; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
 ||||  
 Db 1 FPPP 4

RESULT 15  
 AAY42877  
 ID AAY42877 standard; Peptide; 7 AA.

AC AAY42877;  
 XX 19-JAN-2000 (first entry)  
 DT Vpr-binding peptide, SEQ ID 17.  
 DE Vpr; HIV-1; lentivirus; UDG; uracil DNA glycosylase; inhibition;  
 KW replication; virion; incorporation; uptake; retrovirus; association;  
 KW binding; reactivation; cell cycle arrest; apoptosis; antiviral.  
 XX Synthetic.

XX WO9949891-A1.  
 PN 07-OCT-1999.

XX 30-MAR-1999; 99WO-US06953.  
 XX 30-MAR-1998; 98US-0079822.

XX (UYJE-) UNIV JEFFERSON THOMAS.  
 PA Pomerantz R.J., Bouhamdan M, Duan L, Xue Y;  
 PI WPI; 1999-610824/52.

XX New polypeptide containing a Vpr-binding region -  
 PT Claim 16; Fig 5; 69pp; English.  
 XX This sequence represents a heptapeptide (SEQ ID 17) which can bind

CC lentiviral Vpr protein. Such peptides were identified from a phage  
 CC display library via screening for Vpr-binding activity. Vpr is a human  
 CC immunodeficiency virus type 1 (HIV-1) protein (also found in other  
 CC primate lentiviruses) which is packaged into virions in equal quantities  
 CC to the gag protein. Vpr is expressed relatively late in the lentiviral  
 CC life cycle and encodes a 14 kb protein which is predominantly localised  
 CC in the nucleus of an infected cell. Vpr is able to associate with the  
 CC major uracil DNA glycosylase (UDG) involved in cellular DNA repair, which  
 CC prevents misincorporation of deoxyuracil into DNA during DNA synthesis.  
 CC The association of Vpr with UDG may allow incorporation of UDG into  
 CC HIV-1 virions, resulting in a reduction of uracil misincorporation in  
 CC viral RNA-derived DNA during a subsequent infection cycle. Vpr-binding  
 CC peptides can be fused to polypeptides which do not normally contain a  
 CC Vpr-binding region, rendering the polypeptides susceptible to uptake  
 CC into a virion. Such Vpr-binding polypeptides may be useful for inhibiting  
 CC replication of a virus in a human cell, and for determining whether other  
 CC polypeptides contain a Vpr-binding region. The invention removes the  
 CC requirement to use chimeric proteins containing a portion of the Vpr  
 CC protein to incorporate a protein into a virion, thus avoiding problems  
 CC such as cell cycle arrest, apoptosis or reactivation of a latent  
 CC retrovirus.

XX SQ Sequence 7 AA;

Query Match 80.0%; Score 4; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
 ||||  
 Db 4 FPPP 7

RESULT 16  
 AAW98983  
 ID AAW98983 standard; peptide; 7 AA.

XX AAW98983;  
 AC 11-MAY-1999 (first entry)

DE FAM-(Pro)6-Lys(epsilon-TMR) peptide.

XX Energy transfer; DNA base sequencing; reporter; donor; acceptor;  
 KW terminator; chain terminator method.

XX Synthetic.

XX WO9902544-A1.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-JP03093.

XX 11-JUL-1997; 97JP-0186886.

XX (RIKA ) INST PHYSICAL & CHEM RES.  
 PA (WAKP ) WAKO PURE CHEM IND LTD.

XX Hayaahizaki Y, Tanaka T;

XX WPI; 1999-120768/10.

XX New nucleotide derivatives having energy transfer function - contain  
 PT reporters to serve as donor and acceptor, useful in chain  
 PT termination DNA base sequencing

XX Example; Page 36; 75pp; Japanese.

XX The present invention describes nucleotide compounds of formula (I):  
 CC Q-V-CO-R1 (NH-W2)-NH-(CO-CHR2-NR3)m-W1 (I) Q = mono or oligonucleotide;  
 CC V = C triple bond C-(CH2)n2NH or CH=CH(CH2)n2NH; n1, n2, m = integer;  
 CC R1 = trivalent group; R2, R3 = H or hydrocarbonyl; or CHR2NR3 = a ring;

CC W1, W2 = fluorescent group. Also described is the use of RNA polymerase  
 CC and a mono or oligonucleotide compound (I') as initiator in a chain  
 CC terminator method for DNA base sequencing. (I') has: (i) a 5'-phosphate  
 CC group; and (ii) two reporters capable of serving as a donor and an  
 CC acceptor in energy transfer. (I') including (I) have improved uptake  
 CC efficiency by RNA polymerases and can so be used with RNA polymerases  
 CC as terminators in DNA base sequencing methods. The present sequence  
 CC represents a peptide used in an example from the present invention.  
 XX  
 SQ

Sequence 7 AA;

Query Match 80.0%; Score 4; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 ||||  
 Db 4 PPPK 7

# RESULT 17

AAR43504  
 ID AAR43504 standard; peptide; 8 AA.

XX AAR43504;

AC AAR43504;

XX 25-MAR-2003 (updated)

DT 12-MAY-1994 (first entry)

DE Sm B/B' epitope 83.

XX Linear; epitope; 60 kD; Ro/SSA; La/SSB; autoantigen; E/F; G; 70 kD;  
 XX nuclear ribonucleoprotein; nRNP; Sm B/B'; polypeptide; antigen; D;  
 KW systemic lupus erythematosus; SLE; autoantibody; U4/U6; U5; B; B';  
 XX RNA polymerase III; U1; U2; Sjogrens syndrome; SS; human; vaccine; ss.

OS Homo sapiens.

XX WO9321223-A1.

XX 28-OCT-1993.

XX 13-APR-1993; 93WO-US03484.

XX 13-APR-1992; 92US-0867819.

XX (OKLA ) UNIV OKLAHOMA STATE.

PA Harley JB;

XX WPI; 1993-351658/44.

XX New linear epitope(s) for human auto-antibodies - from the

PT Ro/SSA, La/SSB and Sm B/B' antigens and ribonucleoprotein, used  
 PT for diagnosing and treating auto-immune disorders e.g. systemic  
 PT lupus erythematosus

XX Claim 1; Page 31; 43pp; English.

XX The sequences given in AAR43391-562 are linear epitopes which are  
 CC derived from the 60 kD Ro/SSA peptide, the La/SSB autoantigen,  
 CC the 70 kD nuclear ribonucleoprotein (nRNP) and the Sm B/B'  
 CC polypeptide. These antigens are common in systemic lupus  
 CC erythematosus (SLE) and closely related disorders. The Ro/SSA family  
 CC of proteins has been shown to have several molecular forms which are  
 CC defined by the molecular weight of the antigen identified. The major  
 CC form has a molecular weight of 60 kD and two additional forms have  
 CC molecular weights of 52 and 54 kD. La/SSB is also a member of this  
 CC group of autoantibodies and binds small RNAs with a pyrimidine  
 CC terminus. La/SSB is bound by a third of the anti-Ro/SSA precipitin  
 CC positive sera. La/SSB has been shown to be a 46-50 kD monomeric  
 CC phosphoprotein which associates with RNA polymerase III transcripts.  
 CC Anti-Sm antibodies precipitate snRNPs containing the U1, U2, U4/U6 and

CC U5 RNA. Anti-Sm antibodies may be directed against one or a  
 CC combination of the polypeptides: B (26 kD), B' (27 kD), D (13 kD),  
 CC E/F (11 kD doublet) and G (less than 10 kD). These epitopes may be  
 CC used for preventing, treating or screening autoimmune disorders,  
 CC especially SLE or Sjogrens syndrome (SS). They bind to a human  
 CC autoantibody and may therefore be used as vaccines.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 8 AA;

Query Match 80.0%; Score 4; DB 14; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 ||||  
 Db 3 PPPK 6

# RESULT 18

AAB97318

ID AAB97318 standard; peptide; 8 AA.

XX AAB97318;

XX 13-AUG-2001 (first entry)

DT U3 RNP epitope peptide.

DE U3 RNP epitope peptide.

XX B cell; toxin; antigen specific; antibody mediated disease; virucide;

XX immunosuppressive; antiinflammatory; antiallergic; antidiabetic;

XX thymomimetic; antithyroid; vasotropic; cardiant; antiulcer;

XX neuroprotective; antirheumatic; antiarthritic; dermatological;

XX ophthalmological; nephrotropic; allergy; autoimmune disorder;

XX skin diseases; autoimmune endocrinopathy; vasculitic syndrome;

XX cardiovascular disease; immunohaematologic disorder; neurologic disease;

XX gastrointestinal disease; collagen vascular disease; renal diseases;

XX pulmonary disease; infertility disorder; U3 RNP;

XX mixed connective tissue disorder.

XX Unidentified.

XX WO200132853-A1.

XX 10-MAY-2001.

XX 12-OCT-2000; 2000WO-US28157.

XX 29-OCT-1999; 99US-0162464.

XX (BIOM-) INST APPLIED BIOMEDICINE.

XX Chaplin JW;

XX WPI; 2001-316435/33.

XX B cell clonal toxin useful for treating autoimmune disorders such as

XX Grave's disease, myocardial infarction, Crohn's disease, multiple

XX sclerosis, comprises a group that causes toxin to be internalized by B

XX cell -

XX Disclosure; Page 31; 46pp; English.

XX This invention relates to a B cell clonal toxin. The toxin is made from

XX two moieties, the first causes the toxin to be internalized by a B cell,

XX and the second is a biologically acceptable toxin. The invention

XX includes a method for inactivating/killing an antigen specific B cell. A

XX target B cell is contacted with an effective amount of a B cell clonal

XX toxin. The method is useful for selective immunosuppression in conditions

XX characterized by the presence of an unwanted or deleterious immune

XX response, e.g. in the treatment of antigen specific antibody mediated

XX disease conditions. Use of the B cell clonal toxin can result in

XX immunosuppressive; antiinflammatory; antiallergic; virucide;

CC antidiabetic; thyromimetic; antithyroid; vasotropic; cardiant; antiulcer;  
 CC neuroprotective; antirheumatic; antiarthritic; dermatological;  
 CC ophthalmological; and nephrotropic activity. The toxin is particularly  
 CC useful for treating a host suffering from an antigen specific antibody  
 CC mediated disease condition, where the antigen specific antibody is  
 CC produced by an antigen-reactive B cell population present in a host. The  
 CC toxin is useful for treating allergies, viral disease conditions, and  
 CC autoimmune disorders. Also treated are skin diseases; autoimmune  
 CC endocrinopathies; vasculitic syndromes; cardiovascular disease;  
 CC immunohaematologic disorders; gastrointestinal diseases; neurologic  
 CC diseases; collagen vascular diseases; renal diseases; pulmonary diseases;  
 CC and infertility disorders. The present sequence represents a U3 RNP  
 CC epitope. An antibody response to this antigen is implicated in mixed  
 CC connective tissue disorders, which may be treated using the toxin of the  
 CC invention.

XX SQ Sequence 8 AA;  
 Query Match 80.0%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 Db 5 PPPK 8  
 ||||

## RESULT 19

AAW98979

ID AAW98979 standard; peptide; 9 AA.

XX AC AAW98979;

XX AC AAW98979;

XX DT 11-MAY-1999 (first entry)

XX XX

XX FAM-(Pro)8-Lys(epsilon-TMR) peptide.

XX XX Energy transfer; DNA base sequencing; reporter; donor; acceptor;

XX KW Energy transfer; DNA base sequencing; reporter; donor; acceptor;

XX KW terminator; chain terminator method.

XX XX Synthetic.

XX OS

XX PN WO9902544-A1.

XX XX

XX PD 21-JAN-1999.

XX XX

XX PF 10-JUL-1998; 98WO-JP03093.

XX XX

XX PR 11-JUL-1997; 97JP-0186886.

XX XX

XX PA (RIKA ) INST PHYSICAL &amp; CHEM RES.

XX PA (WAKP ) WAKO PURE CHEM IND LTD.

XX XX

XX PI Hayashizaki Y, Tanaka T;

XX XX

XX DR WPI; 1999-120768/10.

XX XX

XX PT New nucleotide derivatives having energy transfer function - contain

XX PT reporters to serve as donor and acceptor, useful in chain

XX PT termination DNA base sequencing

XX XX

XX PS Example; Page 36; 75pp; Japanese.

XX XX

XX CC The present invention describes nucleotide compounds of formula (I):

XX CC Q-V-CO-R1(NH-W2)-NH-CO-CHR2-NR3m-W1 (I) Q = mono or oligonucleotide;

XX CC V = C triple bond C-(CH2)mNH or CH-CH(CH2)n2NH; n1, n2, m = integer;

XX CC R1 = trivalent group; R2, R3 = H or hydrocarbyl; or CHR2NR3 = a ring;

XX CC W1, W2 = fluorescent group. Also described is the use of RNA polymerase

XX CC and a mono or oligonucleotide compound (I') as initiator in a chain

XX CC terminator method for DNA base sequencing. (I') has: (i) a 5'-phosphate

XX CC group; and (ii) two reporters capable of serving as a donor and an

XX CC acceptor in energy transfer. (I') including (I) have improved uptake

XX CC efficiency by RNA polymerases and can so be used with RNA polymerases

XX CC

CC as terminators in DNA base sequencing methods. The present sequence  
 CC represents a peptide used in an example from the present invention.

XX SQ Sequence 9 AA;

Query Match 80.0%; Score 4; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5

Db 6 PPPK 9

||||

## RESULT 20

AAU09144

ID AAU09144 standard; peptide; 9 AA.

XX AC AAU09144;

XX AC AAU09144;

XX DT 19-DEC-2001 (first entry)

XX XX

XX DE Ena/VASP homology (EVH) proline-rich motif #3.

XX XX

XX KW Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;

XX KW cell migration; Ena/VASP; wound healing; actin polymerisation;

XX KW neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke;

XX KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;

XX KW Huntington's disease; ALS-parkinsonism-dementia complex; bulbar palsy;

XX KW Tourette's syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;

XX KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;

XX KW inflammatory disorder; arthritis; allergy; gout; organ transplant;

XX KW cancer; ischaemia.

XX XX

XX OS Synthetic.

XX XX

XX FH Key Location/Qualifiers

XX FT Misc-difference 9

XX FT /label= OTHER

XX FT /note= "Other = any amino acid"

XX XX

XX PN WO200174853-A2.

XX XX

XX PD 11-OCT-2001.

XX XX

XX PF 30-MAR-2001; 2001WO-US10249.

XX XX

XX PR 03-APR-2000; 2000US-194564P.

XX XX

XX PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.

XX PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.

XX XX

XX PI Gertler FB, Bear JE, Wehland J, Loureiro JJ;

XX XX

XX DR WPI; 2001-626380/72.

XX XX

XX PT Regulating cell motility for promoting wound healing and tissue

XX PT regeneration, treating, neurodegenerative disease and metastasis, by

XX PT inducing or depleting a functional enabled/vasodilator-stimulated

XX PT phosphoprotein -

XX XX

XX PS Example 6; Page 66; 107pp; English.

XX XX

XX CC The invention relates to a method of preventing mammalian cell migration,

XX CC comprising inducing a functional Ena(enabled)/vasodilator-stimulated

XX CC phosphoprotein (VASP) or promoting cell migration comprising depleting

XX CC functional Ena/VASP protein in the mammalian cell. The method is useful

XX CC for preventing or promoting mammalian cell migration, preferably tumour

XX CC cell migration in vitro or in vivo and to prevent tumour cell metastasis

XX CC in a subject. An Ena/VASP activator or inhibitor is useful for promoting

XX CC wound healing, preferably fibroblasts or nerve cells of a tissue type

XX CC with the inhibitor to promote actin polymerisation and tissue formation

XX CC on a scaffold. The inhibitor is also useful for preventing

XX CC

CC neurodegeneration such as in Alzheimer's disease, Down Syndrome,  
 CC Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct  
 CC trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia  
 CC complex, progressive supranuclear palsy, progressive bulbar palsy,  
 CC spinocerebellar atrophy, cerebellar amyloidosis, Pick's atrophy, Rett's  
 CC cerebellar degeneration, Tourette's syndrome, hypoglycaemia, hypoxia,  
 CC Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP  
 CC inhibitor is further useful for enhancing learning and memory in a  
 CC subject having or at risk of developing a learning disorder such as  
 CC Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile  
 CC dementia, Korsakow's disorder and age-related memory loss. The inhibitor  
 CC is administered in an amount for inhibiting the activity of Mena in a  
 CC synapse. Ena/VASP activator is useful for disrupting learning and memory  
 CC and the activator is administered in an amount to promote Ena/VASP  
 CC protein-PE65 interaction. Inducing the activity of Ena/VASP protein  
 CC in immune or haematopoietic cells reduces the ability of the cells to  
 CC migrate and this is useful for treating and preventing inflammatory  
 CC disorders such as arthritis, allergy, gout, organ transplant,  
 CC ulcerative colitis and ischaemic diseases and also for treating cancer  
 CC metastasis. The present sequence represents the amino acid sequence  
 CC of Ena/VASP homology (EVH) proline-rich motif #3.

SQ Sequence 9 AA;

Query Match 80.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
 ||||  
 Db 1 FPPP 4

#### RESULT 21

AAB76143  
 ID AAB76143 standard; Peptide; 9 AA.

XX AAB76143;

AC AAB76143;

DT 10-APR-2001 (first entry)

DE Tumour associated antigen Her2/neu immunogenic peptide.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;  
 KW HLA binding peptide; immune response; glycoprotein; cytostatic;  
 KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;  
 KW human immunodeficiency virus; protozoicide; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;  
 KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;  
 KW renal carcinoma; cervical carcinoma; lymphoma; malaria;  
 KW condyloma acuminatum.

XX Homo sapiens.

OS WO200100225-A1.

PN 04-JAN-2001.

PD 28-JUN-2000; 2000WO-US17842.

XX 29-JUN-1999; 99US-0141422.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S;

XX WPI; 2001-112389/12.

XX Composition comprising human leukocyte antigen binding peptide which  
 PT comprises isolated, prepared epitope useful for treating viral  
 PT infections such as acquired immunodeficiency syndrome, and cancer -

PS Claim 1; Page 48; 58pp; English.

XX The present invention describes a composition (I) which comprises at  
 CC least one human leukocyte antigen (HLA) binding peptide comprising an  
 CC isolated, prepared epitope comprising one of 547, 8-11 residue amino acid  
 CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,  
 CC virucide, hepatotropic, antiinflammatory, anti-HIV (human  
 CC immunodeficiency virus) and protozoicide activities, which can be used  
 CC in vaccine production and is an inducer of cytotoxic T-cell response.  
 CC (I) is useful for inducing a cytotoxic T cell response against a  
 CC preselected antigen in a patient expressing a specific major  
 CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic  
 CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to  
 CC treat and/or prevent viral infection and cancer such as prostate cancer,  
 CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,  
 CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal  
 CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma  
 CC acuminatum.

XX Sequence 9 AA;

Query Match 80.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
 ||||  
 Db 1 FPPP 4

#### RESULT 22

AAB76144  
 ID AAB76144 standard; Peptide; 9 AA.

XX AAB76144;

DT 10-APR-2001 (first entry)

DE Tumour associated antigen Her2/neu immunogenic peptide.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;  
 KW HLA binding peptide; immune response; glycoprotein; cytostatic;  
 KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;  
 KW human immunodeficiency virus; protozoicide; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;  
 KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;  
 KW renal carcinoma; cervical carcinoma; lymphoma; malaria;  
 KW condyloma acuminatum.

XX Homo sapiens.

OS WO200100225-A1.

PN 04-JAN-2001.

PD 28-JUN-2000; 2000WO-US17842.

XX 29-JUN-1999; 99US-0141422.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S;

XX WPI; 2001-112389/12.

XX Composition comprising human leukocyte antigen binding peptide which  
 PT comprises isolated, prepared epitope useful for treating viral  
 PT infections such as acquired immunodeficiency syndrome, and cancer -

PS Claim 1; Page 48; 58pp; English.

XX The present invention describes a composition (I) which comprises at

CC least one human leukocyte antigen (HLA) binding peptide comprising an  
 CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid  
 CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,  
 CC virucide, hepatotropic, antiinflammatory, anti-HIV (human  
 CC immunodeficiency virus) and protozoacide activities, which can be used  
 CC in vaccine production and is an inducer of cytotoxic T-cell response.  
 CC (I) is useful for inducing a cytotoxic T cell response against a  
 CC preselected antigen in a patient expressing a specific major  
 CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic  
 CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to  
 CC treat and/or prevent viral infection and cancer such as prostate cancer,  
 CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,  
 CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal  
 CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma  
 CC acuminatum.

SQ Sequence 9 AA;  
 Query Match 80.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
 Db 1 FPPP 4

## RESULT 23

AAE17284  
 ID AAE17284 standard; peptide; 9 AA.

XX AAE17284;

AC AAE17284;

XX 18-APR-2002 (first entry)

XX Human leukocyte antigen (HLA-B7) Ribo'al S26 peptide.

XX Human, artificial antigen presenting cell; AAPC; beta2-microglobulin;  
 KW human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW cytotoxic T lymphocyte; CTL; T cell-specific antigen; TCA; antitumour;  
 KW immune response; cancer.

XX Homo sapiens.

OS WO200194944-A2.

XX 13-DEC-2001.

XX 01-JUN-2001; 2001WO-US17981.

XX 02-JUN-2000; 2000US-209157P.

XX (SLOK ) SLOAN KETTERING INST CANCER RES.

XX Sadelain M, Latouche J;

XX WPI; 2002-139667/18.

XX Artificial antigen presenting cells for activating T lymphocytes,  
 PT comprises eukaryotic cell expressing antigen presenting complex having  
 PT beta2-microglobulin, exogenous accessory molecule, human leukocyte  
 PT antigen molecule and protein -

XX Disclosure; Page 4; 75pp; English.

XX The present invention relates to an artificial antigen presenting cell  
 CC (AAPC) comprising a eukaryotic cell expressing an antigen presenting  
 CC complex comprising beta2-microglobulin, an exogenous accessory molecule,  
 CC a human leukocyte antigen, HLA (major histocompatibility complex, MHC),  
 CC molecule of a single type and a protein that is processed intracellularly  
 CC to produce an exogenous T cell-specific epitope. The invention also  
 CC relates to methods for activation of T lymphocytes. The method is also  
 CC useful for identifying within a test population of cytotoxic T

CC lymphocytes (CTLs), CTLs specifically activated against a known T-cell  
 CC specific antigen (TCA), which is useful for diagnostic purposes. AAPC is  
 CC also useful for activating CTLs, by contacting AAPC with a suitable  
 CC population of T lymphocytes under conditions suitable for the activation  
 CC and isolating the activated CTLs. AAPC is further useful for the  
 CC investigation of primary T cell activation and diagnostic applications  
 CC here primary T cell activation allow discovery of antigens and accessory  
 CC molecules, and diagnostic applications include cell-based assays for  
 CC quantifying immune response in normal, infected or treated (vaccinated)  
 CC patients. Composition comprising AAPC or activated T cells produced by  
 CC utilising AAPC is useful for eliciting an antitumour response. The  
 CC invention is used for the treatment of cancer. The present sequence is  
 CC human HLA-B7 Ribo'al S26 peptide.

XX Sequence 9 AA;

Query Match 80.0%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5  
 Db 4 PPK 7

## RESULT 24

ABJ20100  
 ID ABJ20100 standard; Peptide; 9 AA.

XX ABJ20100;

XX 10-APR-2003 (first entry)

XX MHC binding peptide SEQ ID No 265.

XX Antirheumatic; antiarthritis; antiarthritic; nootropic; neuroprotective;  
 KW antiinflammatory; major histocompatibility complex; MHC;  
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;  
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;  
 KW inflammation; gene therapy; MHC binding peptide.

XX Synthetic.

XX WO200294981-A2.

XX 28-NOV-2002.

XX 16-MAY-2002; 2002WO-IL00383.

XX 16-MAY-2001; 2001US-290958P.

XX 29-MAY-2001; 2001US-0865548.

XX (TECR ) TECHNION RES & DEV FOUND LTD.

XX Barnea E, Beer I, Ziv T, Admon A, Dasseau L, Buchsbaum S;

XX WPI; 2003-210043/20.

XX Identifying peptides that are capable of binding to major  
 PT histocompatibility complex (MHC) molecules of a particular haplotype by  
 PT analyzing peptides bound to the soluble and secreted form of the MHC  
 PT molecules of the particular haplotype -

XX Claim 51; Page 211; 238pp; English.

XX The invention relates to a novel method for identifying peptides  
 CC originating from a particular cell type, which are capable of binding to  
 CC major histocompatibility complex (MHC) molecules of a particular  
 CC haplotype. The method comprises analysing peptides bound to the soluble  
 CC and secreted form of the MHC molecules of the particular haplotype. The  
 CC method is useful for identifying peptides for treating an autoimmune  
 CC disease, such as T or B cell and/or allergic disease or condition,  
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,

CC e.g. Alzheimer's disease, or diseases associated with inflammation. The  
CC sequences of the invention may be used in a gene therapy application.  
CC -This sequence represents a peptide relating to the method for identifying  
CC MHC binding peptides of the invention.

XX Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
DB 4 PPPK 7

RESULT 25

ABP58250  
ID ABP58250 standard; Peptide; 9 AA.

XX AC ABP58250;

XX DT 07-APR-2003 (first entry)

XX DE Human pre-gastrokine (pre-AMP-18) peptide 109-117.

XX KW Human; gastrokine; AMP-18; gastric antrum mucosal protein; mitogen;  
XX growth factor; vulnery.

XX OS Homo sapiens.

XX PN WO200292758-A2.

XX PD 21-NOV-2002.

XX PF 29-MAR-2002; 2002WO-US10148.

XX PR 29-MAR-2001; 2001US-0821726.

XX PA (UYCH-) UNIV CHICAGO.

XX PI Toback FG, Martin TE, Powell CT, Agarwal K;

XX DR WPI; 2003-120666/11.

XX ST Gastric Antrum Mucosal Protein 18, useful for preparing a composition  
PT for healing of the injured gastrointestinal tract -

XX PS Disclosure; Page 24; 67pp; English.

XX CC The present sequence is that of a peptide comprising amino acids  
CC 109-117 of human gastric antrum mucosal protein 18 (AMP-18)  
CC precursor polypeptide (see AMP58250), a novel gastrokine. The  
CC AMP-18 protein, and active peptides derived from its sequence,  
CC are cellular growth factors and can be used to stimulate the  
CC growth of epithelial cells of the gastrointestinal tract (claimed).  
CC The concentration of peptide 109-117 for half-maximal growth  
CC stimulation (K<sub>1/2</sub>) of BSC-1 epithelial cells was 2.5 uM.

XX Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
DB 6 PPPK 9

RESULT 26

AAE33297  
ID AAE33297 standard; peptide; 9 AA.

XX AAE33297;

XX DT 02-APR-2003 (first entry)

XX DE Human pre-AMP-18 peptide #9.

XX KW Cellular growth stimulating protein; gastric antrum mucosal protein;  
XX gastrokine; AMP-18 protein; gastro-intestinal disorder; cell therapy;  
XX ulcer; human.

XX OS Homo sapiens.

XX PN WO200278640-A2.

XX PD 10-OCT-2002.

XX PF 29-MAR-2002; 2002WO-US09885.

XX PR 29-MAR-2001; 2001US-0821726.

XX PA (UYCH-) UNIV CHICAGO.

XX PI Toback GF, Martin TE, Walsh-Reitz M;

XX DR WPI; 2003-103239/09.

XX ST Protein inhibitor, useful for treating gastrointestinal disorders or  
PT diseases comprises isolated homologous cellular stimulating proteins -  
XX Disclosure; Page 35; 84pp; English.

XX CC The invention relates to a protein inhibitor which comprises homologous  
CC cellular growth stimulating proteins designated gastrokines. The  
CC invention also provides gastric antrum mucosal proteins designated  
CC AMP-18 which belongs to the novel group of gastrokines and nucleic acid  
CC molecules encoding such proteins. Pharmaceutical composition comprising  
CC growth stimulating peptide derived from a gastrokine protein is useful  
CC for treating gastro-intestinal disorder or diseases associated with  
CC overgrowth of gastric epithelia e.g. ulcer. The invention is useful in  
CC cell therapy. The present sequence is human pre-AMP-18 peptide.

XX Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
DB 6 PPPK 9

RESULT 27

AAP80874

ID AAP80874 standard; protein; 10 AA.

XX AC AAP80874;

XX DT 25-MAR-2003 (updated)

XX DT 06-NOV-1990 (first entry)

XX DE Hook region #5 contg cleavage site and hinge region.

XX KW hook region; peptide cleavage site; hinge region.

XX OS synthetic.

XX Key Location/Qualifiers

XX FT Cleavage-site 1..1

XX FT /label=potential cleavage site

XX FT /note="linked to leader encoding beta-gal"

XX FT Cleavage-site 10..10





AC AAB76191;  
 XX  
 DT 10-APR-2001 (first entry)  
 XX  
 DE Tumour associated antigen Her2/neu immunogenic peptide.  
 XX  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;  
 KW HLA binding peptide; immune response; glycoprotein; cytostatic;  
 KW viricide; hepatotropic; antiinflammatory; anti-HIV; vaccine;  
 KW human immunodeficiency virus; protozoicide; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;  
 KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;  
 KW renal carcinoma; cervical carcinoma; lymphoma; malaria;  
 KW condyloma acuminatum.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200100225-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 28-JUN-2000; 2000WO-US17842.  
 XX  
 PR 29-JUN-1999; 99US-0141422.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S;  
 XX  
 DR WPI; 2001-112389/12.  
 XX  
 PT Composition comprising human leukocyte antigen binding peptide which  
 PT comprises isolated, prepared epitope useful for treating viral  
 PT infections such as acquired immunodeficiency syndrome, and cancer -  
 XX  
 PS Claim 1; Page 49; 58pp; English.  
 XX  
 CC The present invention describes a composition (I) which comprises at  
 CC least one human leukocyte antigen (HLA) binding peptide comprising an  
 CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid  
 CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,  
 CC viricide, hepatotropic, antiinflammatory, anti-HIV (human  
 CC immunodeficiency virus) and protozoicide activities, which can be used  
 CC in vaccine production and is an inducer of cytotoxic T-cell response.  
 CC (I) is useful for inducing a cytotoxic T cell response against a  
 CC preslected antigen in a patient expressing a specific major  
 CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic  
 CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to  
 CC treat and/or prevent viral infection and cancer such as prostate cancer,  
 CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,  
 CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal  
 CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma  
 CC acuminatum.  
 XX  
 SQ Sequence 10 AA;  
 XX  
 Query Match 80.0%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 ||||  
 Db 1 FPPP 4  
 ||||  
 RESULT 30  
 AAW98980  
 ID AAW98980 standard; peptide; 11 AA.  
 AC  
 XX AAW98980;  
 XX  
 DT 11-MAY-1999 (first entry)

XX FAM-(Pro)10-Lys(epsilon-TMR) peptide.  
 DE  
 XX Energy transfer; DNA base sequencing; reporter; donor; acceptor;  
 KW terminator; chain terminator method.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9902544-A1.  
 PN  
 XX 21-JAN-1999.  
 PD  
 XX 10-JUL-1998; 98WO-JP03093.  
 PF  
 XX 11-JUL-1997; 97JP-0186886.  
 PR  
 XX (RIKA ) INST PHYSICAL & CHEM RES.  
 PA (WAKP ) WAKO PURE CHEM IND LTD.  
 XX  
 PI Hayashizaki Y, Tanaka T;  
 XX  
 DR WPI; 1999-120768/10.  
 XX  
 XX New nucleotide derivatives having energy transfer function - contain  
 PT reporters to serve as donor and acceptor, useful in chain  
 PT termination DNA base sequencing  
 XX  
 PS Example; Page 38; 75pp; Japanese.  
 XX  
 CC The present invention describes nucleotide compounds of formula (I):  
 CC Q-V-CO-R1(NH-W2)-NH(CO-CHR2-NR3)m-W1 (I) Q = mono or oligonucleotide;  
 CC V = C triple bond C-(CH2)nNH or CH=CH(CH2)n2NH; n1, n2, m = integer;  
 CC R1 = trivalent group; R2, R3 = H or hydrocarbyl; or CHR2NR3 = a ring;  
 CC W1, W2 = fluorescent group. Also described is the use of RNA polymerase  
 CC and a mono or oligonucleotide compound (I') as initiator in a chain  
 CC terminator method for DNA base sequencing. (I') has: (i) a 5'-phosphate  
 CC group; and (ii) two reporters capable of serving as a donor and an  
 CC acceptor in energy transfer. (I') including (I) have improved uptake  
 CC efficiency by RNA polymerases and can so be used with RNA polymerases  
 CC as terminators in DNA base sequencing methods. The present sequence  
 CC represents a peptide used in an example from the present invention.  
 XX  
 SQ Sequence 11 AA;  
 XX  
 Query Match 80.0%; Score 4; DB 20; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPPK 5  
 ||||  
 Db 8 PPPK 11  
 ||||  
 RESULT 31  
 AAY56001  
 ID AAY56001 standard; peptide; 11 AA.  
 XX  
 AC AAY56001;  
 XX  
 DT 15-MAR-2000 (first entry)  
 XX  
 DE Mucor hiemalis endo-beta-N-acetylglucosaminidase peptide p60-AP-2.  
 XX  
 KW Endo-beta-N-acetylglucosaminidase; enzyme; cleavage; sugar chain;  
 KW carbohydrate; glycoprotein; disease; cancer.  
 XX  
 OS Mucor hiemalis.  
 XX  
 PN WO9961591-A1.  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 20-MAY-1999; 99WO-JP02644.

XX 22-MAY-1998; 98JP-0141717.  
 PR (KIRI ) KIRIN BEER KK.  
 PA Kobayashi K, Takeuchi M, Iwamatsu A, Yamamoto K, Kumagai H;  
 PI Yoshida S;  
 XX WPI; 2000-062704/05.  
 DR Polynucleotides encoding endo-beta-N-acetylglucosaminidase, useful for  
 PT the specific cleavage of complex sugar chains -  
 PT Example 4; Page 22; 72pp; Japanese.  
 XX Peptides AAY55994-Y56014 represent fragments of the Mucor hiemalis  
 CC endo-beta-N-acetylglucosaminidase protein derived by cleavage with  
 CC Lys-C protease and subsequent amino acid sequencing. The peptide  
 CC sequences were then used to generate primers to isolate the coding  
 CC sequence for isolating the corresponding gene. The protein is useful  
 CC for the specific cleavage of complex sugar chains for the preparation,  
 CC investigation and modification of these chains, especially in complex  
 CC carbohydrates forming part of a glycoprotein molecule which undergoes  
 CC modification in diseases such as cancer.  
 XX SQ Sequence 11 AA;  
 Query Match 80.0%; Score 4; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPK 5  
 DB 8 PPK 11  
 RESULT 32  
 AAW32743  
 ID AAW32743 standard; peptide; 12 AA.  
 XX AC AAW32743;  
 XX 30-JAN-1998 (first entry)  
 XX Human platelet glycoprotein Ib/IX complex epitope mimotope.  
 DE Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;  
 KW monoclonal antibody S2-2; anti mimotope; binding site; antibody;  
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;  
 KW anti thrombotic drug; ristocetin.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9718236-A1.  
 XX 22-MAY-1997.  
 XX 08-NOV-1996; 96WO-US17882.  
 XX 13-NOV-1995; 95US-0556597.  
 XX (UTNY ) UNIV NEW YORK STATE RES FOUND.  
 PA Lyle VA, Miller JL;  
 XX WPI; 1997-289227/26.  
 XX Peptide which mimics human platelet glycoprotein Ib/IX complex  
 PT epitope - also anti-mimotope molecule capable of binding to the  
 PT peptide and useful to modulate platelet adhesion, aggregation or  
 PT agglutination

PS Claim 8; Page 99; 115pp; English.  
 XX The present sequence represents a mimotope which functionally mimics a  
 CC binding site for a monoclonal antibody (Mab) which recognises an epitope  
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More  
 CC specifically the Mab is S2-2. The mimotope peptide can be used for  
 CC raising antibodies, as probes to search for anti-mimotopes and to  
 CC neutralise the inhibitory activity of those antibodies which recognise  
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used  
 CC to modulate the adhesion, aggregation or agglutination of platelets by  
 CC affecting von Willebrand factor interaction with the platelets through  
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits  
 CC the ristocetin induced aggregation of platelets.  
 XX SQ Sequence 12 AA;  
 Query Match 80.0%; Score 4; DB 18; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 DB 5 FPPP 8  
 RESULT 33  
 AAW23206  
 ID AAW23206 standard; peptide; 12 AA.  
 XX AC AAW23206;  
 XX 28-OCT-1997 (first entry)  
 XX Terminal peptide extension for lipolytic enzyme.  
 DE Lipolytic enzyme; modification; peptide extension; detergent;  
 KW washing powder; dishwashing composition; pitch removal; paper;  
 KW pulp; manufacture; degreasing; hide; sheepskin; wool; catalysis;  
 KW organic synthesis; transesterification; esterification;  
 KW ester hydrolysis; baking; defatting.  
 XX Synthetic.  
 OS WO9704078-A1.  
 XX 06-FEB-1997.  
 XX 12-JUL-1996; 96WO-DK00321.  
 XX 01-APR-1996; 96DK-0000372.  
 PR 14-JUL-1995; 95DK-0000832.  
 PR 13-SEP-1995; 95DK-0001013.  
 PR 29-SEP-1995; 95DK-0001096.  
 PR 21-NOV-1995; 95DK-0001306.  
 PR 14-FEB-1996; 96US-0011634.  
 XX (NOVO ) NOVO-NORDISK AS.  
 PA Fuglsang CC, Halkier T, Jorgensen ST, Okkels JS;  
 PI Patkar SA, Perteresen DA, Thellersen M, Vind J;  
 XX WPI; 1997-132621/12.  
 XX Modified lipolytic enzymes with peptide extensions at one or both  
 PT ends - esp. for use in detergent and dishwashing compsn., have  
 PT improved substrate affinity, stability and wash performance  
 XX Claim 12; Page 179; 197pp; English.  
 XX A lipolytic enzyme, modified by a peptide extension, e.g. the  
 CC present sequence, of its carboxy and/or amino terminus, can be used  
 CC in detergents, particularly in washing powders or dishwashing  
 CC compositions. It may also be used to remove pitch in paper and

CC pulp manufacture, to degrease hides, sheepskins and wool, to  
 CC catalyze organic synthesis, e.g. (trans)esterification or ester  
 CC hydrolysis, in baking and in other degreasing/defaulting processes.  
 CC The peptide extension(s) increases substrate affinity, confers  
 CC stability and especially improves wash performance, i.e. better  
 CC lipid soil removal, reducing the amount of enzyme used.  
 CC  
 SQ Sequence 12 AA;

Query Match 80.0%; Score 4; DB 18; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 ||||  
 DB 2 PPPK 5

RESULT 34  
 AAW21083  
 ID AAW21083 standard; peptide; 12 AA.  
 XX  
 AC AAW21083;  
 XX  
 DT 19-JUN-1997 (first entry)  
 XX  
 DE Lipolytic enzyme opt. N- or C-terminal extension peptide #51.  
 XX  
 KW Lipolytic enzyme; detergent; lard; cotton swatch; laundry;  
 KW dishwashing.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9707202-A.  
 XX  
 PD 27-FEB-1997.  
 XX  
 PF 12-AUG-1996; 96WO-DK00341.  
 XX  
 PR 07-MAY-1996; 96US-0016754.  
 PR 11-AUG-1995; 95DK-0000905.  
 PR 29-SEP-1995; 95DK-0001096.  
 PR 14-FEB-1996; 96US-0011627.  
 PR 01-APR-1996; 96DK-0000374.  
 XX  
 PA (NOVO ) NOVO-NORDISK AS.  
 XX  
 PI Borch K, Kretzschmar T, Okkels JS, Patkar SA, Petersen DA;  
 PI Royer JC, Svendsen A, Thellersen M;  
 XX  
 DR WPI; 1997-165287/15.  
 XX  
 XX Lipolytic enzyme with high capacity to remove lard in one wash cycle -  
 PT also related DNA, vectors and transformed cells, useful in laundry and  
 PT dishwashing formulations  
 XX  
 PS Claim 17; Page 245; 274pp; English.  
 XX  
 CC The sequences given in AAW21033-92 are peptides which may be added to  
 CC the N- or C-terminal of the lipolytic enzyme of the invention. The  
 CC lipolytic enzyme, when present in a specified detergent composition,  
 CC is able to remove at least 15% more lard from soiled cotton swatches  
 CC (9 by 9 cm) than an equiv. enzyme-free compsn. in a one-cycle wash  
 CC assay. The assay uses 7 lard-stained cotton swatches in 1000 ml  
 CC water (3.2 mM Ca2+/Mg2+, ratio 5:1; 5 g/l detergent; pH 10 plus 12500 LU  
 CC of enzyme/l) for 20 min at 30 deg.C, in a thermostated Terg-O-to-Meter,  
 CC then 15 min rinsing, drying overnight and soxhlet extn. and  
 CC quantification of fatty material. The enzyme may be used in laundry  
 CC and dishwashing formulations. It is able to remove a substantial  
 CC amount of lard in a single cycle under realistic washing conditions.  
 CC  
 SQ Sequence 12 AA;

Query Match 80.0%; Score 4; DB 18; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 ||||  
 DB 2 PPPK 5

RESULT 35  
 AAY67258  
 ID AAY67258 standard; protein; 12 AA.  
 XX  
 AC AAY67258;  
 XX  
 DT 05-APR-2000 (first entry)  
 XX  
 DE PTP-PEST substrate competition peptide.  
 XX  
 KW Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion;  
 KW cell migration; division; cytostatic; antiinflammatory; angiogenesis;  
 KW cancer; enzyme substrate identification.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9961467-A2.  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 21-MAY-1999; 99WO-CA00461.  
 XX  
 PR 21-MAY-1998; 98CA-2238654.  
 PR 11-DEC-1998; 98US-0111993.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Tremblay ML, Cote J, Angers-Lousteau A, Charest A;  
 XX  
 DR WPI; 2000-097104/08.  
 XX  
 XX Novel therapeutic agents for treating diseases which are related to  
 PT cell proliferation, migration, inflammation and angiogenesis especially  
 PT cancer -  
 XX  
 PS Example 5; Page 41; 91pp; English.  
 XX  
 CC This peptide is used to compete with protein tyrosine phosphatase (PTP)  
 CC PEST for its natural substrates (e.g. p130Cas). PTP-PEST is a soluble  
 CC PTP that is ubiquitously expressed throughout embryonic development and  
 CC in murine adult tissues. The N-terminal portion of the enzyme encodes  
 CC for the catalytic domain, while the C-terminal portion is composed of 5  
 CC proline rich domains, and a binding site for the adaptor protein Shc.  
 CC The pro 2 domain is required for paxillin binding, and the synthesis of  
 CC mutant PTP-PEST have shown that proline 362 is important for paxillin  
 CC binding activity. The invention relates to a compound that is capable of  
 CC interfering with the binding of PTP-PEST to signalling molecules  
 CC (e.g. paxillin) that are involved in cell migration, adhesion or  
 CC division. The compound can be derived from minimal sequences (see  
 CC AAY67254 and AAY67255) found in binding sites of PTP-PEST. The invention  
 CC also relates to a method for finding a genuine substrate for an enzyme in  
 CC a cell that normally expresses the wild type form of the enzyme. A  
 CC mutant version of PTP-PEST (see AAY67251 and AAY67253) is used in this  
 CC method. The compounds have cytostatic and antiinflammatory activity. The  
 CC compounds are used for making medicaments for treating a disease related  
 CC with cell proliferation, migration, inflammation and angiogenesis,  
 CC especially cancer. The novel method is used for identifying a genuine  
 CC substrate for an enzyme.  
 XX  
 SQ Sequence 12 AA;

Query Match 80.0%; Score 4; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 4 PPPK 7

RESULT 36  
AAR74384  
ID AAR74384 standard; peptide; 13 AA.  
XX  
AC  
XX AAR74384;  
XX 23-JAN-1996 (first entry)  
DT  
XX HTLV-1 p27(rex) protein antigenic peptide rex13.  
DE Human T-cell lymphotropic virus type I; HTLV-I; p27(rex) protein;  
KW antigenic peptide; rex13; residues 177-189; adult T-cell leukaemia;  
KW HTLV-I associated myelopathy.  
XX  
OS Human lymphotropic virus type I.  
XX  
XX US5420244-A.  
PN  
XX 30-MAY-1995.  
PD  
XX  
XX 06-AUG-1993; 93US-0103742.  
PF  
XX  
PR 06-AUG-1993; 93US-0103742.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX Lal RB, Rudolph DL;  
PI  
XX WPI; 1995-206307/27.  
DR  
XX New HTLV-I antigenic peptide(s) - used for diagnosing HTLV-I  
PT infection(s), partic. HTLV-I associated myelopathy and adult T-cell  
XX leukemia  
XX  
XX Example 1; Columns 11-12; 21pp; English.  
PS  
XX AAR74376-R74384 are human T-cell lymphotropic virus type I (HTLV-I)  
CC p27(rex) protein antigenic peptides. They can be used to diagnose  
CC diseases caused by HTLV-I, e.g. adult T-cell leukaemia, and HTLV-I  
CC associated myelopathy.  
XX  
XX Sequence 13 AA;  
SQ

Query Match 80.0%; Score 4; DB 16; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
Db 2 FPPP 5

RESULT 37  
AAW38122  
ID AAW38122 standard; Peptide; 13 AA.  
XX  
AC AAW38122;  
XX  
DT 23-APR-1998 (first entry)  
XX  
DE - PPPPY motif containing peptide ENAC-beta.  
XX  
XX Peptide recognition unit; WW domain; cell signalling; growth regulation;  
KW cytoskeleton organisation; targeted drug screening; modulator;  
KW WW domain interaction; YAP protein; dystrophin;  
KW epithelial sodium channel protein.  
XX

OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Region 4..8  
FT /note= "PPPPY motif"  
XX  
XX W09737223-A1.  
PN  
XX 09-OCT-1997.  
PD  
XX 03-APR-1997; 97WO-US05547.  
PF  
XX 03-APR-1996; 96US-0630916.  
PR  
XX (CYTO-) CYTOGEN CORP.  
PA (OYNC-) UNIV NORTH CAROLINA.  
XX  
XX Fowlkes DM, Kay BK, Pirozzi G;  
PI  
XX WPI; 1997-503234/46.  
DR  
XX Identifying cell signalling and growth regulatory polypeptides by  
PT reaction with multivalent recognition complex - polypeptides are  
PT useful in targetted drug selection  
XX  
XX Example 6.3; Fig 24B; 220pp; English.  
PS  
XX Peptides AAW38115-28 are derived from epithelial sodium channel alpha  
CC (ENAC-alpha), beta (ENAC-beta) and gamma (ENAC-gamma) proteins. The  
CC peptides contain PPPPY-like motifs, which are found in the proline rich  
CC regions of WBP-1 and WBP-2 proteins. Peptides containing this residue  
CC bind to the YAP WW domain, but not the WW domain from dystrophin  
CC or to a panel of SH3 domains. Peptides AAW38115-28 were biotinylated and  
CC complexed with alkaline streptavidin, and used in a cross affinity  
CC mapping experiment. They were tested for their ability to bind to the 3  
CC individual novel WW domains of WWP4 (AAW36797), which were expressed as  
CC glutathione-S-transferase expression proteins. The present peptide does  
CC not bind to the WW domains of the WWP4 protein. The WW domain is a  
CC small functional domain. Its name is derived from the observation that  
CC two tryptophan residues, one in the amino terminal portion of the WW  
CC domain and one in the carboxyl terminal portion, are conserved. Most  
CC proteins containing WW domains have a function involving cell signalling  
CC and growth regulation or the organisation of the cytoskeleton.  
CC Polypeptides containing a WW domain are identified by treating a  
CC multivalent recognition unit complex that has selective binding affinity  
CC for a WW domain, with many polypeptides and identifying those with  
CC selective affinity for the complex. Proteins containing WW domains are  
CC used for targeted drug screening, i.e. to identify potential modulators  
CC of specific WW domain interactions.  
XX  
XX Sequence 13 AA;  
SQ

Query Match 80.0%; Score 4; DB 18; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 4 PPPK 7

RESULT 38  
AAW38064  
ID AAW38064 standard; peptide; 13 AA.  
XX  
AC AAW38064;  
XX  
XX 23-APR-1998 (first entry)  
DT  
XX Peptide recognition unit ENAC-gamma used to identify WW domains.  
DE  
XX Peptide recognition unit; YAP WW domain binding protein; WBP-1; WBP-2;  
KW WW domain; cell signalling; growth regulation; cytoskeleton organisation;  
KW

targeted drug screening; modulator; WW domain interaction.

XX Synthetic.  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "residue is biotinylated"  
 XX  
 PN WO9737223-A1.  
 XX  
 PD 09-OCT-1997.  
 XX  
 XX 03-APR-1997; 97WO-US05547.  
 PF  
 XX 03-APR-1996; 96US-0630916.  
 PR  
 XX (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Fowlkes DM, Kay BK, Pirozzi G;  
 XX  
 XX WPI; 1997-503234/46.  
 DR  
 XX  
 XX Identifying cell signalling and growth regulatory polypeptides by  
 PT reaction with multivalent recognition complex - polypeptides are  
 PT useful in targetted drug selection  
 PT  
 XX  
 XX Example 1; Page 71; 220pp; English.  
 PS  
 XX Peptides AAW38063-64 are peptide recognition units that are based on  
 CC the sequences of WW domain binding domains of the alpha and gamma  
 CC subunits of epithelial sodium channel protein. They were used to  
 CC screen a cDNA expression library generated from LNCap prostate  
 CC cancer cell line. A novel human gene WWP4 (AAW36797) was identified. The  
 CC WW domain is a small functional domain found in a large number of  
 CC proteins from a variety of species including humans, nematodes and  
 CC yeast. Its name is derived from the observation that two tryptophan  
 CC residues, one in the amino terminal portion of the WW domain and one in  
 CC the carboxyl terminal portion, are conserved. Most proteins containing  
 CC WW domains have a function involving cell signalling and growth  
 CC regulation or the organisation of the cytoskeleton. Polypeptides  
 CC containing a WW domain are identified by treating a multivalent  
 CC recognition unit complex that has selective binding affinity for a WW  
 CC domain, with many polypeptides and identifying those with selective  
 CC affinity for the complex. Proteins containing WW domains are used for  
 CC targeted drug screening, i.e. to identify potential modulators of  
 CC specific WW domain interactions. The valency of the recognition unit is  
 CC important in determining specificity of interaction with WW domains. In  
 CC multivalent form specificity is relaxed, but not lost, so proteins  
 CC containing WW domains similar, but not identical, to the sequence of the  
 CC peptides' target WW can be detected, including new polypeptides.  
 XX  
 XX  
 SQ Sequence 13 AA;  
 Query Match 80.0%; Score 4; DB 18; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 PPK 5  
 Db |||||  
 4 PPK 7  
 RESULT 39  
 AAW98981  
 ID AAW98981 standard; peptide; 13 AA.  
 XX  
 AC AAW98981;  
 XX  
 XX 11-MAY-1999 (first entry)  
 DT  
 XX FAM- (Pro)12-Lys (epsilon-TMR) peptide.  
 DE  
 XX

KW Energy transfer; DNA base sequencing; reporter; donor; acceptor;  
 KW terminator; chain terminator method.  
 XX  
 XX Synthetic.  
 XX  
 PN WO9902544-A1.  
 XX  
 PD 21-JAN-1999.  
 XX  
 XX 10-JUL-1998; 98WO-JP03093.  
 PF  
 XX 11-JUL-1997; 97JP-0186886.  
 PR  
 XX (RIKA ) INST PHYSICAL & CHEM RES.  
 PA (WAKP ) WAKO PURE CHEM IND LTD.  
 XX  
 PI Hayashizaki Y, Tanaka T;  
 XX  
 XX WPI; 1999-120768/10.  
 DR  
 XX New nucleotide derivatives having energy transfer function - contain  
 PT reporters to serve as donor and acceptor, useful in chain  
 PT termination DNA base sequencing  
 PT  
 XX  
 XX Example; Page 39; 75pp; Japanese.  
 PS  
 XX The present invention describes nucleotide compounds of formula (I):  
 CC Q-V-CO-R1(NH-W2)-NH(CO-CHR2-NR3)m-W1 (I) Q = mono or oligonucleotide;  
 CC V = C triple bond C-(CH2)nmNH or CH=CH(CH2)n2NH; n1, n2, m = integer;  
 CC R1 = trivalent group; R2, R3 = H or hydrocarbyl; or CHR2NR3 = a ring;  
 CC W1, W2 = fluorescent group. Also described is the use of RNA polymerase  
 CC and a mono or oligonucleotide compound (I') as initiator in a chain  
 CC terminator method for DNA base sequencing. (I') has: (i) a 5'-phosphate  
 CC group; and (ii) two reporters capable of serving as a donor and an  
 CC acceptor in energy transfer. (I') including (I) have improved uptake  
 CC efficiency by RNA polymerases and can so be used with RNA polymerases  
 CC as terminators in DNA base sequencing methods. The present sequence  
 CC represents a peptide used in an example from the present invention.  
 XX  
 XX  
 SQ Sequence 13 AA;  
 Query Match 80.0%; Score 4; DB 20; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 PPK 5  
 Db |||||  
 10 PPK 13  
 RESULT 40  
 AAR06249  
 ID AAR06249 standard; protein; 14 AA.  
 XX  
 AC AAR06249;  
 XX  
 XX 09-JAN-2003 (updated)  
 DT 07-DEC-1990 (first entry)  
 DT  
 XX Antigenic peptide fragment selected from the 12 N-terminal AAs of  
 DE heptadecagastrin (G17).  
 DE  
 XX Gastrin; tumours; peptic ulcers; diphtheria toxoid; tetanus toxin;  
 KW  
 XX Unidentified.  
 OS  
 XX EP380230-A.  
 PN  
 XX 01-AUG-1990.  
 PD  
 XX 17-JAN-1990; 90EP-0300456.  
 PF  
 XX 12-MAY-1989; 89US-0351193.  
 PR

```

PR 24-JAN-1989; 89US-0301353.
XX (APHT-) APHTON CORP.
XX
XX Gevas PC, Grimes S, Karr SL, Littenberg RL;
PI WPI; 1990-233029/31.
DR
XX Immunogens against gastrin peptide(s) - used to induce antibodies
PT that specifically neutralise single form of gastrin, G17 or G34
XX
XX Claim 8; Page 19; 32pp; English.
XX
XX Antigenic fragments may be attached to an immunogenic carrier
CC and used to raise Abs to a specific single form of Gastrin
CC ie. G17 or G34. Peptide fragments capable of binding to these
CC Abs are useful in neutralising anti-gastrin Abs in vivo.
CC (Updated on 09-JAN-2003 to add missing OS field.)
XX
XX Sequence 14 AA;
SQ
Query Match 80.0%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PPK 5
DB 11 PPK 14

RESULT 41
AAG79174
ID AAG79174 standard; peptide; 14 AA.
XX
XX AAG79174;
XX
XX 03-JAN-2002 (first entry)
XX
XX Peptide derived from ActA, and containing EVH1-binding site.
XX
XX ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;
XX enabled/vasodilator-stimulated phosphoprotein protein; T cell;
XX T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
XX infectious disease; cancer; autoimmune disease; inflammation;
XX platelet aggregation; wound healing; clotting.
XX
XX Listeria monocytogenes.
XX
XX WO200174858-A2.
XX
XX 11-OCT-2001.
XX
XX 03-APR-2001; 2001WO-US10753.
XX
XX 03-APR-2000; 2000US-194215P.
XX
XX (NASI ) MASSACHUSETTS INST TECHNOLOGY.
XX (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX
XX Krause M, Sechi AS, Gertler FB, Wehland J;
XX WPI; 2001-616686/71.
XX
XX Modulating cytoskeletal rearrangement to regulate T cell and macrophage
XX activation for treating cancer, autoimmune disease, and infectious
XX disease, comprises contacting with a Fyb/SLAP complex modulator
XX
XX Example 5; Page 43; 79pp; English.
XX
XX The specification describes Fyb/SLAP proteins. Fyb/SLAP proteins are
XX ligands for the EVH1 domains of Ena(enabled)/vasodilator-stimulated
XX phosphoprotein (VASP) proteins. The specification describes a method for
XX modulating cytoskeletal rearrangement in a cell, or T cell response to T

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CC cell receptor stimulation. The method comprises contacting the cell or T
CC cell with a Fyb/SLAP complex modulator sufficient to modulate the
CC formation of a complex of an Ena/VASP protein and a Fyb/SLAP protein.
CC The method is useful for modulating cytoskeletal rearrangement in a cell
CC such as a lymphocyte, preferably a T cell, a macrophage or a cell
CC fragment such as a platelet and for modulating T cell response to a
CC T cell receptor stimulation. T cell response is increased in a subject
CC having or at risk of developing infectious disease or cancer and T cell
CC response is inhibited in a subject having or is at risk of developing an
CC autoimmune disease or a condition characterized by inflammation. A
CC composition comprising a Fyb/SLAP complex inhibitor is useful for
CC increasing platelet aggregation for promoting wound healing or
CC clotting. The present sequence represents a peptide derived from
CC ActA, which is used in the course of the invention.
XX
XX Sequence 14 AA;
SQ
Query Match 80.0%; Score 4; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PPK 4
DB 3 PPK 6

RESULT 42
ABP58245
ID ABP58245 standard; Peptide; 14 AA.
XX
XX ABP58245;
XX
XX 07-APR-2003 (first entry)
XX
XX Human pre-gastrokine (pre-AMP-18) peptide 104-117.
XX
XX Human; gastrokine; AMP-18; gastric antrum mucosal protein; mitogen;
XX growth factor; vulnerary.
XX
XX Homo sapiens.
XX
XX WO200292758-A2.
XX
XX 21-NOV-2002.
XX
XX 29-MAR-2002; 2002WO-US10148.
XX
XX 29-MAR-2001; 2001US-0821726.
XX (UYCH-) UNIV CHICAGO.
XX
XX Toback FG, Martin TE, Powell CT, Agarwal K;
XX WPI; 2003-120666/11.
XX
XX Gastric Antrum Mucosal Protein 18, useful for preparing a composition
XX for healing of the injured gastrointestinal tract
XX
XX Claim 11; Page 41; 67pp; English.
XX
XX The present sequence is that of a peptide comprising amino acids
XX 104-117 of human gastric antrum mucosal protein 18 (AMP-18)
XX precursor polypeptide (see AMP58257), a novel gastrokine. The
XX AMP-18 protein and active peptides derived from its sequence, and can
XX be used to stimulate the growth of epithelial cells of the
XX gastrointestinal tract (claimed). The concentration of peptide
XX 104-117 for half-maximal growth stimulation (K1/2) of BSC-1
XX epithelial cells was 0.8 uM.
XX
XX Sequence 14 AA;
SQ
Query Match 80.0%; Score 4; DB 24; Length 14;

```

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Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
DB 11 PPPK 14

RESULT 43
AAE33291
ID AAE33291 standard; peptide; 14 AA.
XX AC AAE33291;
XX DT 02-APR-2003 (first entry)
XX DE Human pre-AMP-18 peptide #3.
XX KW Cellular growth stimulating protein; gastric antrum mucosal protein;
KW gastrokine; AMP-18 protein; gastro-intestinal disorder; cell therapy;
KW ulcer; human.
XX OS Homo sapiens.
XX PN WO200278640-A2.
XX PD 10-OCT-2002.
XX PF 29-MAR-2002; 2002WO-US09885.
XX PR 29-MAR-2001; 2001US-0821726.
XX PA (UYCH-) UNIV CHICAGO.
XX PI Toback GF, Martin TE, Walsh-Reitz M;
XX DR WPI; 2003-103239/09.
XX PT Protein inhibitor, useful for treating gastrointestinal disorders or
XX diseases comprises isolated homologous cellular stimulating proteins -
XX Claim 1; Page 51; 84pp; English.
XX The invention relates to a protein inhibitor which comprises homologous
XX cellular growth stimulating proteins designated gastrokines. The
XX invention also provides gastric antrum mucosal proteins designated
XX AMP-18 which belongs to the novel group of gastrokines and nucleic acid
XX molecules encoding such proteins. Pharmaceutical composition comprising
XX growth stimulating peptide derived from a gastrokine protein is useful
XX for treating gastro-intestinal disorder or diseases associated with
XX overgrowth of gastric epithelia e.g. ulcer. The invention is useful in
XX cell therapy. The present sequence is human pre-AMP-18 peptide.
XX SQ Sequence 14 AA;

Query Match 80.0%; Score 4; DB 24; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
DB 11 PPPK 14

RESULT 44
AAR02172
ID AAR02172 standard; protein; 15 AA.
XX AC AAR02172;
XX DT 10-MAR-2003 (updated)
XX DT 02-AUG-1990 (first entry)
XX

Peptide which binds to Immunoglobulin E (IgE) receptors inhibiting IgE
binding.
Immunoglobulin E (IgE); anti-allergic drug; IgE binding inhibitor.
Unidentified.
Key Location/Qualifiers
Misc-difference 1..1 /label=OTHER
FT /note="H-Phe"
FT Misc-difference 15..15 /label=OTHER
FT /note="Thr-OH"
PN JP01299298-A.
XX
XX 04-DEC-1989.
XX PF 27-MAY-1988; 88JP-0129721.
XX PR 27-MAY-1988; 88JP-0129721.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX WPI; 1990-019330/03.
XX PT Peptides which bind to IgE receptors inhibiting IgE binding -
XX used as anti-allergic drug having no side effects
XX Claim 2; Page 843; 8pp; Japanese.
XX CC It is the new sequence No 4 and has an anti-allergic effect. It binds to
XX IgE receptors on cell surfaces and inhibits IgE binding to receptors. It
XX can be used as an anti-allergic drug, having no side effects.
XX CC (Updated on 10-MAR-2003 to add missing OS field.)
XX SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4
DB 1 FPPP 4

RESULT 45
AAW38996
ID AAW38996 standard; peptide; 15 AA.
XX AC AAW38996;
XX DT 27-MAR-1998 (first entry)
XX DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:393.
XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX OS Synthetic.
XX PN WO9730074-A1.
XX PD 21-AUG-1997.
XX PF 14-FEB-1997; 97WO-US02298.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.

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PA (UUNC-) UNIV NORTH CAROLINA.  
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JW;  
 XX WPI; 1997-424972/39.  
 XX  
 XX Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX  
 PS Claim 22; Page 92; 131pp; English.  
 XX  
 CC The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 80.0%; Score 4; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 DB 6 FPPP 9  
 RESULT 46  
 AAW38935  
 ID AAW38935 standard; peptide; 15 AA.  
 XX  
 AC AAW38935;  
 XX  
 DT 27-MAR-1998 (first entry)  
 XX  
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:332.  
 XX  
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9730074-A1.  
 XX  
 PD 21-AUG-1997.  
 XX  
 PF 14-FEB-1997; 97WO-US02298.  
 XX  
 PR 16-FEB-1996; 96US-0602999.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UUNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JW;  
 XX

DR WPI; 1997-424972/39.  
 XX  
 XX Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX  
 XX Claim 22; Page 91; 131pp; English.  
 PS  
 XX The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 80.0%; Score 4; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPKK 5  
 DB 7 PPKK 10  
 RESULT 47  
 AAG79166  
 ID AAG79166 standard; peptide; 15 AA.  
 XX  
 AC AAG79166;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Synthetic antigenic peptide derived from ActA.  
 XX  
 KW ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;  
 KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;  
 KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;  
 KW infectious disease; cancer; autoimmune disease; inflammation;  
 KW platelet aggregation; wound healing; clotting.  
 XX  
 OS Synthetic.  
 OS Listeria monocytogenes.  
 XX  
 PN WO200174858-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 03-APR-2001; 2001WO-US10753.  
 XX  
 PR 03-APR-2000; 2000US-194215P.  
 XX  
 PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 XX  
 PI Krause M, Sechi AS, Gertler FB, Wehland J;  
 XX  
 DR WPI; 2001-616686/71.  
 XX  
 PT Modulating cytoskeletal rearrangement to regulate T cell and macrophage



PT activation for treating cancer, autoimmune disease, and infectious  
 XX disease, comprises contacting with a Fyb/SLAP complex modulator -  
 PS Example 1; Page 36; 79pp; English.  
 XX  
 CC The present sequence represents an antigenic peptide derived from ActA.  
 CC polyclonal antibodies raised against this peptide were used to screen  
 CC mouse embryo expression library to isolate Fyb/SLAP clones. Fyb/SLAP  
 CC proteins are ligands for the EVH1 domains of  
 CC Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins.  
 CC The specification describes a method for modulating cytoskeletal  
 CC rearrangement in a cell, or T cell response to T cell receptor  
 CC stimulation. The method comprises contacting the cell or T cell with a  
 CC Fyb/SLAP complex modulator sufficient to modulate the formation of a  
 CC complex of an Ena/VASP protein and a Fyb/SLAP protein. The method is  
 CC useful for modulating cytoskeletal rearrangement in a cell such as a  
 CC lymphocyte, preferably a T cell, a macrophage or a cell fragment such  
 CC as a platelet and for modulating T cell response to a T cell receptor  
 CC stimulation. T cell response is increased in a subject having or at  
 CC risk of developing infectious disease or cancer and T cell response  
 CC is inhibited in a subject having or is at risk of developing an  
 CC autoimmune disease or a condition characterized by inflammation. A  
 CC composition comprising a Fyb/SLAP complex inhibitor is useful for  
 CC increasing platelet aggregation for promoting wound healing or  
 CC clotting.  
 CC  
 XX  
 SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
 ||||  
 Db 4 FPPP 7

RESULT 48  
 AAG64569  
 ID AAG64569 standard; Peptide; 15 AA.  
 XX  
 AC AAG64569;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human vacuole protein 13 peptide 2.  
 XX  
 KW Human; vacuole protein 13; malignant tumour; cancer; nosohaemia; HIV;  
 KW human immunodeficiency virus; infection; immunological disease;  
 KW inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN CN1297899-A.  
 XX  
 XX 06-JUN-2001.  
 XX  
 XX 24-NOV-1999; 99CN-0124091.  
 XX  
 XX 24-NOV-1999; 99CN-0124091.  
 XX  
 PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2001-489648/54.  
 XX  
 XX Human vacuole protein 13 and its encoding polynucleotides, useful for  
 PT treating tumours, human immunodeficiency virus infections and  
 PT inflammation -  
 PT  
 XX  
 PS Example 6; Page 18 Disclosure; 28pp; Chinese.

CC The invention relates to the human vacuole protein 13. The protein and  
 CC polynucleotide are useful in treating various diseases, such as malignant  
 CC tumour, nosohaemia, human immunodeficiency virus infections,  
 CC immunological diseases and inflammations. The present sequence is that of  
 CC the human vacuole protein 13 peptide  
 CC Note: the present sequence given as SEQ ID NO 7 in the examples differs  
 CC from that given as SEQ ID NO 7 in the sequence listing (AAG64568).  
 XX  
 SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
 ||||  
 Db 11 PPPK 14

RESULT 49  
 AAB72252  
 ID AAB72252 standard; peptide; 15 AA.  
 XX  
 AC AAB72252;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrin derived cytokine inducing peptide SEQ ID 7.  
 XX  
 KW Colostrin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22818.  
 XX  
 PR 17-AUG-1999; 99US-0149311.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGC-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 DR WPI; 2001-202804/20.  
 XX  
 XX Inducing a cytokine and modulating an immune response; useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrin as an immunological  
 PT regulator -  
 XX  
 XX Claim 1; Page 34; 50pp; English.  
 PS  
 XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.  
 XX  
 SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPPP 4  
Db 6 FPPP 9

## RESULT 50

AAB72506  
ID AAB72506 standard; Peptide; 15 AA.

AC AAB72506;

DT 09-MAY-2001 (first entry)

DE Colostrinin peptide #7.

KW Dermatological; oxidative stress regulator; colostrinin.

OS Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US222665.

XX 17-AUG-1999; 99US-0149310.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations -

PS Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), CC to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient.

XX Sequence 15 AA;

Query Match 80.0%; Score 4; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPPP 4  
Db 6 FPPP 9

## RESULT 51

AAB72538  
ID AAB72538 standard; Peptide; 15 AA.

AC AAB72538;

DT 09-MAY-2001 (first entry)

XX Colostrinin peptide #7.

DE Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.

XX

OS Unidentified.

PN WO200112651-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US222774.

XX 17-AUG-1999; 99US-0149633.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I;

XX WPI; 2001-226545/23.

XX Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient -

PS Claim 6; Page 21; 35pp; English.

XX The present invention relates to a method for promoting neural cell differentiation and treating damaged neural cells, using colostrinin and colostrinin constituent peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum.

XX Sequence 15 AA;

Query Match 80.0%; Score 4; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPPP 4  
Db 6 FPPP 9

## RESULT 52

AAB59312  
ID AAB59312 standard; Peptide; 15 AA.

XX AAB59312;

XX 21-MAR-2001 (first entry)

DT Ewe colostrinin peptide fragment A-3.

XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX Ovis sp.

XX WO200075173-A2.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-GB02128.

XX 02-JUN-1999; 99GB-0012852.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques -

XX

PS Claim 7; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.

XX Sequence 15 AA;

Query Match 80.0%; Score 4; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4

Db |||||

6 FPPP 9

RESULT 53

ABG72860

ID ABG72860 standard; Peptide; 15 AA.

XX AC

XX ABG72860;

XX 26-FEB-2003 (first entry)

XX DE

XX Human ribosomal protein 17.05 N-terminal.

XX KW

XX Human; ribosomal protein 17.05; malignant tumour; haemopathy;

XX KW human immunodeficiency virus; HIV; immunological disease;

XX KW inflammation.

XX OS

XX Homo sapiens.

XX PN

XX CN1352106-A.

XX XX

XX 05-JUN-2002.

XX PF

XX 06-NOV-2000; 2000CN-0127235.

XX PR

XX 06-NOV-2000; 2000CN-0127235.

XX PA

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX PI

XX Mao Y, Xie Y;

XX WPI; 2002-683308/74.

XX XX

XX New human ribosomal protein 17.05 polypeptide for treating malignant

XX tumors, hemopathy, human immunodeficiency virus infection,

XX PT immunological diseases and various inflammations -

XX XX

XX Example 5; Page 18 (Disclosure); 33pp; Chinese.

XX PS

XX The present invention discloses a new kind of polypeptide, human

XX ribosomal protein 17.05, polynucleotides encoding the polypeptide and a

XX DNA recombination process to produce the polypeptide. The present

XX invention also describes applying the polypeptide in treating various

XX diseases, such as malignant tumours, haemopathy, human immunodeficiency

XX virus (HIV) infection, immunological diseases and various inflammations.

XX Also discloses is the antagonist resisting the polypeptide and its

XX treatment effect, and the application of the polynucleotides encoding

XX human ribosomal protein 17.05. This is the amino acid sequence of the

XX novel human ribosomal protein 17.05 N-terminal.

XX XX

XX Sequence 15 AA;

XX Query Match

XX 80.0%; Score 4; DB 23; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4

Db |||||

5 FPPP 8

RESULT 54

ABP59535

ID ABP59535 standard; Peptide; 15 AA.

XX AC

XX ABP59535;

XX XX

XX 03-MAR-2003 (first entry)

XX DE

XX Human ribonucleotide protein RBM856.43 N-terminal peptide.

XX KW

XX Human; ribonucleotide protein RBM856.43; infection; cancer; diabetes;

XX KW arrhythmia; hyperthyroidism.

XX OS

XX Homo sapiens.

XX PN

XX CN1345752-A.

XX XX

XX 24-APR-2002.

XX PF

XX 29-SEP-2000; 2000CN-0125516.

XX PR

XX 29-SEP-2000; 2000CN-0125516.

XX PA

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX PI

XX Mao Y, Xie Y;

XX WPI; 2002-675774/73.

XX DR

XX Novel polypeptide-ribonucleotide protein RBM 856.43 for curing several

XX PT diseases, such as diabetes, hyperthyroidism, arrhythmic, tumor and

XX PT various infections -

XX XX

XX Example 5; Page 18 (disclosure); 33pp; Chinese.

XX PS

XX The present invention provides the protein and coding sequences of human

XX ribonucleotide protein RBM856.43. The sequences are useful in the

XX treatment of diabetes, hyperthyroidism, arrhythmia, cancer and

XX infections. The present sequence is the N-terminus of the protein of the

XX CC invention.

XX XX

XX SQ Sequence 15 AA;

XX Query Match

XX 80.0%; Score 4; DB 23; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 FPPP 4

XX |||||

XX 7 FPPP 10

RESULT 55

ABB81220

ID ABB81220 standard; Peptide; 15 AA.

XX AC

XX ABB81220;

XX XX

XX 14-AUG-2002 (first entry)

XX DE

XX Human ciliary rootlet protein 45.98 N-terminal peptide SEQ ID NO:7.

XX KW

XX Human; ciliary rootlet protein 45.98; neuroprotective; nontropic;

XX KW antiarrhythmic; antiasthmatic; antiulcer; gene therapy; paralysis;

XX KW nervous system development abnormality; arrhythmia; bronchial asthma;

XX KW digestive ulcer; dementia.

XX OS Homo sapiens.  
 XX PN WO200238604-A1.  
 XX PD 16-MAY-2002.  
 XX PF 09-NOV-2001; 2001WO-CN01543.  
 XX PR 10-NOV-2000; 2000CN-0127410.  
 XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 XX PI Mao Y, Xie Y;  
 XX PX WPI; 2002-394823/42.  
 XX PT New cicliary rootlet protein 45.98 polypeptide for diagnosing and  
 PT treating malignant tumors, hemopathy, human immunodeficiency virus  
 PT infection, immunological diseases and inflammation -  
 XX PS Example 6; Page 19; 37pp; Chinese.  
 XX PX The present invention describes cicliary rootlet protein 45.98 (I).  
 CC (I) and the polynucleotide encoding it (II) have neuroprotective,  
 CC nootropic, antiarrhythmic, antiasthmatic and antitumor activities,  
 CC and can be used in gene therapy. (I) and (II) can be used in the  
 CC diagnosis and treatment of nervous system development abnormality,  
 CC paralysis, arrhythmia, bronchial asthma, digestive ulcer, and dementia.  
 CC The present sequence represents the N-terminal peptide of (I), which  
 CC is used in an example from the present invention.  
 XX SQ Sequence 15 AA;  
 XX SQ

Query Match 80.0%; Score 4; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPPK 5  
 DB 7 PPPK 10

RESULT 56  
 AAEE20234  
 ID AAEE20234 standard; peptide; 15 AA.  
 XX AC  
 XX AAE20234;  
 XX DT 18-JUN-2002 (first entry)  
 XX DE Colostrinin constituent peptide #7.  
 XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulneryary.  
 XX OS Unidentified.  
 XX XX

Key Location/Qualifiers  
 Modified-site 15  
 /note= "Optionally C-terminal amide"  
 FT FT  
 XX XX  
 XX PN WO200213850-A1.  
 XX PD 21-FEB-2002.  
 XX PF 17-AUG-2000; 2000WO-US22776.  
 XX PR 17-AUG-2000; 2000WO-US22776.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2002-269151/31.  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX PX Claim 6; Page 25; 51pp; English.  
 XX XX

The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/  
 CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.  
 XX SQ Sequence 15 AA;  
 XX SQ

Query Match 80.0%; Score 4; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 DB 6 FPPP 9

RESULT 57  
 AAMS1042  
 ID AAMS1042 standard; Peptide; 15 AA.  
 XX AC  
 XX AAMS1042;  
 XX DT 30-MAY-2002 (first entry)  
 XX DE Colostrinin constituent peptide.  
 XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; human.  
 XX OS Homo sapiens.  
 XX XX

Key Location/Qualifiers  
 Modified-site 15  
 /note= "Optional C-terminal amidation"  
 FT FT  
 XX XX  
 XX PN WO200213849-A1.  
 XX PD 21-FEB-2002.  
 XX PF 17-AUG-2000; 2000WO-US22775.  
 XX PR 17-AUG-2000; 2000WO-US22775.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX XX

DR WPI; 2002-269150/31.  
 XX  
 PT Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue  
 XX  
 PS Claim 1; Page 34; 54pp; English.  
 XX  
 CC The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions  
 CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patient. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide. Cytokines induced by this peptide in human  
 CC leucocyte cultures include interferon-gamma, tumour necrosis  
 CC factor-alpha, interleukin-4, interleukin-6 and interleukin-10.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 80.0%; Score 4; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 Db ||||  
 6 FPPP 9  
 RESULT 58  
 AAO14583  
 ID AAO14583 standard; peptide; 15 AA.  
 XX  
 AC AAO14583;  
 XX  
 DT 27-MAY-2002 (first entry)  
 XX  
 DE Neural cell regulatory colostrinin peptide 7.  
 XX  
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 15  
 FT /note= "Optional C-terminal amide"  
 XX  
 PN WO200213851-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22777.  
 XX  
 PR 17-AUG-2000; 2000WO-US22777.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX

PI Boldogh I, Stanton JG, Hughes TK;  
 XX WPI; 2002-269152/31.  
 XX  
 PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog  
 XX  
 PS Claim 7; Page 21; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 80.0%; Score 4; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 Db ||||  
 6 FPPP 9  
 RESULT 59  
 AAU09832  
 ID AAU09832 standard; Protein; 15 AA.  
 XX  
 AC AAU09832;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Human quinine reductase 9, N-terminal region.  
 XX  
 KW Human; quinine reductase 9; cytostatic; virucidal; immunomodulatory;  
 KW antiinflammatory; haemostatic; malignant tumour; haemopathy; HIV;  
 KW human immunodeficiency virus; immunological disease; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175055-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 26-MAR-2001; 2001WO-CN00520.  
 XX  
 PR 29-MAR-2000; 2000CN-0115266.  
 XX  
 PA (BIOV-) BIOWINDOW GENE DEV INC SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 XX WPI; 2002-025851/03.  
 XX  
 PT Human quinine reductase 9 and encoded polynucleotide, applicable in  
 PT diagnosis and treatment of malignant tumour, haemopathy, HIV infection,  
 PT immunological diseases and various inflammations  
 XX  
 PS Example 5; Page 14; 33pp; Chinese.  
 XX  
 CC The invention relates to an isolated polypeptide of human quinine  
 CC reductase 9. The polypeptide and encoded polynucleotide are applicable  
 CC in diagnosis and treatment of malignant tumour, haemopathy, human  
 CC immunodeficiency virus (HIV) infection, immunological diseases and  
 CC various inflammations. The present sequence represents the N-terminal  
 CC 15 amino acid sequence of human quinine reductase 9.

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XX      SQ      Sequence      15 AA;
SQ
Query Match      80.0%; Score 4; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FPPP-4
Db      7 FPPP 10

RESULT 60
AAW39031
ID      AAW39031 standard; peptide; 16 AA.
XX
AC      AAW39031;
XX
DT      27-MAR-1998 (first entry)
XX
DE      Peptide resembling an SH3 domain binding peptide SEQ ID NO:432.
XX
KW      Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW      tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW      Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
OS      Synthetic.
XX
PN      WO9730074-A1.
XX
PD      21-AUG-1997.
XX
PF      14-FEB-1997; 97WO-US02298.
XX
PR      16-FEB-1996; 96US-0602999.
XX
PA      (CYTO-) CYTOGEN CORP.
PA      (UYNC-) UNIV NORTH CAROLINA.
XX
PI      Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI      Sparks AB, Thorn JM;
XX
DR      WPI; 1997-424972/39.
XX
PT      Src homology region 3 binding peptide - used to activate Src
PT      tyrosine kinase(s) and to stimulate immune response by increasing
PT      production of certain lymphokine(s), e.g. interleukin-1
XX
PS      Claim 22; Page 93; 131pp; English.
XX
CC      The present sequence represents a peptide which resembles a Src homology
CC      region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC      (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC      bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
CC      domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
CC      peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
CC      the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
CC      domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
CC      peptides which bind the amino-terminal SH3 domain of Grb2. The purified
CC      binding peptides can be used in the method to identify inhibitors of
CC      their binding to their respective SH3 domains, which could be used to
CC      modulate the pharmacological activity of proteins or polypeptide
CC      containing the SH3 domain. The peptides can also be used to activate
CC      Src or Src-related protein tyrosine kinases, to stimulate the immune
CC      response by increasing the production of certain lymphokines, e.g.
CC      tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC      conjugated molecule to certain cellular compartments containing Src or
CC      Src related proteins.
XX
SQ      Sequence      16 AA;

Query Match      80.0%; Score 4; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPK 5
Db      9 PPK 12

RESULT 61
AAW38989
ID      AAW38989 standard; peptide; 16 AA.
XX
AC      AAW38989;
XX
DT      27-MAR-1998 (first entry)
XX
DE      Peptide resembling an SH3 domain binding peptide SEQ ID NO:386.
XX
KW      Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW      tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW      Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
OS      Synthetic.
XX
PN      WO9730074-A1.
XX
PD      21-AUG-1997.
XX
PF      14-FEB-1997; 97WO-US02298.
XX
PR      16-FEB-1996; 96US-0602999.
XX
PA      (CYTO-) CYTOGEN CORP.
PA      (UYNC-) UNIV NORTH CAROLINA.
XX
PI      Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI      Sparks AB, Thorn JM;
XX
DR      WPI; 1997-424972/39.
XX
PT      Src homology region 3 binding peptide - used to activate Src
PT      tyrosine kinase(s) and to stimulate immune response by increasing
PT      production of certain lymphokine(s), e.g. interleukin-1
XX
PS      Claim 22; Page 92; 131pp; English.
XX
CC      The present sequence represents a peptide which resembles a Src homology
CC      region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC      (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC      bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
CC      domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
CC      peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
CC      the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
CC      domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
CC      peptides which bind the amino-terminal SH3 domain of Grb2. The purified
CC      binding peptides can be used in the method to identify inhibitors of
CC      their binding to their respective SH3 domains, which could be used to
CC      modulate the pharmacological activity of proteins or polypeptide
CC      containing the SH3 domain. The peptides can also be used to activate
CC      Src or Src-related protein tyrosine kinases, to stimulate the immune
CC      response by increasing the production of certain lymphokines, e.g.
CC      tumour necrosis factor-alpha and interleukin-1, or to deliver a
CC      conjugated molecule to certain cellular compartments containing Src or
CC      Src related proteins.
XX
SQ      Sequence      16 AA;

Query Match      80.0%; Score 4; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPK 5
Db      9 PPK 12

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XX AC AAY87908;
XX DT 01-SEP-2000 (first entry)
XX DE AAV-2 antigenic peptide AAV-2-1.
XX KW Antigenic; capsid; monoclonal antibody; anticancer; anti-inflammatory;
XX KW anti-anemic; gene therapy; tumor; cystic fibrosis; sickle cell anemia.
XX OS Adeno associated virus.
XX PN DE19849643-A1.
XX PD 04-MAY-2000.
XX PF 29-OCT-1998; 98DE-1049643.
XX PR 29-OCT-1998; 98DE-1049643.
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX PI Kleinschmidt J, Wobus C, Kern A;
XX DR WPI; 2000-330206/29.
XX PT New monoclonal antibody that binds to adeno-associated virus, useful
XX PT for preparing gene therapy vectors, is used to alter tropism of the
XX PT virus for specific gene delivery -
XX PS Example 1; Page 6; 12pp; German.
XX CC This invention describes a novel monoclonal antibody (MAB), or its
XX CC fragments, that bind to the capsid of an adeno-associated virus (AAV)
XX CC and inhibit binding of AAV to a receptor on its original target cell.
XX CC The products of the invention have anticancer, anti-inflammatory and
XX CC anti-anemic activity. MAB are used to treat AAV that are used for
XX CC directed gene transfer, especially gene therapy of e.g. tumors, cystic
XX CC fibrosis and sickle cell anemia. AAV treated with MAB have altered
XX CC tropism, i.e. they no longer bind to their original host cell but can
XX CC bind to selected target cells, particularly defined by the nature of a
XX CC receptor ligand bound to MAB. The Raji cell line (Burkitt lymphoma) is
XX CC hardly infected by wild-type AAV-2. When recombinant AAV-2 was incubated
XX CC with a bispecific single-chain antibody, comprising the variable heavy
XX CC chain region of an anti-AAV-2 monoclonal antibody and the variable light
XX CC chain region of an anti-CD19 antibody, the treated vectors were able to
XX CC infect Raji cells efficiently. This sequence represents an antigenic
XX CC peptide derived from AAV-2 which is used to illustrate the method of the
XX SQ Sequence 16 AA;
XX Query Match 80.0%; Score 4; DB 21; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 4.3e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 2 PPK 5
XX DB 3 PPK 6
XX RESULT 64
XX AAB59343
XX ID AAB59343 standard; Peptide; 16 AA.
XX AC AAB59343;
XX XX
XX DT 21-MAR-2001 (first entry)
XX DE Ewe colostrin peptide fragment derived sequence #3.
XX KW Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder;
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX SQ Sequence 16 AA;
XX Query Match 80.0%; Score 4; DB 18; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 4.3e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 2 PPK 5
XX DB 9 PPK 12
XX RESULT 63
XX AAY87908
XX ID AAY87908 standard; peptide; 16 AA.
XX AC AAW38947
XX DT 27-MAR-1998 (first entry)
XX DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:344.
XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX OS Synthetic.
XX PN WO9730074-A1.
XX PD 21-AUG-1997.
XX PF 14-FEB-1997; 97WO-US02298.
XX PR 16-FEB-1996; 96US-0602999.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX PI Sparks AB, Thorn JM;
XX DR WPI; 1997-424972/39.
XX PT Src homology region 3 binding peptide - used to activate Src
XX PT tyrosine kinase(s) and to stimulate immune response by increasing
XX PT production of certain lymphokine(s), e.g. interleukin-1
XX PS Claim 22; Page 91; 131pp; English.
XX CC The present sequence represents a peptide which resembles a Src homology
XX CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
XX CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
XX CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
XX CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX CC binding peptides can be used in the method to identify inhibitors of
XX CC their binding to their respective SH3 domains, which could be used to
XX CC modulate the pharmacological activity of proteins or polypeptide
XX CC containing the SH3 domain. The peptides can also be used to activate
XX CC Src or Src-related protein tyrosine kinases, to stimulate the immune
XX CC response by increasing the production of certain lymphokines, e.g.
XX CC tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX CC conjugated molecule to certain cellular compartments containing Src or
XX CC Src related proteins.
XX SQ Sequence 16 AA;
XX Query Match 80.0%; Score 4; DB 18; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 4.3e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 2 PPK 5
XX DB 9 PPK 12
XX RESULT 63
XX AAY87908
XX ID AAY87908 standard; peptide; 16 AA.

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XX OS Ovis sp.  
 XX PN WO200075173-A2.  
 XX PD 14-DEC-2000.  
 XX PF 02-JUN-2000; 2000WO-GB02128.  
 XX PR 02-JUN-1999; 99GB-0012852.  
 XX PS (REG- ) REGEN THERAPEUTICS PLC.  
 XX PI Georgiades JA;  
 XX DR WPI; 2001-071058/08.  
 XX PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques  
 XX PS Claim 8; Page 27; 63pp; English.  
 XX CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX SQ Sequence 16 AA;  
 Query Match 80.0%; Score 4; DB 22; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 Db |||||  
 7 FPPP 10  
 RESULT 65  
 AAO15252  
 ID AAO15252 standard; peptide; 16 AA.  
 XX AC AAO15252;  
 XX DT 05-SEP-2002 (first entry)  
 XX DE Human papillomavirus 16 E6 protein-binding peptide 11.  
 XX KW E6 protein binding peptide; protein-ligand interaction;  
 XX KW perturbagen library; target molecule identification; drug development.  
 XX OS Unidentified.  
 XX PN US2002045188-A1.  
 XX PD 18-APR-2002.  
 XX PF 25-MAY-2001; 2001US-085644.  
 XX PR 17-NOV-1998; 98US-0193759.  
 XX PR 17-NOV-1999; 99WO-US27409.  
 XX PA (KAMB/) KAMB C A.  
 XX PA (CAPO/) CAPONIGRO G M.  
 XX PA (TENG/) TENG D H.  
 XX PA (SAND/) SANDROCK T M.  
 XX PA (STUM/) STUMP M.

XX PI Kamb CA, Caponigro GM, Teng DH, Sandrock TM, Stump M;  
 XX DR WPI; 2002-507237/54.  
 XX PT A new method for identifying a physiological target molecule that  
 PT correlates to a phenotype of interest involves using a library of  
 PT putative perturbagen probes against target molecules, and is useful in  
 PT drug development  
 XX PS Example 10; Page 20; 37pp; English.  
 XX CC The invention comprises a method for identifying a physiologically  
 CC relevant target molecule that correlates to a phenotype of interest. The  
 CC method involves determining protein-ligand interactions between a target  
 CC candidate and a library of perturbagens and performing a phenotypic assay  
 CC to determine physiologically relevant perturbagens. The method of the  
 CC invention results in fewer false positive results than prior art methods  
 CC and can be used in drug development. The present amino acid sequence  
 CC represents a peptide that binds to the E6 protein from human  
 CC papillomavirus 16.  
 XX SQ Sequence 16 AA;  
 Query Match 80.0%; Score 4; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FPPP 4  
 Db |||||  
 11 FPPP 14  
 RESULT 66  
 AAW38983  
 ID AAW38983 standard; peptide; 17 AA.  
 XX AC AAW38983;  
 XX DT 27-MAR-1998 (first entry)  
 XX DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:380.  
 XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 XX KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 XX KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX OS Synthetic.  
 XX PN WO9730074-A1.  
 XX PD 21-AUG-1997.  
 XX PF 14-FEB-1997; 97WO-US02298.  
 XX PR 16-FEB-1996; 96US-0602999.  
 XX PA (CYTO-) CYTOGEN CORP.  
 XX PA (UYNC-) UNIV NORTH CAROLINA.  
 XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 XX PI Sparks AB, Thorn JM;  
 XX DR WPI; 1997-424972/39.  
 XX CC Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX PS Claim 22; Page 92; 131pp; English.  
 XX CC The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:



CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

XX Sequence 17 AA;  
 SQ

Query Match 80.0%; Score 4; DB 18; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5  
 DB 9 PPK 12

RESULT 67  
 AAW38939  
 ID AAW38939 standard; peptide; 17 AA.

AC AAW38939;  
 XX  
 DT 27-MAR-1998 (first entry)

DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:336.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX Synthetic.

XX WO9730074-A1.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US02298.

XX 16-FEB-1996; 96US-0602999.

XX (CYTO-) CYTOGEN CORP.

PA (UNNC-) UNIV NORTH CAROLINA.

PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JB;  
 PI Sparks AB, Thorn JM;

XX WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1

XX Claim 22; Page 91; 131pp; English.

XX The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3

CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

XX Sequence 17 AA;  
 SQ

Query Match 80.0%; Score 4; DB 18; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5  
 DB 9 PPK 12

RESULT 68  
 AAW83313  
 ID AAW83313 standard; peptide; 17 AA.

AC AAW83313;  
 XX

DT 10-FEB-1999 (first entry)

DE LRP5 protein fragment #1.

XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;  
 KW endocytosis; insulin dependent diabetes mellitus; autoimmune disease;  
 KW glomerulonephritis; inflammation; viral infection; osteoporosis;  
 KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein.

XX Homo sapiens.

XX WO9846743-A1.

XX 22-OCT-1998.

XX 15-APR-1998; 98WO-GB01102.

XX 05-JUN-1997; 97US-0048740.

XX 15-APR-1997; 97US-0043553.

XX (MERI ) MERCK & CO INC.

PA (WELL ) WELLCOME TRUST LTD.

XX Caskey CT, Cox RD, Gerhold D, Hammond H, Hess JW;  
 PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;  
 PI Phillips MS, Todd JA, Twells RCJ;

XX WPI; 1998-594573/50.

XX New isolated LDL-receptor related protein - used to develop products  
 PT for treating, e.g. elevated triglyceride levels, diabetes,  
 PT autoimmune disorders, inflammation or Alzheimer's disease

XX Claim 20; Page 126; 200pp; English.

XX The present invention describes LRP5 (low density lipoprotein (LDL)  
 CC receptor related protein, previously designated LRP-3). The present  
 CC sequence represents a specifically claimed LRP5 protein fragment.  
 CC Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining  
 CC if an individual is susceptible to insulin dependent diabetes mellitus  
 CC (IDDM). The NAMS or proteins can be used for reducing triglyceride levels  
 CC in the serum of an individual. Therapies that affect LRP5 may also be  
 CC useful in the treatment of autoimmune diseases such as  
 CC glomerulonephritis, diseases and disorders involving disruption of

CC endocytosis and/or antigen presentation, cytokine clearance and/or  
 CC inflammation, viral infection, pathogenic bacterial toxin contamination,  
 CC elevation of free fatty acids or hypercholesterolemia, type 2 diabetes,  
 CC osteoporosis, Alzheimer's disease and cardiovascular disease. Products  
 CC from the present invention can also be used for detection, diagnosis and  
 CC drug screening.

XX  
 SQ Sequence 17 AA;

Query Match 80.0%; Score 4; DB 19; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
 |||||  
 Db 6 FPPP 9

## RESULT 69

AAU01833  
 ID AAU01833 standard; peptide; 17 AA.

XX AC AAU01833;

XX DT 07-SEP-2001 (first entry)

XX DE Wheat Gliadin peptide J.

XX Wheat; A-gliadin; peptide J; coeliac disease; gluten intolerance;  
 KW T-cell binding; antagonist; transglutaminase; transgenic plant.

XX OS Triticum aestivum.

XX PN WO200125793-A2.

XX PD 12-APR-2001.

XX PF 02-OCT-2000; 2000WO-GB03760.

XX PR 01-OCT-1999; 99GB-0023306.

XX (ISIS-) ISIS INNOVATION LTD.

XX PI Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2001-300179/31.

XX Diagnosing coeliac disease or susceptibility to the disease in an  
 PT individual, by detecting in vitro or in vivo T cells which bind  
 PT immunodominant T cell epitope obtained from naturally occurring homolog  
 PT of gliadin -

XX Example 8; Fig 14; 107pp; English.

XX The sequence represents wheat Gliadin peptide J, corresponding to  
 CC A-gliadin 57-73 and containing a natural polymorphism.  
 CC The peptides of the invention are used to test mammalian (preferably  
 CC human) susceptibility to coeliac disease (gluten intolerance). The  
 CC peptides are contacted with a blood sample and T cell recognition  
 CC measured, a positive T-cell recognition indicating a susceptibility to  
 CC coeliac disease. The peptides are useful for inducing tolerance in an  
 CC individual and antagonists to the peptides are useful for treating or  
 CC preventing coeliac disease in an individual and for producing an antibody  
 CC specific to them or a wild-type sequence. A mutant gliadin protein (or  
 CC its fragment of 15 amino acids in length) whose wild-type sequence can be  
 CC modified by transglutaminase to a sequence that comprises the epitope,  
 CC but which has been modified in such a way that it does not contain  
 CC sequence which can be modified by transglutaminase to a sequence that  
 CC comprise the epitope is useful for decreasing the ability of gliadin  
 CC protein to cause Coeliac disease. Nucleic acids encoding proteins  
 CC antagonistic to the T-cell binding of the epitopes are useful for  
 CC obtaining a transgenic plant cell or seed and for the production of a  
 CC protein. The resultant crop plant is useful for obtaining a product of a

CC wheat plant, especially grain, which is optionally processed into flour  
 CC or another grain product. Food comprising the antagonistic protein is  
 CC useful instead of a wild-type gliadin.

XX Sequence 17 AA;

Query Match 80.0%; Score 4; DB 22; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
 |||||  
 Db 5 FPPP 8

## RESULT 70

AAU01840  
 ID AAU01840 standard; peptide; 17 AA.

XX AC AAU01840;

XX DT 07-SEP-2001 (first entry)

XX Wheat peptide antagonist for A-gliadin 57-73 QE65 #2.

XX Wheat; A-gliadin; 57-75 QE65; coeliac disease; gluten intolerance;  
 KW T-cell binding; antagonist; transglutaminase; transgenic plant.

XX OS Triticum aestivum.

XX PN WO200125793-A2.

XX PD 12-APR-2001.

XX PF 02-OCT-2000; 2000WO-GB03760.

XX PR 01-OCT-1999; 99GB-0023306.

XX (ISIS-) ISIS INNOVATION LTD.

XX PI Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2001-300179/31.

XX Diagnosing coeliac disease or susceptibility to the disease in an  
 PT individual, by detecting in vitro or in vivo T cells which bind  
 PT immunodominant T cell epitope obtained from naturally occurring homolog  
 PT of gliadin -

XX Example 11; Page 58; 107pp; English.

XX The sequence represents a gliadin peptide corresponding to A-gliadin  
 CC 57-73 which is naturally polymorphic in that region and is antagonistic  
 CC to A-gliadin 57-73 QE65 interferon gamma ELISpot (not defined) response.  
 CC The peptides of the invention are used to test mammalian (preferably  
 CC human) susceptibility to coeliac disease (gluten intolerance). The  
 CC peptides are contacted with a blood sample and T cell recognition  
 CC measured, a positive T-cell recognition indicating a susceptibility to  
 CC coeliac disease. The peptides are useful for inducing tolerance in an  
 CC individual and antagonists to the peptides are useful for treating or  
 CC preventing coeliac disease in an individual and for producing an antibody  
 CC specific to them or a wild-type sequence. A mutant gliadin protein (or  
 CC its fragment of 15 amino acids in length) whose wild-type sequence can be  
 CC modified by transglutaminase to a sequence that comprises the epitope,  
 CC but which has been modified in such a way that it does not contain  
 CC sequence which can be modified by transglutaminase to a sequence that  
 CC comprise the epitope is useful for decreasing the ability of gliadin  
 CC protein to cause Coeliac disease. Nucleic acids encoding proteins  
 CC antagonistic to the T-cell binding of the epitopes are useful for  
 CC obtaining a transgenic plant cell or seed and for the production of a  
 CC protein. The resultant crop plant is useful for obtaining a product of a  
 CC wheat plant, especially grain, which is optionally processed into flour  
 CC or another grain product. Food comprising the antagonistic protein is

CC useful instead of a wild-type gliadin.

XX Sequence 17 AA;  
SQ Query Match 80.0%; Score 4; DB 22; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 5 FPPP 8

RESULT 71  
AAW05469  
ID AAW05469 standard; Peptide; 18 AA.

XX AC AAW05469;  
XX DT 24-FEB-1998 (first entry)  
XX DE SH3-binding peptide bSH3020.  
XX KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;  
XX KW cellular signalling element; cellular structural element; malignancy;  
XX KW protein identification; functional domain; protein screening;  
XX KW cellular signal transduction process; binding peptide.

XX OS Synthetic.

XX PN WO9631625-A1.

XX PD 10-OCT-1996.

XX PF 04-APR-1996; 96WO-US04454.

XX PR 03-APR-1996; 96US-0630915.

XX PR 07-APR-1995; 95US-0417872.

XX PA (CYTO-) CYTOGEN CORP.

XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;

XX PI WPI; 1996-465045/46.

XX PT Identifying polypeptide(s) having specific functional domain (esp. SH3 domain) - comprises detecting selective binding to recognition unit, regardless of sequence homology

XX PS Example; Fig 12B; 174pp; English.

XX CC AAW05445-W05492 represent Src-homology region 3 (SH3) domain binding peptides. These sequences were used as parts of multivalent recognition unit complexes used in the method of the invention. The method of the invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). It comprises contacting a multivalent recognition unit (RU) complex with a number of peptides and identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for identifying proteins containing an SH3 domain due to the minimal sequence homology among known SH3 proteins. Multivalent RU complexes are particularly suited to screening for polypeptides containing functional domains that are similar to, but not identical in sequence to, the original target functional domain. The new method enables proteins having a common function to be identified. Identification of novel SH3 proteins will be useful for a better understanding of cell growth, malignancy, signal transduction processes, etc. New candidate drugs can be identified, and their specificities (e.g. pharmacological activities) can be assessed using the method of the invention.

XX SQ Sequence 18 AA;

Query Match 80.0%; Score 4; DB 18; Length 18;

Query Match 80.0%; Score 4; DB 17; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 10 FPPP 13

RESULT 72  
AAW37677  
ID AAW37677 standard; Peptide; 18 AA.

XX AC AAW37677;

XX DT 23-APR-1998 (first entry)

XX DE PPPY motif containing peptide bSH3020 used to bind WW domains.

XX KW Peptide recognition unit; WW domain; cell signalling; growth regulation;  
XX KW cytoskeleton organisation; targeted drug screening; modulator;  
XX KW WW domain interaction; YAP protein; dystrophin.

XX OS Synthetic.

XX PN WO9737223-A1.

XX PD 09-OCT-1997.

XX PF 03-APR-1997; 97WO-US05547.

XX PR 03-APR-1996; 96US-0630916.

XX PA (CYTO-) CYTOGEN CORP.

XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Fowlkes DM, Kay BK, Pirozzi G;

XX PI WPI; 1997-503234/46.

XX PT Identifying cell signalling and growth regulatory polypeptides by reaction with multivalent recognition complex - polypeptides are useful in targeted drug selection

XX PS Example 6.3; Fig 7; 220pp; English.

XX CC Peptides AAW37653-77 contain PPPY-like motifs. The PPPY motif is found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides containing this residue have been shown to bind the YAP WW domain, but not the WW domain from dystrophin or to a panel of SH3 domains. Peptides AAW37653-77 were biotinylated and complexed with alkaline streptavidin, and used in a cross affinity mapping experiment. They were tested for their ability to bind to the 12 individual novel WW domains of WWP1 (AAW36794), WWP2 (AAW36795), WWP3 (AAW37696) and WWP4 (AAW36797), which were expressed as glutathione-S-transferase expression proteins. The present peptide, derived from a vinculin protein, does not bind to WW domains of the novel proteins. The WW domain is a small functional domain. Its name is derived from the observation that two tryptophan residues, one in the amino terminal portion of the WW domain and one in the carboxyl terminal portion, are conserved. Most proteins containing WW domains have a function involving cell signalling and growth regulation or the organisation of the cytoskeleton. Polypeptides containing a WW domain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW domain, with many polypeptides and identifying those with selective affinity for the complex. Proteins containing WW domains are used for targeted drug screening, i.e. to identify potential modulators of specific WW domain interactions.

XX SQ Sequence 18 AA;

Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
|||  
DB 10 FPPP 13

RESULT 73  
AAW38909  
ID AAW38909 standard; peptide; 18 AA.  
XX AC AAW38909;  
XX DT 27-MAR-1998 (first entry)  
XX DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.  
XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
XX OS Synthetic.  
XX PN WO9730074-A1.  
XX PD 21-AUG-1997.  
XX PF 14-FEB-1997; 97WO-US02298.  
XX PR 16-FEB-1996; 96US-0602999.  
XX PA (CYTO-) CYTOGEN CORP.  
XX PY (UYNC-) UNIV NORTH CAROLINA.  
XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
XX PI Sparks AB, Thorn JM;  
XX DR WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src  
XX tyrosine kinase(s) and to stimulate immune response by increasing  
XX production of certain lymphokine(s), e.g. interleukin-1  
XX  
XX Claim 22; Page 90; 131pp; English.  
XX  
XX The present sequence represents a peptide which resembles a Src homology  
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified  
XX binding peptides can be used in the method to identify inhibitors of  
XX their binding to their respective SH3 domains, which could be used to  
XX modulate the pharmacological activity of proteins or polypeptide  
XX containing the SH3 domain. The peptides can also be used to activate  
XX Src or Src-related protein tyrosine kinases, to stimulate the immune  
XX response by increasing the production of certain lymphokines, e.g.  
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a  
XX conjugated molecule to certain cellular compartments containing Src or  
XX Src related proteins.

SQ Sequence 18 AA;

Query Match 80.0%; Score 4; DB 18; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
|||

DB 7 FPPP 10

RESULT 74  
AAW47567  
ID AAW47567 standard; peptide; 18 AA.  
XX AC AAW47567;  
XX DT 03-JUL-1998 (first entry)  
XX DE Exendin agonist (18).

XX KW Exendin agonist; gastric motility; gastric emptying; treatment;  
KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;  
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;  
KW obesity; Gila monster venom.  
XX OS Synthetic.  
XX PN WO9805351-A1.  
XX PD 12-FEB-1998.  
XX PF 08-AUG-1997; 97WO-US14199.  
XX PR 08-AUG-1996; 96US-0694954.  
XX PA (AMYL-) AMYLIN PHARM INC.  
XX PI Bealey NRA, Gedulin B, Prickett KS, Young AA;  
XX DR WPI; 1998-145351/13.

XX PT Regulating gastrointestinal motility using exendins or their  
XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,  
XX impaired glucose tolerance etc., also in diagnostic investigations  
XX  
XX Example 21; Fig 8; 70pp; English.

XX The present sequence is an exendin agonist, which reduces gastric  
XX motility and delays gastric emptying. It can be used to treat spasm  
XX (where associated with acute diverticulitis or disorders of the  
XX biliary tract or sphincter of Oddi), postprandial dumping syndrome  
XX and hyperglycaemia (particularly associated with type 2 diabetes),  
XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an  
XX exendin agonist is administered to prevent stomach contents passing  
XX into the intestines, then the stomach pumped) and obesity. It can  
XX also be administered to subjects undergoing gastrointestinal  
XX diagnostic investigation, particularly radiological or by magnetic  
XX resonance imaging.  
XX Exendins, components of Gila monster venom, have some sequence  
XX similarity to glucagon-like peptides (GLP). They are GLP agonists  
XX and have been suggested (US5424286) for treatment of diabetes and  
XX prevention of hyperglycaemia.

SQ Sequence 18 AA;

Query Match 80.0%; Score 4; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
|||  
DB 13 FPPP 16

RESULT 75  
AAW47569

ID AAW47569 standard; peptide; 18 AA.  
XX  
AC AAW47569;  
XX  
XX  
DT 03-JUL-1998 (first entry)  
XX  
DE Exendin agonist (20).  
XX  
KW Exendin agonist; gastric motility; gastric emptying; treatment;  
KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;  
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;  
KW obesity; Gila monster venom.  
XX  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT Modified-site 11  
FT /note= "tert-butylglycine"  
FT Modified-site 18  
FT /note= "amidated"  
XX  
PN WO9805351-A1.  
XX  
PD 12-FEB-1998.  
XX  
PF 08-AUG-1997; 97WO-US14199.  
XX  
PR 08-AUG-1996; 96US-0694954.  
XX  
PA (AMYL-) AMYLIN PHARM INC.  
XX  
PI Beiley NRA, Gedulin B, Prickett KS, Young AA;  
XX  
XX WPI; 1998-145351/13.  
XX  
PT Regulating gastrointestinal motility using exendins or their  
PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,  
PT impaired glucose tolerance etc., also in diagnostic investigations  
XX  
PS Example 23; Fig 8; 70pp; English.  
XX  
CC The present sequence is an exendin agonist, which reduces gastric  
CC motility and delays gastric emptying. It can be used to treat spasm  
CC (where associated with acute diverticulitis or disorders of the  
CC biliary tract or sphincter of Oddi), postprandial dumping syndrome  
CC and hyperglycaemia (particularly associated with type 2 diabetes),  
CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an  
CC exendin agonist is administered to prevent stomach contents passing  
CC into the intestines, then the stomach pumped) and obesity. It can  
CC also be administered to subjects undergoing gastrointestinal  
CC diagnostic investigation, particularly radiological or by magnetic  
CC resonance imaging.  
CC Exendins, components of Gila monster venom, have some sequence  
CC similarity to glucagon-like peptides (GLP). They are GLP agonists  
CC and have been suggested (US5424286) for treatment of diabetes and  
CC prevention of hyperglycaemia.  
XX  
SQ Sequence 18 AA;

Query Match 80.0%; Score 4; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
    |||||  
Db 13 FPPP 16

Search completed: November 25, 2003, 18:15:55  
Job time : 17.1968 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 9.94681 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-12

Perfect score: 5

Sequence: 1 FPPK 5

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	15	US-10-281-652-12
2	4	80.0	5	9	US-09-825-144-15
3	4	80.0	5	9	US-09-823-240-3
4	4	80.0	5	12	US-10-192-381-47
5	4	80.0	7	11	US-09-281-495-17
6	4	80.0	8	12	US-10-376-121A-16
7	4	80.0	9	9	US-09-825-144-10
8	4	80.0	9	9	US-09-823-240-7
9	4	80.0	10	10	US-09-872-832-32
10	4	80.0	10	9	US-09-823-240-1
11	4	80.0	12	11	US-09-845-612B-4
12	4	80.0	12	12	US-10-232-544-67
13	4	80.0	13	15	US-10-185-050-60
14	4	80.0	13	15	US-10-185-050-167
15	4	80.0	14	9	US-09-825-144-12

16	4	80.0	15	9	US-09-825-144-1	Sequence 1, Appli
17	4	80.0	15	12	US-10-161-791-393	Sequence 393, App
18	4	80.0	15	15	US-10-281-652-7	Sequence 7, Appli
19	4	80.0	16	9	US-09-865-644-11	Sequence 11, Appli
20	4	80.0	16	12	US-10-161-791-332	Sequence 332, App
21	4	80.0	16	12	US-10-161-791-344	Sequence 344, App
22	4	80.0	16	12	US-10-161-791-386	Sequence 386, App
23	4	80.0	16	12	US-10-161-791-432	Sequence 432, App
24	4	80.0	16	15	US-10-057-789-223	Sequence 223, App
25	4	80.0	16	15	US-10-212-628-223	Sequence 223, App
26	4	80.0	17	12	US-10-331-907-403	Sequence 403, App
27	4	80.0	17	12	US-10-161-791-336	Sequence 336, App
28	4	80.0	17	12	US-10-161-791-380	Sequence 380, App
29	4	80.0	18	9	US-09-879-957-165	Sequence 165, App
30	4	80.0	18	12	US-10-161-791-305	Sequence 305, App
31	4	80.0	18	15	US-10-185-050-109	Sequence 109, App
32	4	80.0	19	9	US-09-879-957-162	Sequence 162, App
33	4	80.0	19	15	US-10-185-050-106	Sequence 106, App
34	4	80.0	19	15	US-10-226-007-1542	Sequence 1542, Ap
35	4	80.0	20	9	US-09-735-450-4	Sequence 4, Appli
36	4	80.0	20	10	US-09-941-611-20	Sequence 20, Appli
37	4	80.0	20	15	US-10-044-995-20	Sequence 20, Appli
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42	3	60.0	4	12	US-10-376-121A-130	Sequence 130, App
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44	3	60.0	4	12	US-10-376-121A-135	Sequence 135, App
45	3	60.0	4	15	US-10-096-986-106	Sequence 106, App
46	3	60.0	4	15	US-10-185-815-99	Sequence 99, Appli
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49	3	60.0	4	15	US-09-823-240-4	Sequence 4, Appli
50	3	60.0	5	9	US-09-858-754-9	Sequence 9, Appli
51	3	60.0	5	9	US-09-785-921A-15	Sequence 15, Appli
52	3	60.0	5	12	US-10-352-704-23	Sequence 23, Appli
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57	3	60.0	5	15	US-10-185-050-233	Sequence 233, App
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59	3	60.0	5	15	US-10-096-986-9	Sequence 9, Appli
60	3	60.0	5	15	US-10-226-007-5	Sequence 5, Appli
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62	3	60.0	5	15	US-10-226-007-7	Sequence 7, Appli
63	3	60.0	6	9	US-09-803-126-21	Sequence 21, Appli
64	3	60.0	6	10	US-09-859-053-41	Sequence 41, Appli
65	3	60.0	6	10	US-09-871-106B-10	Sequence 10, Appli
66	3	60.0	6	10	US-09-814-777A-29	Sequence 29, Appli
67	3	60.0	6	10	US-09-990-574-1	Sequence 1, Appli
68	3	60.0	6	10	US-09-990-574-2	Sequence 2, Appli
69	3	60.0	6	11	US-09-774-639-225	Sequence 225, App
70	3	60.0	6	11	US-09-969-730-321	Sequence 321, App
71	3	60.0	6	12	US-10-032-214-297	Sequence 297, App
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73	3	60.0	6	12	US-10-352-704-25	Sequence 25, Appli
74	3	60.0	6	12	US-10-376-121A-119	Sequence 119, App
75	3	60.0	6	12	US-10-376-121A-125	Sequence 125, App
76	3	60.0	6	12	US-10-376-121A-207	Sequence 207, App
77	3	60.0	6	12	US-10-376-121A-212	Sequence 212, App
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87	3	60.0	6	14	US-10-078-547-19	Sequence 19, Appli
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Sequence 20, Appl  
Sequence 21, Appl  
Sequence 15, Appl  
Sequence 5, Appl  
Sequence 18, Appl  
Sequence 21, Appl  
Sequence 8, Appl  
Sequence 11, Appl  
Sequence 15, Appl  
Sequence 16, Appl  
Sequence 18, Appl  
Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-10-281-652-12  
; Sequence 12, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/05/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-12

Query Match 100.0%; Score 5; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPK 5  
Db 1 FPPPK 5

RESULT 2  
US-09-825-144-15  
; Sequence 15, Application US/09825144  
; Patent No. US20020037286A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthias Krause  
; APPLICANT: Antonio S. Sechi  
; APPLICANT: Frank B. Gertler  
; APPLICANT: Jorgen Wehland  
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
; FILE REFERENCE: M0656/7065  
; CURRENT APPLICATION NUMBER: US/09/825,144  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,215  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 5

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-825-144-15

Query Match 80.0%; Score 4; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
Db 1 FPPP 4

RESULT 3  
US-09-823-240-3  
; Sequence 3, Application US/09823240  
; Patent No. US20020048813A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: Jorgen Wehland  
; APPLICANT: Joseph Loureio  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; TITLE OF INVENTION: Motility  
; FILE REFERENCE: M0656/7064 (HCL)  
; CURRENT APPLICATION NUMBER: US/09/823,240  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/194,564  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-09-823-240-3

Query Match 80.0%; Score 4; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
Db 1 FPPP 4

RESULT 4  
US-10-192-381-47  
; Sequence 47, Application US/10192381  
; Publication No. US20030170807A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WORLEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENEKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS  
; FILE REFERENCE: JHUI580-4  
; CURRENT APPLICATION NUMBER: US/10/192,381  
; CURRENT FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: US/09/377,285  
; PRIOR FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/138,426  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,493  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,494  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/097,334  
; PRIOR FILING DATE: 1998-08-18



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; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: optimal ligand
US-10-192-381-47

Query Match      80.0%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FPPP 4
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Db      1 FPPP 4

RESULT 5
US-09-281-495-17
; Sequence 17, Application US/09281495
; Publication No. US20030059765A1
; GENERAL INFORMATION:
; APPLICANT: Pomerantz, Roger J
; APPLICANT: Bouhamdan, Mohamad
; APPLICANT: Duan, Ling-Xun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROVIDING A PROTEIN TO A
; TITLE OF INVENTION: VIRION
; FILE REFERENCE: 9855-25U1
; CURRENT APPLICATION NUMBER: US/09/281,495
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,822
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vpr-Specific
; OTHER INFORMATION: Polypeptide Binding Region
US-09-281-495-17

Query Match      80.0%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FPPP 4
      ||||
Db      4 FPPP 7

RESULT 6
US-10-376-121A-16
; Sequence 16, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMREF114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1..8
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-376-121A-16

Query Match      80.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPK 5
      ||||
Db      3 PPPK 6

RESULT 7
US-09-825-144-10
; Sequence 10, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehland
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7085
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-10

Query Match      80.0%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FPPP 4
      ||||
Db      1 FPPP 4
```

```
RESULT 8
US-09-823-240-7
; Sequence 7, Application US/098232240
; Patent No. US20020048813A1
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jurgen Wehland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M0656/7064 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,240
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa is any amino acid
US-09-823-240-7

Query Match      80.0%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4
Db 1 FPPP 4

RESULT 9
US-09-872-832-32
; Sequence 32, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-832-32

Query Match      80.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5
Db 4 PPK 7

RESULT 10
US-09-823-240-1
; Sequence 1, Application US/098232240
; Patent No. US20020048813A1
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
```

```
; APPLICANT: James E. Bear
; APPLICANT: Jurgen Wehland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M0656/7064 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,240
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa is Asp or Glu
; NAME/KEY: UNSURE
; LOCATION: (7)...(7)
; OTHER INFORMATION: Xaa is any amino acid
US-09-823-240-1

Query Match      80.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4
Db 2 FPPP 5

RESULT 11
US-09-845-612B-4
; Sequence 4, Application US/09845612B
; Publication No. US20030083261A1
; GENERAL INFORMATION:
; APPLICANT: YU, HONGTAO
; APPLICANT: TANG, ZHANYUN
; APPLICANT: LUO, XUELIAN
; APPLICANT: RIZO-REY, JOSE
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOT
; TITLE OF INVENTION: POINT PROTEIN MAD2
; FILE REFERENCE: UTSD:795
; CURRENT APPLICATION NUMBER: US/09/845,612B
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(12)
; OTHER INFORMATION: synthetic peptide
US-09-845-612B-4

Query Match      80.0%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5
Db 9 PPK 12

RESULT 12
US-10-232-544-67
; Sequence 67, Application US/10232544
; Publication No. US20030199069A1
```

GENERAL INFORMATION:  
APPLICANT: Fuglsang, Claus  
APPLICANT: Okkels, Jens  
APPLICANT: Petersen, Dorte  
APPLICANT: Patkar, Shankant  
APPLICANT: Thellersen, Marianne  
APPLICANT: Svendsen, Allan  
APPLICANT: Borch, Kim  
APPLICANT: Royer, John  
APPLICANT: Kretzschmar, Titus  
APPLICANT: Halkier, Torben  
APPLICANT: Vind, Jesper  
APPLICANT: Jorgensen, Steen  
TITLE OF INVENTION: No. US20030199069A1el Lipolytic Enzymes  
FILE REFERENCE: 4455.404-US  
CURRENT APPLICATION NUMBER: US/10/232,544  
CURRENT FILING DATE: 2002-08-30  
PRIOR APPLICATION NUMBER: US/09/007,288  
PRIOR FILING DATE: 2000-01-14  
NUMBER OF SEQ ID NOS: 162  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 67  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Peptide addition  
US-10-232-544-67

Query Match 80.0%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPK 5  
Db 2 PPPK 5

RESULT 13  
US-10-185-050-60  
Sequence 60, Application US/10185050  
Publication No. US20030077577A1  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
Kay, Brian K.  
Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 167:  
US-10-185-050-167

Query Match 80.0%; Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 60:  
US-10-185-050-60

Query Match 80.0%; Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPK 5  
Db 4 PPPK 7

RESULT 14  
US-10-185-050-167  
Sequence 167, Application US/10185050  
Publication No. US20030077577A1  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
Kay, Brian K.  
Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 167:  
US-10-185-050-167

Query Match 80.0%; Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
DB 4 PPPK 7

RESULT 15  
US-09-825-144-12  
; Sequence 12, Application US/09825144  
; Patent No. US20020037286A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthias Krause  
; APPLICANT: Antonio S. Sechi  
; APPLICANT: Frank B. Gertler  
; APPLICANT: Jorgen Wehland  
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
; FILE REFERENCE: M0656/7065  
; CURRENT APPLICATION NUMBER: US/09/825,144  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,215  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-09-825-144-12

Query Match 80.0%; Score 4; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 3 FPPP 6

RESULT 16  
US-09-825-144-1  
; Sequence 1, Application US/09825144  
; Patent No. US20020037286A1  
; GENERAL INFORMATION:  
; APPLICANT: Matthias Krause  
; APPLICANT: Antonio S. Sechi  
; APPLICANT: Frank B. Gertler  
; APPLICANT: Jorgen Wehland  
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation  
; FILE REFERENCE: M0656/7065  
; CURRENT APPLICATION NUMBER: US/09/825,144  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,215  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-09-825-144-1

Query Match 80.0%; Score 4; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 4 FPPP 7

RESULT 17  
US-10-161-791-393  
; Sequence 393, Application US/10161791

Publication No. US2003018663A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leelie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 393:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-393

Query Match 80.0%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 6 FPPP 9

RESULT 18  
US-10-281-652-7  
; Sequence 7, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17

```
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-7

Query Match      80.0%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4
Db 6 FPPP 9

RESULT 19
US-09-865-644-11
; Sequence 11, Application US/09865644
; Patent No. US20020045188A1
; GENERAL INFORMATION:
; APPLICANT: Kamb et al
; TITLE OF INVENTION: METHODS FOR VALIDATING POLYPEPTIDE TARGETS THAT CORRELATE TO
; FILE REFERENCE: 29345/37561
; CURRENT APPLICATION NUMBER: US/09/865,644
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Peptide Binder of HPV B6
US-09-865-644-11

Query Match      80.0%; Score 4; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4
Db 11 FPPP 14

RESULT 20
US-10-161-791-332
; Sequence 332, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 332:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-332

Query Match      80.0%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 8 PPPK 11

RESULT 21
US-10-161-791-344
; Sequence 344, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 344:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-344

Query Match 80.0%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
|||  
Db 9 PPPK 12

## RESULT 22

US-10-161-791-386  
Sequence 386, Application US/10161791  
Publication No. US2003018683A1

GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 386:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-386

Query Match 80.0%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
|||  
Db 9 PPPK 12

## RESULT 23

US-10-161-791-432  
Sequence 432, Application US/10161791  
Publication No. US2003018683A1

GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 432:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-432

Query Match 80.0%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
|||  
Db 9 PPPK 12

## RESULT 24

US-10-057-789-223  
Sequence 223, Application US/10057789  
Publication No. US20030082522A1

GENERAL INFORMATION:  
APPLICANT: Paul Haynes  
APPLICANT: Jing Wei  
APPLICANT: John Yates

APPLICANT: Nancy Andon  
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE  
; FILE REFERENCE: NADII.022A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 60/264,576  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/305,232  
; PRIOR FILING DATE: 2001-07-13  
; NUMBER OF SEQ ID NOS: 311  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 223  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 6  
; OTHER INFORMATION: Xaa = Modified Cysteine  
US-10-057-789-223

Query Match 80.0%; Score 4; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
|||  
DB 13 PPPK 16

RESULT 25  
US-10-212-628-223  
; Sequence 223, Application US/10212628  
; Publication No. US20030087329A1  
; GENERAL INFORMATION:  
; APPLICANT: Paul Haynes  
; APPLICANT: Jing Wei  
; APPLICANT: John Yates  
; APPLICANT: Nancy Andon  
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE  
; FILE REFERENCE: NADII.022CP1  
; CURRENT APPLICATION NUMBER: US/10/212,628  
; CURRENT FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 60/264,576  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/305,232  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 10/057,789  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 311  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 223  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 6  
; OTHER INFORMATION: Xaa = Modified Cysteine  
US-10-212-628-223

Query Match 80.0%; Score 4; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
|||  
DB 13 PPPK 16

RESULT 26

US-10-331-907-403  
; Sequence 403, Application US/10331907  
; Publication No. US20030181660A1  
; GENERAL INFORMATION:  
; APPLICANT: Todd, John A  
; Hees, John W  
; Caskey, Charles T  
; Cox, Roger D  
; Gerhold, David  
; Hammond, Holly  
; Hey, Patricia  
; Kawaguchi, Yoshihiko  
; Merriman, Tony R  
; Metzker, Michael L  
; TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor  
; NUMBER OF SEQUENCES: 455  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon and Vanderhye  
; STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: US  
; ZIP: VA 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA: US/10/331,907  
; APPLICATION NUMBER: US/10/331,907  
; FILING DATE: 31-Dec-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/402,923A  
; FILING DATE: 14-Feb-2001  
; APPLICATION NUMBER: PCT/GB98/01102  
; FILING DATE: 15-APR-1998  
; APPLICATION NUMBER: US 60/043,553  
; FILING DATE: 15-APR-1997  
; APPLICATION NUMBER: US 60/048,740  
; FILING DATE: 05-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: B.J.Sadoff  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 620-81  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4091  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 403:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 403:  
US-10-331-907-403

Query Match 80.0%; Score 4; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
|||  
DB 6 FPPP 9

RESULT 27  
US-10-161-791-336  
; Sequence 336, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.

APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 336:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-336

Query Match 80.0%; Score 4; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPK 5  
Db 9 PPPK 12

RESULT 28  
US-10-161-791-380  
Sequence 380, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 380:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-380

Query Match 80.0%; Score 4; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPK 5  
Db 9 PPPK 12

RESULT 29  
US-09-879-957-165  
Sequence 165, Application US/09879957  
Patent No. US20020034755A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: HOFFMAN, No. US20020034755A1h  
APPLICANT: KAY, Brian K.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: MCCONNELL, Stephen J.  
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
USING SAME  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,957  
FILING DATE: 13-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,915  
FILING DATE: 03-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-174



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 165:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 165:  
US-09-879-957-165

Query Match 80.0%; Score 4; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
Db 10 FPPP 13

RESULT 30  
US-10-161-791-305  
; Sequence 305, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 305:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-10-161-791-305

Query Match 80.0%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
Db 7 FPPP 10

RESULT 31  
US-10-185-050-109  
; Sequence 109, Application US/10185050  
; Publication No. US2003007577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; KAY, Brian K.  
; FOLKES, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 233  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/185,050  
; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-208-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:  
US-10-185-050-109

Query Match 80.0%; Score 4; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
Db 10 FPPP 13

RESULT 32  
US-09-879-957-162  
; Sequence 162, Application US/09879957  
; Patent No. US20020034755A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; HOFFMAN, No. US20020034755A1h

KAY, Brian K.  
FOWLES, Dana M.  
MCCONNELL, Stephen J.  
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
USING SAME  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,957  
FILING DATE: 13-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,915  
FILING DATE: 03-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-09-879-957-162  
Query Match 80.0%; Score 4; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FPPP 4  
Db 8 FPPP 11  
RESULT 33  
US-10-185-050-106  
; Sequence 106, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowles, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
MEDIUM TYPE: Floppy disk  
COMPUTER READABLE FORM:  
KAY, Brian K.  
FOWLES, Dana M.  
MCCONNELL, Stephen J.  
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
USING SAME  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,957  
FILING DATE: 13-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,915  
FILING DATE: 03-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 162:  
US-09-879-957-162  
Query Match 80.0%; Score 4; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FPPP 4  
Db 8 FPPP 11  
RESULT 33  
US-10-185-050-106  
; Sequence 106, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowles, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
MEDIUM TYPE: Floppy disk  
COMPUTER READABLE FORM:  
KAY, Brian K.  
FOWLES, Dana M.  
MCCONNELL, Stephen J.  
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
USING SAME  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 106:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 106:  
US-10-185-050-106  
Query Match 80.0%; Score 4; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FPPP 4  
Db 8 FPPP 11  
RESULT 34  
US-10-226-007-1542  
; Sequence 1542, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1542  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Unidentified ssDNA virus TA278  
US-10-226-007-1542  
Query Match 80.0%; Score 4; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 PPKK 5  
Db 16 PPKK 19  
RESULT 35  
US-09-735-450-4  
; Sequence 4, Application US/09735450  
; Patent No. US20020025323A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Paterson, Yvonne
/ APPLICANT: Gunn III, George R
/ APPLICANT: Peters, Christian
/ TITLE OF INVENTION: Compositions and Methods for Enhancing Immunogenicity
/ TITLE OF INVENTION: of Antigens
/ FILE REFERENCE: PENN-0741
/ CURRENT APPLICATION NUMBER: US/09/735,450
/ CURRENT FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: 09/537,642
/ PRIOR FILING DATE: 2000-03-29
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Listeria monocytogenes
/ US-09-735-450-4

Query Match      80.0%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FPPP 4
        ||||
Db      10 FPPP 13

RESULT 36
US-09-941-611-20
; Sequence 20, Application US/09941611
; Patent No. US20020106640A1
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; POLLET, DIRK
; MAERTENS, GEERT
; VAN HEUVERSWUN, HUGO
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/941,611
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/391,671
; FILING DATE: 1995-02-21
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Query Match      80.0%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-941-611-20

Query Match      80.0%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPK 5
        ||||
Db      7 PPPK 10

RESULT 37
US-10-044-995-20
; Sequence 20, Application US/10044995
; Publication No. US20030049685A1
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; POLLET, DIRK
; MAERTENS, GEERT
; VAN HEUVERSWUN, HUGO
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,995
; FILING DATE: 15-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/391,671
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/920,286
; FILING DATE: 14-OCT-1992
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-044-995-20

Query Match      80.0%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2 PPPK 5  
|||||  
Db 7 PPPK 10

## RESULT 38

US-10-226-007-1543  
; Sequence 1543, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1543  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Unidentified ssDNA virus TA278  
US-10-226-007-1543

Query Match 80.0%; Score 4; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
|||||  
Db 16 PPPK 19

## RESULT 39

US-10-226-007-1556  
; Sequence 1556, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1556  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Unidentified ssDNA virus TA278  
US-10-226-007-1556

Query Match 80.0%; Score 4; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
|||||  
Db 17 PPPK 20

## RESULT 40

US-10-352-704-21  
; Sequence 21, Application US/10352704

; Publication No. US20030176690A1  
; GENERAL INFORMATION:  
; APPLICANT: Chatelain, Francois  
; APPLICANT: Kumarev, Viktor  
; TITLE OF INVENTION: Process for Preparing Polynucleotides on  
; a Solid Support and Apparatus Permitting its  
; Implementation  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/10/352,704

FILING DATE: 28-Jan-2003

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/358,556A

FILING DATE: 14-DEC-1994

APPLICATION NUMBER: FR 9315164

FILING DATE: 16-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Player, William E.

REGISTRATION NUMBER: 31,409

REFERENCE/DOCKET NUMBER: 10577/P58418

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)638-6666

TELEFAX: (202) 393-5350

TELEX: RCA 248593 IDEA UR

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-352-704-21

Query Match 60.0%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 1 PPP 3

## RESULT 41

US-10-299-991-11

; Sequence 11, Application US/10299991

; Publication No. US20030194725A1

; GENERAL INFORMATION:

; APPLICANT: Greener et al.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING AND VALIDATING POTENTIAL DRUG TARGETS

; FILE REFERENCE: PROI-P01-004

; CURRENT APPLICATION NUMBER: US/10/299,991

; CURRENT FILING DATE: 2002-11-19

; PRIOR APPLICATION NUMBER: 60/331701

; PRIOR FILING DATE: 2001-11-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Retroviral

## US-10-299-991-11

Query Match 60.0%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 1 PPP 3

## RESULT 42

US-10-376-121A-130  
; Sequence 130, Application US/10376121A  
; Publication No. US20030216544A1  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; AUTOANTIBODIES

NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3400

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV(2)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 130:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 130:

## US-10-376-121A-130

Query Match 60.0%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 1 PPP 3

## RESULT 43

US-10-376-121A-134  
; Sequence 134, Application US/10376121A  
; Publication No. US20030216544A1

GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTOANTIBODIES

NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3400

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV(2)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 134:

## US-10-376-121A-134

Query Match 60.0%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 1 PPP 3

## RESULT 44

US-10-376-121A-135  
; Sequence 135, Application US/10376121A  
; Publication No. US20030216544A1  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; AUTOANTIBODIES

NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3400

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 135:  
US-10-376-121A-135

Query Match 60.0%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 1 PPP 3

RESULT 45  
US-10-097-534-41  
Sequence 41, Application US/10097534  
Publication No. US20030049607A1  
GENERAL INFORMATION:  
APPLICANT: GREENER, TSVIKA  
APPLICANT: MOSKOWITZ, HAIM  
APPLICANT: REISS, YUVAL  
APPLICANT: ALROY, IRIS  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL  
TITLE OF INVENTION: MATURATION  
FILE REFERENCE: PLV-001.01  
CURRENT APPLICATION NUMBER: US/10/097,534  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/275,224  
PRIOR FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: 60/308,958  
PRIOR FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: 60/340,170  
PRIOR FILING DATE: 2001-12-07  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Illustrative  
OTHER INFORMATION: Gag protein motif  
US-10-097-534-41

Query Match 60.0%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 1 PPP 3

RESULT 46  
US-10-096-986-106  
Sequence 106, Application US/10096986  
Publication No. US20030083464A1  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
Chambers, Charles  
Causey, Stuart  
Pollock, Thomas J.  
Cappello, Joseph  
Crissman, John W.  
TITLE OF INVENTION: No. US20030083464A1 Peptides Comprising Repetitive  
Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/10/096,986  
FILING DATE: 12-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/444,791  
FILING DATE: 22-No. US20030083464A1-1999  
APPLICATION NUMBER: US 08/482,085  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 106:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..4  
OTHER INFORMATION: /note= "X = any amino acid"  
SEQUENCE DESCRIPTION: SEQ ID NO: 106:  
US-10-096-986-106

Query Match 60.0%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 2 PPP 4

## RESULT 47

US-10-185-815-99  
; Sequence 99, Application US/10185815  
; Publication No. US20030096354A1  
; GENERAL INFORMATION:  
; APPLICANT: Elan Corporation, plc  
; APPLICANT: O'Mahony, Daniel  
; APPLICANT: Lambkin, Imelda  
; APPLICANT: Higgins, Lisa  
; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands  
; FILE REFERENCE: E1067-20093  
; CURRENT APPLICATION NUMBER: US/10/185,815  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: 60/302,591  
; PRIOR FILING DATE: 2001-07-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 99  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: polypeptide ligand

## US-10-185-815-99

Query Match 60.0%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 2 PPP 4

## RESULT 48

US-10-222-455-33  
; Sequence 33, Application US/10222455  
; Publication No. US20030099983A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Cyclic and Substituted Immobilized  
; Molecular Synthesis  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3814  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/222,455  
; FILING DATE: 16-Aug-2002  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/647,618  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: US 07/972,007  
; FILING DATE: 05-NOV-1992  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991

; APPLICATION NUMBER: US 07/805,727  
; FILING DATE: 06-DEC-1991  
; APPLICATION NUMBER: US 07/624,120  
; FILING DATE: 06-DEC-1990  
; APPLICATION NUMBER: US 07/492,462  
; FILING DATE: 07-MAR-1990  
; APPLICATION NUMBER: US 07/362,901  
; FILING DATE: 07-JUN-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy, Matthew B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 16528J-000141US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-10-222-455-33

Query Match 60.0%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 1 PPP 3

## RESULT 49

US-10-226-007-1  
; Sequence 1, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005, 01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-226-007-1

Query Match 60.0%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 1 PPP 3

## RESULT 50

US-09-823-240-4  
; Sequence 4, Application US/09823240  
; Patent No. US20020048813A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank B. Gertler  
; APPLICANT: James E. Bear

; APPLICANT: Jurgen Wehland  
; APPLICANT: Joseph Loureiro  
; TITLE OF INVENTION: Methods and Products for Regulating Cell  
; TITLE OF INVENTION: Motility  
; FILE REFERENCE: M0656/7064 (HCL)  
; CURRENT APPLICATION NUMBER: US/09/823,240  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 60/194,564  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Listeria monocytogenes  
US-09-823-240-4

Query Match 60.0%; Score 3; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
DB 2 PPP 4

RESULT 51  
US-09-858-754-9  
; Sequence 9, Application US/09858754  
; Patent No. US2002005130A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Gary L.  
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS  
; FILE REFERENCE: CPI-042  
; CURRENT APPLICATION NUMBER: US/09/858,754  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/023,130  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: 60/039,740  
; PRIOR FILING DATE: 1997-02-14  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: synthetic construct  
US-09-858-754-9

Query Match 60.0%; Score 3; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
DB 1 PPP 3

RESULT 52  
US-09-785-921A-15  
; Sequence 15, Application US/09785921A  
; Patent No. US20020094334A1  
; GENERAL INFORMATION:  
; APPLICANT: Keener, William K.  
; APPLICANT: Ward, Thomas E.  
; TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN  
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS  
; FILE REFERENCE: LIT-PI-529  
; CURRENT APPLICATION NUMBER: US/09/785,921A  
; CURRENT FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PRT

; ORGANISM: Rous sarcoma virus  
US-09-785-921A-15  
Query Match 60.0%; Score 3; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
DB 1 PPP 3

RESULT 53  
US-10-352-704-23  
; Sequence 23, Application US/10352704  
; Publication No. US20030176690A1  
; GENERAL INFORMATION:  
; APPLICANT: Chatelain, Francois  
; APPLICANT: Kumarev, Viktor  
; TITLE OF INVENTION: Process for Preparing Polynucleotides on  
; a Solid Support and Apparatus Permitting its  
; Implementation  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/352,704  
FILING DATE: 28-Jan-2003  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,556A  
FILING DATE: 14-DEC-1994  
APPLICATION NUMBER: FR 9315164  
FILING DATE: 16-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Playex, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: 10577/P58418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-6666  
TELEFAX: (202) 393-5350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-10-352-704-23

Query Match 60.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
DB 1 PPP 3

RESULT 54  
US-10-376-121A-120  
; Sequence 120, Application US/10376121A



Publication No. US20030216544A1  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTOANTIBODIES  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV(2)  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 120:  
US-10-376-121A-120  
Query Match 60.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db 1 PPP 3  
RESULT 55  
US-10-376-121A-129  
Sequence 129, Application US/10376121A  
Publication No. US20030216544A1  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTOANTIBODIES  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV(2)  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
US-10-376-121A-129  
Query Match 60.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db 1 PPP 3  
RESULT 56  
US-10-185-050-3  
Sequence 3, Application US/10185050  
Publication No. US20030077577A1  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
Kay, Brian K.  
Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: <unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-185-050-3

Query Match 60.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 PPP 4  
|||  
Db 1 PPP 3

## RESULT 57

US-10-185-050-231  
; Sequence 231, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.

TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997

ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 231:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 231:  
US-10-185-050-231

Query Match 60.0%; Score 3; DB 15; Length 5;

Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
QY 2 PPP 4  
|||  
Db 1 PPP 3

## RESULT 58

US-10-185-050-233  
; Sequence 233, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.

TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 233

CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997

ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 233:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 233:  
US-10-185-050-233

Query Match 60.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 PPP 4  
|||  
Db 1 PPP 3

## RESULT 59

US-10-074-225A-10  
; Sequence 10, Application US/10074225A  
; Publication No. US20030082740A1  
; GENERAL INFORMATION:  
; APPLICANT: DONATE, Fernando  
; APPLICANT: PLUNKETT, Marian L  
; APPLICANT: HARRIS, Scott

APPLICANT: MAZAR, Andrew P  
TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC  
FILE OF INVENTION: ANTI-TUMOR AGENT  
FILE REFERENCE: 38342-178463  
CURRENT APPLICATION NUMBER: US/10/074.225A  
CURRENT FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/268,370  
PRIOR FILING DATE: 2001-02-14  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-10-074-225A-10

Query Match 60.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
Db 1 PPP 3

RESULT 60  
US-10-096-986-9  
Sequence 9, Application US/10095986  
Publication No. US20030083464A1  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
Richardson, Charles  
Chambers, James  
Causley, Stuart  
Pollock, Thomas J.  
Cappelletto, Joseph  
Crisman, John W.  
TITLE OF INVENTION: No. US20030083464A1 Peptides Comprising Repetitive  
Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/096.986  
FILING DATE: 12-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/444.791  
FILING DATE: 22-No. US20030083464A1-1999  
APPLICATION NUMBER: US 08/482,085  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.

REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-096-986-9

Query Match 60.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
Db 2 PPP 4

RESULT 61  
US-10-226-007-5  
Sequence 5, Application US/10226007  
Publication No. US20030105277A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
FILE REFERENCE: 5005.01  
CURRENT APPLICATION NUMBER: US/10/226,007  
CURRENT FILING DATE: 2002-11-15  
PRIOR APPLICATION NUMBER: US 60/313,883  
PRIOR FILING DATE: 2001-08-21  
NUMBER OF SEQ ID NOS: 1673  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-226-007-5

Query Match 60.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
Db 1 PPP 3

RESULT 62  
US-10-226-007-6  
Sequence 6, Application US/10226007  
Publication No. US20030105277A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
FILE REFERENCE: 5005.01  
CURRENT APPLICATION NUMBER: US/10/226,007  
CURRENT FILING DATE: 2002-11-15  
PRIOR APPLICATION NUMBER: US 60/313,883  
PRIOR FILING DATE: 2001-08-21  
NUMBER OF SEQ ID NOS: 1673  
SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-226-007-6

Query Match      60.0%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPP 4
Db      1 PPP 3

RESULT 63
US-10-226-007-7
; Sequence 7, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-226-007-7

Query Match      60.0%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPP 4
Db      1 PPP 3

RESULT 64
US-09-803-126-21
; Sequence 21, Application US/09803126
; Patent No. US20020099190A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Alan R.
; APPLICANT: Deng, Gary G.
; APPLICANT: Rubanyi, Gabor M.
; TITLE OF INVENTION: Estrogen-Regulated Unconventional Myosin-Related
; FILE REFERENCE: 015303-000310US
; CURRENT APPLICATION NUMBER: US/09/803,126
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/188,488
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Peptide
US-09-803-126-21
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Query Match      60.0%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPP 4
Db      1 PPP 3

RESULT 65
US-09-859-053-41
; Sequence 41, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Teuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, NO. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-41

Query Match      60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPP 4
Db      3 PPP 5

RESULT 66
US-09-873-106B-10
; Sequence 10, Application US/09873106B
; Patent No. US20020127657A1
; GENERAL INFORMATION:
; APPLICANT: Reinherz, Ellis L.
; APPLICANT: Freund, Christian
; APPLICANT: Li, Jing
; APPLICANT: Nishizawa, Kazuhisa
; APPLICANT: Wagner, Gerhard
; TITLE OF INVENTION: Cloning and Characterization of a CD2
; FILE REFERENCE: 1062.1021-004
; CURRENT APPLICATION NUMBER: US/09/873,106B
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/111,007
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: US 60/115,647
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/26993
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD2BP2 binding region
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## US-09-873-106B-10

Query Match 60.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
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Db 1 PPP 3

## RESULT 67

US-09-814-777A-29

; Sequence 29, Application US/09814777A  
; Patent No. US20020142415A1  
; GENERAL INFORMATION:  
; APPLICANT: KOOPMAN, Peter Anthony  
; APPLICANT: MUSCAT, George Eugene Orlando  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM  
; FILE REFERENCE: 21415-0003  
; CURRENT APPLICATION NUMBER: US/09/814,777A  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: AU P06457  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Human  
US-09-814-777A-29

Query Match 60.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 3 PPP 5

## RESULT 68

US-09-990-574-1

; Sequence 1, Application US/09990574  
; Patent No. US20020156008A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaumaya, Pravin T.P.  
; APPLICANT: Carolyn, Whitacre C.  
; TITLE OF INVENTION: Agents for blocking T cell mediated immune reactions  
; FILE REFERENCE: 18525/04028  
; CURRENT APPLICATION NUMBER: US/09/990,574  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/252744  
; PRIOR FILING DATE: 2000-12-04  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-574-1

Query Match 60.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 3 PPP 5

## RESULT 69

US-09-990-574-2

; Sequence 2, Application US/09990574  
; Patent No. US20020156008A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaumaya, Pravin T.P.  
; APPLICANT: Carolyn, Whitacre C.  
; TITLE OF INVENTION: Agents for blocking T cell mediated immune reactions  
; FILE REFERENCE: 18525/04028  
; CURRENT APPLICATION NUMBER: US/09/990,574  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/252744  
; PRIOR FILING DATE: 2000-12-04  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-574-2

Query Match 60.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
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Db 2 PPP 4

## RESULT 70

US-09-774-639-225

; Sequence 225, Application US/09774639  
; Publication No. US20030003555A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 90 Human Secreted Proteins  
; FILE REFERENCE: P2013P1  
; CURRENT APPLICATION NUMBER: US/09/774,639  
; CURRENT FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 371  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 225  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-774-639-225

Query Match 60.0%; Score 3; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPP 3  
|||  
Db 3 PPP 5

## RESULT 71

US-09-969-730-321

; Sequence 321, Application US/09969730  
; Publication No. US2003005443A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 90 Human Secreted Proteins  
; FILE REFERENCE: P2013P2  
; CURRENT APPLICATION NUMBER: US/09/969,730  
; CURRENT FILING DATE: 2001-10-04  
; PRIOR APPLICATION NUMBER: 09/774,639  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/238,291  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 09/244,112  
; PRIOR FILING DATE: 1999-02-04

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; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
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; PRIOR APPLICATION NUMBER: 60/056,365
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; PRIOR APPLICATION NUMBER: 60/056,563
; PRIOR FILING DATE: 1997-08-19
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; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,311
; PRIOR FILING DATE: 1997-08-05
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; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,809
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,806
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,310
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,798
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,309
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,312
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,807
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,386
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 321
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-969-730-321

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Query Match 60.0%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 PPP 3
Db 3 PPP 5

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RESULT 72
US-10-032-214-297
; Sequence 297, Application US/10032214
; Publication No. US20030138881A1
; GENERAL INFORMATION:
; APPLICANT: PUNNONEN, JUHA

```

```

; APPLICANT: LAZETIC, ALEXANDRA
; APPLICANT: LEONG, STEVEN R.
; APPLICANT: CHANG, CHIA-CHUN
; APPLICANT: APT, DORIS
; APPLICANT: GUSTAFSSON, CLAES
; TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
; FILE REFERENCE: 02-106730US
; CURRENT APPLICATION NUMBER: US/10/032,214
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 09/888,324
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: PCT/US01/19973
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,946
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/241,245
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 297
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: conserved peptide
; US-10-032-214-297

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Query Match 60.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 PPP 4
Db 3 PPP 5

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RESULT 73
US-10-072-622-11
; Sequence 11, Application US/10072622
; Publication No. US20030158102A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; APPLICANT: Bajorath, Jurgen
; TITLE OF INVENTION: ICOS Mutants
; FILE REFERENCE: 07039-331001
; CURRENT APPLICATION NUMBER: US/10/072,622
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-072-622-11

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Query Match 60.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 PPP 4
Db 3 PPP 5

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RESULT 74
US-10-352-704-25
; Sequence 25, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on

```

```

1 a Solid Support and Apparatus Permitting its
2 Implementation
3
4 NUMBER OF SEQUENCES: 31
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Jacobson, Price, Holman & Stern
7 STREET: 400 Seventh St. N.W.
8 CITY: Washington D.C
9 STATE: D.C
10 COUNTRY: U.S.A.
11 ZIP: 20004
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.25
18
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/10/352,704
21 FILING DATE: 28-Jan-2003
22 CLASSIFICATION: 536
23
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US/08/358,556A
26 FILING DATE: 14-DEC-1994
27 APPLICATION NUMBER: FR 9315164
28 FILING DATE: 16-DEC-1993
29
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Player, William E.
32 REGISTRATION NUMBER: 31,409
33 REFERENCE/DOCKET NUMBER: 10577/P58418
34
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (202) 638-6666
37 TELEFAX: (202) 393-5350
38
39 TELEX: RCA 248593 IDEA UR
40
41 INFORMATION FOR SEQ ID NO: 25:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 6 amino acids
44 TYPE: amino acid
45 TOPOLOGY: linear
46
47 MOLECULE TYPE: protein
48 SEQUENCE DESCRIPTION: SEQ ID NO: 25:
49 US-10-352-704-25

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 5.45213 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-12

Perfect score: 5

Sequence: 1 FPPPK 5

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued\_Patents\_AA.\*

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3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	4	US-09-641-803-12
2	5	100.0	14	1	US-08-211-070A-1
3	5	100.0	14	2	US-08-859-183-8
4	4	80.0	7	4	US-09-281-495-17
5	4	80.0	9	2	US-08-146-028-443
6	4	80.0	9	2	US-08-146-028-445
7	4	80.0	9	2	US-08-146-028-446
8	4	80.0	9	2	US-08-146-028-447
9	4	80.0	9	3	US-08-723-425A-443
10	4	80.0	9	3	US-08-723-425A-444
11	4	80.0	9	3	US-08-723-425A-445
12	4	80.0	9	3	US-08-723-425A-446
13	4	80.0	9	3	US-08-723-425A-447
14	4	80.0	9	3	US-08-723-425A-448
15	4	80.0	9	3	US-09-112-206-443
16	4	80.0	9	3	US-09-112-206-445
17	4	80.0	9	3	US-09-112-206-446
18	4	80.0	9	3	US-09-112-206-447
19	4	80.0	9	3	US-09-112-206-448
20	4	80.0	10	2	US-08-146-028-444
21	4	80.0	10	3	US-08-723-425A-444
22	4	80.0	10	3	US-09-112-206-444
23	4	80.0	12	2	US-08-666-473-113
24	4	80.0	12	2	US-08-556-597-138
25	4	80.0	12	4	US-09-007-288E-67
26	4	80.0	13	1	US-08-103-742-37
27	4	80.0	13	3	US-08-630-916A-60

28	4	80.0	15	3	US-08-602-999A-393	Sequence 393, App
29	4	80.0	15	4	US-09-500-124-393	Sequence 393, App
30	4	80.0	15	4	US-09-641-803-7	Sequence 7, Appli
31	4	80.0	16	3	US-08-602-999A-332	Sequence 332, App
32	4	80.0	16	3	US-08-602-999A-344	Sequence 344, App
33	4	80.0	16	3	US-08-602-999A-386	Sequence 386, App
34	4	80.0	16	3	US-08-602-999A-432	Sequence 432, App
35	4	80.0	16	4	US-09-500-124-332	Sequence 332, App
36	4	80.0	16	4	US-09-500-124-344	Sequence 344, App
37	4	80.0	16	4	US-09-500-124-386	Sequence 386, App
38	4	80.0	16	4	US-09-500-124-432	Sequence 432, App
39	4	80.0	16	4	US-09-023-905A-28	Sequence 28, Appl
40	4	80.0	17	3	US-08-602-999A-336	Sequence 336, App
41	4	80.0	17	3	US-08-602-999A-380	Sequence 380, App
42	4	80.0	17	4	US-09-500-124-336	Sequence 336, App
43	4	80.0	17	4	US-09-500-124-380	Sequence 380, App
44	4	80.0	17	4	US-09-060-299-403	Sequence 403, App
45	4	80.0	17	4	US-09-402-923A-403	Sequence 403, App
46	4	80.0	18	3	US-08-630-916A-109	Sequence 109, App
47	4	80.0	18	3	US-08-881-094-11	Sequence 11, Appl
48	4	80.0	18	3	US-08-881-094-12	Sequence 12, Appl
49	4	80.0	18	3	US-08-602-999A-105	Sequence 105, App
50	4	80.0	18	4	US-08-630-915A-165	Sequence 165, App
51	4	80.0	18	4	US-09-500-124-305	Sequence 305, App
52	4	80.0	19	3	US-08-630-916A-106	Sequence 106, App
53	4	80.0	19	4	US-08-103-742-36	Sequence 36, Appl
54	4	80.0	20	1	US-08-466-975A-20	Sequence 20, Appl
55	4	80.0	20	2	US-08-391-671A-20	Sequence 20, Appl
56	4	80.0	20	3	US-08-467-902A-20	Sequence 20, Appl
57	4	80.0	20	3	US-09-275-265-20	Sequence 20, Appl
58	4	80.0	20	4	US-08-850-328-13	Sequence 13, Appl
59	4	80.0	20	4	US-09-941-611-20	Sequence 20, Appl
60	3	60.0	4	1	US-07-972-007-33	Sequence 33, Appl
61	3	60.0	4	1	US-08-351-058A-1	Sequence 1, Appl
62	3	60.0	4	1	US-08-477-509B-106	Sequence 106, App
63	3	60.0	4	1	US-08-477-509B-9	Sequence 9, Appl
64	3	60.0	4	2	US-08-482-085B-106	Sequence 106, App
65	3	60.0	4	3	US-09-444-791A-106	Sequence 106, App
66	3	60.0	4	4	US-09-295-996B-6	Sequence 6, Appl
67	3	60.0	4	4	US-09-057-162-33	Sequence 33, Appl
68	3	60.0	4	4	PCT-US92-09964-1	Sequence 1, Appl
69	3	60.0	4	4	US-08-351-058A-5	Sequence 5, Appl
70	3	60.0	5	1	US-08-240-514-31	Sequence 31, Appl
71	3	60.0	5	1	US-08-477-509B-9	Sequence 9, Appl
72	3	60.0	5	2	US-08-612-302A-31	Sequence 31, Appl
73	3	60.0	5	2	US-08-666-473-6	Sequence 6, Appl
74	3	60.0	5	2	US-08-666-473-10	Sequence 10, Appl
75	3	60.0	5	2	US-08-340-283-3	Sequence 3, Appl
76	3	60.0	5	2	US-08-340-283-4	Sequence 4, Appl
77	3	60.0	5	2	US-08-358-556A-23	Sequence 23, Appl
78	3	60.0	5	2	US-08-967-508-12	Sequence 12, Appl
79	3	60.0	5	2	US-08-967-508-13	Sequence 13, Appl
80	3	60.0	5	2	US-08-630-916A-3	Sequence 3, Appl
81	3	60.0	5	3	US-08-482-085B-9	Sequence 9, Appl
82	3	60.0	5	3	US-08-476-509B-38	Sequence 38, Appl
83	3	60.0	5	3	US-08-967-506-12	Sequence 12, Appl
84	3	60.0	5	3	US-08-967-506-13	Sequence 13, Appl
85	3	60.0	5	4	US-09-444-791A-9	Sequence 9, Appl
86	3	60.0	5	4	US-09-295-996B-7	Sequence 7, Appl
87	3	60.0	5	4	US-09-119-507B-3	Sequence 3, Appl
88	3	60.0	5	4	US-09-295-846B-10	Sequence 10, Appl
89	3	60.0	5	4	US-09-551-737C-10	Sequence 10, Appl
90	3	60.0	5	4	US-08-897-556A-3	Sequence 3, Appl
91	3	60.0	5	4	US-08-897-556A-100	Sequence 100, App
92	3	60.0	5	4	US-08-897-556A-105	Sequence 105, App
93	3	60.0	5	4	PCT-US92-09964-5	Sequence 5, Appl
94	3	60.0	5	5	PCT-US94-02552-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
US-09-641-803-12  
; Sequence 12, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641.803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-12

Query Match 100.0%; Score 5; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPK 5  
|||  
Db 1 FPPPK 5

RESULT 2  
US-08-211-070A-1  
; Sequence 1, Application US/08211070A  
; Patent No. 5583350  
; GENERAL INFORMATION:  
; APPLICANT: Friedrich, Thomas  
; APPLICANT: Koerwer, Wolfgang  
; APPLICANT: Kroeger, Burkhard  
; APPLICANT: Bialojan, Siegfried  
; TITLE OF INVENTION: No. 5583350el thrombin-inhibitory protein from ticks.  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Keil & Weinkauf  
; STREET: 1101 Connecticut Avenue  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
; COMPUTER: IBM AT-compatible, 80486 processor  
; OPERATING SYSTEM: MS-DOS version 6.0  
; SOFTWARE: WordPerfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/211.070A  
; FILING DATE: 18-MAR-1994  
; CLASSIFICATION: 435  
; CLASSIFICATION: C12P 21/02  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP92/02198  
; FILING DATE: 23-SEP-1992  
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-211-070A-1

Query Match 100.0%; Score 5; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPK 5  
|||  
Db 5 FPPPK 9

RESULT 3  
US-08-859-183-8  
; Sequence 8, Application US/08859183  
; Patent No. 5827731  
; GENERAL INFORMATION:  
; APPLICANT: Friedrich, Thomas  
; APPLICANT: Bialojan, Siegfried  
; APPLICANT: Bollschweiler, Claus  
; APPLICANT: Kuenast, Christoph  
; TITLE OF INVENTION: No. 5827731el thrombin-inhibitory protein  
; TITLE OF INVENTION: from ticks  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Keil & Weinkauf  
; STREET: 1101 Connecticut Avenue  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage  
; COMPUTER: IBM AT-compatible, 80486 processor  
; OPERATING SYSTEM: MS-DOS version 6.0  
; SOFTWARE: WordPerfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/859,183  
; FILING DATE: 20-MAY-1997  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: 08/415,999  
; FILING DATE: 04-APR-1995  
; APPLICATION NUMBER: PCT/EP92/02179  
; FILING DATE: 21-SEP-1992  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-859-183-8

Query Match 100.0%; Score 5; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPPK 5  
|||  
Db 5 FPPPK 9

RESULT 4  
US-09-281-495-17  
; Sequence 17, Application US/09281495  
; Patent No. 6541002  
; GENERAL INFORMATION:  
; APPLICANT: Pomerantz, Roger J  
; APPLICANT: BouHamdan, Mohamad  
; APPLICANT: Duan, Ling-Xun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROVIDING A PROTEIN TO A

```
; TITLE OF INVENTION: VIRION
; FILE REFERENCE: 9855-25U1
; CURRENT APPLICATION NUMBER: US/09/281.495
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,822
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Vpr-Specific
; OTHER INFORMATION: Polypeptide Binding Region
US-09-281-495-17

Query Match      80.0%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPPP 4
Db 4 FPPP 7

RESULT 5
US-08-146-028-443
; Sequence 443, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,028
; INFORMATION FOR SEQ ID NO: 443:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-146-028-443

Query Match      80.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPK 5
Db 6 PPPK 9

RESULT 6
US-08-146-028-445
; Sequence 445, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
```

```
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,028
; INFORMATION FOR SEQ ID NO: 445:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-146-028-445

Query Match      80.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPK 5
Db 4 PPPK 7

RESULT 7
US-08-146-028-446
; Sequence 446, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,028
; INFORMATION FOR SEQ ID NO: 446:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-146-028-446

Query Match      80.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPK 5
Db 3 PPPK 6

RESULT 8
US-08-146-028-447
; Sequence 447, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
```

;; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
;; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
;; NUMBER OF SEQUENCES: 453  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
;; CURRENT APPLICATION DATA: US/08/146,028  
;; APPLICATION NUMBER: US/08/146,028  
;; INFORMATION FOR SEQ ID NO: 447:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-146-028-447

Query Match 80.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 2 PPPK 5

## RESULT 9

US-08-146-028-448  
; Sequence 448, Application US/08146028  
; Patent No. 5891640  
; GENERAL INFORMATION:  
; APPLICANT:

;; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
;; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
;; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
;; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
;; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
;; NUMBER OF SEQUENCES: 453  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/146,028  
;; INFORMATION FOR SEQ ID NO: 448:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-146-028-448

Query Match 80.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 1 PPPK 4

## RESULT 10

US-08-723-425A-443  
; Sequence 443, Application US/08723425A  
; Patent No. 6165730  
; GENERAL INFORMATION:  
; APPLICANT: DELEYS, ROBERT  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT

;; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
;; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
;; NUMBER OF SEQUENCES: 453  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: NIXON & VANDERHYE, P.C.  
;; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
;; CITY: Arlington  
;; STATE: VA  
;; COUNTRY: USA  
;; ZIP: 22201  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/723,425A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SADOFF, B.J.  
;; REGISTRATION NUMBER: 36,663  
;; REFERENCE/DOCKET NUMBER: 1487-13  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-816-4000  
;; TELEFAX: 703-816-4100  
;; INFORMATION FOR SEQ ID NO: 443:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-723-425A-443

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 6 PPPK 9

## RESULT 11

US-08-723-425A-445  
; Sequence 445, Application US/08723425A  
; Patent No. 6165730  
; GENERAL INFORMATION:  
; APPLICANT: DELEYS, ROBERT

;; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
;; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
;; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
;; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
;; NUMBER OF SEQUENCES: 453  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: NIXON & VANDERHYE, P.C.  
;; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
;; CITY: Arlington  
;; STATE: VA  
;; COUNTRY: USA  
;; ZIP: 22201  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/723,425A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 445:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-723-425A-445

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
DB 4 PPPK 7

RESULT 12  
US-08-723-425A-446  
; Sequence 446, Application US/08723425A  
; Patent No. 6165730  
; GENERAL INFORMATION:  
; APPLICANT: DELEYS, ROBERT  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
; TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
; NUMBER OF SEQUENCES: 453  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE, P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/723,425A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-13  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 446:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-723-425A-446

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
DB 3 PPPK 6

RESULT 13  
US-08-723-425A-447  
; Sequence 447, Application US/08723425A  
; Patent No. 6165730  
; GENERAL INFORMATION:  
; APPLICANT: DELEYS, ROBERT  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
; TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
; NUMBER OF SEQUENCES: 453  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE, P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/723,425A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-13  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 447:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-723-425A-447

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
DB 2 PPPK 5

RESULT 14  
US-08-723-425A-448  
; Sequence 448, Application US/08723425A  
; Patent No. 6165730  
; GENERAL INFORMATION:  
; APPLICANT: DELEYS, ROBERT  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
; TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
; NUMBER OF SEQUENCES: 453  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE, P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
US-08-723-425A-448

QY 2 PPPK 5  
DB 3 PPPK 6

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,425A  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 448:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-723-425A-448

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPKK 5  
|  
|  
|  
|  
Db 1 PPKK 4

## RESULT 15

US-09-112-206-443  
Sequence 443, Application US/09112206  
Patent No. 6210903  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES.  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/112,206  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,028

FILING DATE:  
INFORMATION FOR SEQ ID NO: 443:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-112-206-443

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPKK 5  
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|  
|  
|  
Db 6 PPKK 9

## RESULT 16

US-09-112-206-445  
Sequence 445, Application US/09112206  
Patent No. 6210903  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/112,206  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,028

FILING DATE:  
INFORMATION FOR SEQ ID NO: 445:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-112-206-445

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPKK 5  
|  
|  
|  
|  
Db 4 PPKK 7

## RESULT 17

US-09-112-206-446  
Sequence 446, Application US/09112206  
Patent No. 6210903  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/112,206  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,028

FILING DATE:  
INFORMATION FOR SEQ ID NO: 446:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-112-206-446

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
    ||||  
Db 3 PPPK 6

RESULT 18  
US-09-112-206-447  
; Sequence 447, Application US/09112206  
; Patent No. 6210903  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/112,206  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/146,028  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 447:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-112-206-447

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
    ||||  
Db 2 PPPK 5

RESULT 19  
US-09-112-206-448  
; Sequence 448, Application US/09112206  
; Patent No. 6210903  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/112,206  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/146,028

; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 448:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-112-206-448

Query Match 80.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
    ||||  
Db 1 PPPK 4

RESULT 20  
US-08-146-028-444  
; Sequence 444, Application US/08146028  
; Patent No. 5891640  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146,028  
; INFORMATION FOR SEQ ID NO: 444:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-146-028-444

Query Match 80.0%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
    ||||  
Db 6 PPPK 9

RESULT 21  
US-08-723-425A-444  
; Sequence 444, Application US/08723425A  
; Patent No. 6165730  
; GENERAL INFORMATION:  
; APPLICANT: DELEYS, ROBERT  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
; NUMBER OF SEQUENCES: 453  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: NIXON & VANDERHVE, P. C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA

;; ZIP: 22201.  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/723,425A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SADOFF, B.J.  
;; REGISTRATION NUMBER: 36,663  
;; REFERENCE/DOCKET NUMBER: 1487-13  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-816-4000  
;; TELEFAX: 703-816-4100  
;; INFORMATION FOR SEQ ID NO: 444:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-723-425A-444

Query Match 80.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5

Db 6 PPPK 9

RESULT 22  
US-09-112-206-444  
; Sequence 444, Application US/09112206  
; Patent No. 6210903  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINVLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES.  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/112,206  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/146,028  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 444:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-112-206-444

Query Match 80.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5

||||

Db 6 PPPK 9

RESULT 23  
US-08-666-473-113  
; Sequence 113, Application US/08666473  
; Patent No. 5843713  
; GENERAL INFORMATION:  
; APPLICANT: YOSHIDA, Aruto  
; APPLICANT: TAKEUCHI, Makoto  
; TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR  
; TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED  
; TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/666,473  
; FILING DATE: 19-SEP-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP95/02238  
; FILING DATE: 01-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-22101  
; FILING DATE: 09-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-269111  
; FILING DATE: 01-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 16887/837  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-666-473-113

Query Match 80.0%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
||||

Db 7 PPPK 10

RESULT 24  
US-08-556-597-138  
; Sequence 138, Application US/08556597  
; Patent No. 5877155  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Jonathan L.  
; APPLICANT: Lyle, Vicki A.  
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF  
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN 1B/1X



NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/556,597  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/406,330  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Timian, Susan J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 20884/101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1636  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 138:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-556-597-138

Query Match 80.0%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 5 FPPP 8

RESULT 25  
US-09-007-288E-67  
Sequence 67, Application US/09007288E  
Patent No. 6495357  
GENERAL INFORMATION:  
APPLICANT: Fuglsang, Claus  
APPLICANT: Orkels, Jens  
APPLICANT: Petersen, Dorte  
APPLICANT: Pakkar, Shamkant  
APPLICANT: Thelliersen, Marianne  
APPLICANT: Svendsen, Allan  
APPLICANT: Borch, Kim  
APPLICANT: Royer, John  
APPLICANT: Kretzschmar, Titus  
APPLICANT: Halkier, Torben  
APPLICANT: Vind, Jesper  
APPLICANT: Jorgensen, Steen  
TITLE OF INVENTION: No. 6495357el Lipolytic Enzymes  
FILE REFERENCE: 4455.404-US  
CURRENT APPLICATION NUMBER: US/09/007,288E  
CURRENT FILING DATE: 2000-01-14  
NUMBER OF SEQ ID NOS: 162  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 67  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:

OTHER INFORMATION: Peptide addition  
US-09-007-288E-67  
Query Match 80.0%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPKK 5  
DB 2 PPKK 5

RESULT 26  
US-08-103-742-37  
Sequence 37, Application 08/103742  
Patent No. 5420244  
GENERAL INFORMATION:  
APPLICANT: RUDOLPH, DONNA L.  
APPLICANT: LAL, RENU B.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TITLE OF INVENTION: DIAGNOSING HTLV-I ASSOCIATED MYELOPATHY AND ADULT T-CELL LEUK  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
STREET: Suite 1200, 127 Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/103,742  
FILING DATE: 06 AUG 1993  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: SPRATT, GWENDOLYN D.  
REGISTRATION NUMBER: 36,016  
REFERENCE/DOCKET NUMBER: 1414.080  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404/688-0770  
TELEFAX: 404/688-9880  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-103-742-37

Query Match 80.0%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 2 FPPP 5

RESULT 27  
US-08-630-916A-60  
Sequence 60, Application US/08630916A  
Patent No. 6011137  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
APPLICANT: Kay, Brian K.  
APPLICANT: Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-60

Query Match 80.0%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPK 5  
Db 4 PPPK 7

RESULT 28  
US-08-602-999A-393  
Sequence 393, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 393:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-393

Query Match 80.0%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPPP 4  
Db 6 FPPP 9

RESULT 29  
US-09-500-124-393  
Sequence 393, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: 08/602,999  
APPLICATION NUMBER:  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 393:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

## US-09-500-124-393

Query Match 80.0%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 6 FPPP 9

## RESULT 30

US-09-641-803-7  
; Sequence 7, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641.803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149.310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-7

Query Match 80.0%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 6 FPPP 9

## RESULT 31

US-08-602-999A-332  
; Sequence 332, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
US-08-602-999A-332

## CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 332:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-602-999A-332

Query Match 80.0%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPKK 5  
DB 8 PPKK 11

## RESULT 32

US-08-602-999A-344  
; Sequence 344, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
US-08-602-999A-344

; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 344:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-602-999A-344

Query Match 80.0%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPK 5  
Db 9 PPK 12

## RESULT 33

US-08-602-999A-386  
Sequence 386, Application US/08602999A

Patent No. 6184205

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.

APPLICANT: QUILLIAM, Lawrence A.

APPLICANT: DER, Channing J.

APPLICANT: FOWLKES, Dana M.

APPLICANT: RIDER, James E.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/602,999A

FILING DATE: 16-FEB-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-202

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 386:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-602-999A-386

Query Match 80.0%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPK 5  
Db 9 PPK 12

## RESULT 34

US-08-602-999A-432

Sequence 432, Application US/08602999A

Patent No. 6184205

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/602,999A

FILING DATE: 16-FEB-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-202

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 432:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-602-999A-432

Query Match 80.0%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPK 5  
Db 9 PPK 12

## RESULT 35

US-09-500-124-332

Sequence 332, Application US/09500124

Patent No. 6432920

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.

APPLICANT: QUILLIAM, Lawrence A.

APPLICANT: DER, Channing J.

APPLICANT: FOWLKES, Dana M.

APPLICANT: RIDER, James E.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME

NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 332:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-332

Query Match      80.0%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPK 5
Db      8 PPPK 11

RESULT 36
US-09-500-124-344
; Sequence 344, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-386
```

```
;
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 344:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-344

Query Match      80.0%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPK 5
Db      9 PPPK 12

RESULT 37
US-09-500-124-386
; Sequence 386, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 386:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-386
```

Query Match 80.0%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 9 PPPK 12

## RESULT 38

US-09-500-124-432  
; Sequence 432, Application US/09500124  
; Patent No. 6432920

## GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467

## CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:

## CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 432:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-09-500-124-432

Query Match 80.0%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 9 PPPK 12

## RESULT 39

US-09-023-905A-28  
; Sequence 88, Application US/09023905A  
; Patent No. 6475778  
; GENERAL INFORMATION:

; APPLICANT: Roberts, Thomas M.  
; APPLICANT: King, Frederick J.  
; APPLICANT: Harris, David P.  
; APPLICANT: Hu, Erding  
; APPLICANT: Spiegelman, Bruce  
; APPLICANT: Chan, Joanne  
; TITLE OF INVENTION: Differentiation Enhancing Factors and Uses  
; TITLE OF INVENTION: Therefor  
; FILE REFERENCE: DFN-021  
; CURRENT APPLICATION NUMBER: US/09/023,905A  
; CURRENT FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/038,191  
; PRIOR FILING DATE: 1997-02-14  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Bos sp.  
; US-09-023-905A-28

Query Match 80.0%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 8 PPPK 11

## RESULT 40

US-08-602-999A-336  
; Sequence 336, Application US/08602999A  
; Patent No. 6184205

## GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467

## CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 336:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid

```
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-336

Query Match      80.0%; Score 4; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5
Db 9 PPK 12

RESULT 41
US-08-602-999A-380
; Sequence 380, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 380:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-380

Query Match      80.0%; Score 4; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5
Db 9 PPK 12

RESULT 42
US-09-500-124-336
; Sequence 336, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-336

Query Match      80.0%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5
Db 9 PPK 12

RESULT 43
US-09-500-124-380
; Sequence 380, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-336

Query Match      80.0%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPK 5
Db 9 PPK 12
```

CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 380:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-380

Query Match 80.0%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
DB 9 PPPK 12

RESULT 44  
US-09-060-299-403  
Sequence 403, Application US/09060299  
Patent No. 6545137  
GENERAL INFORMATION:  
APPLICANT: Todd, John A  
APPLICANT: Hess, John W  
APPLICANT: Caskey, Charles T  
APPLICANT: Cox, Roger D  
APPLICANT: Gerhold, David  
APPLICANT: Hammond, Holly  
APPLICANT: Hey, Patricia  
APPLICANT: Kawaguchi, Yoshihiko  
APPLICANT: Metzker, Michael L  
APPLICANT: Merriman, Tony R  
TITLE OF INVENTION: No. 6545137el Receptor  
NUMBER OF SEQUENCES: 455  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vanderhye  
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: US  
ZIP: VA 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/060,299  
FILING DATE: 15-APR-1998  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/043,553  
FILING DATE: 15-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,740  
FILING DATE: 05-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: B.J.Sadoff  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 620-35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4091  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 403:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-060-299-403

Query Match 80.0%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 6 FPPP 9

RESULT 45  
US-09-402-923A-403  
Sequence 403, Application US/09402923A  
Patent No. 6555654  
GENERAL INFORMATION:  
APPLICANT: Todd, John A  
APPLICANT: Hess, John W  
APPLICANT: Caskey, Charles T  
APPLICANT: Cox, Roger D  
APPLICANT: Gerhold, David  
APPLICANT: Hammond, Holly  
APPLICANT: Hey, Patricia  
APPLICANT: Kawaguchi, Yoshihiko  
APPLICANT: Merriman, Tony R  
APPLICANT: Metzker, Michael L  
TITLE OF INVENTION: No. 6555654el LDL-Receptor  
NUMBER OF SEQUENCES: 455  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vanderhye  
STREET: 1100 No. 6555654th Glebe Road, Eighth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: US  
ZIP: VA 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,923A  
FILING DATE: 14-Feb-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01102  
FILING DATE: 15-APR-1998  
APPLICATION NUMBER: US 60/043,553  
FILING DATE: 15-APR-1997  
APPLICATION NUMBER: US 60/048,740  
FILING DATE: 05-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: B.J.Sadoff  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 620-81  
TELECOMMUNICATION INFORMATION:



```
;
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 403:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 403:
US-09-402-923A-403

Query Match      80.0%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4
Db 6 FPPP 9

RESULT 46
US-08-630-916A-109
; Sequence 109, Application US/08630916A
; Patent No. 601137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-916A-109

Query Match      80.0%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4
Db 10 FPPP 13

RESULT 47
US-08-881-094-11
```

```
; Sequence 11, Application US/08881094A
; Patent No. 6022739
; GENERAL INFORMATION:
; APPLICANT: Ryan, Clarence A
; APPLICANT: Pearce, Gregory L
; APPLICANT: McGurl, Barry F
; TITLE OF INVENTION: Systemin
; FILE REFERENCE: 7555-000001CPB
; CURRENT APPLICATION NUMBER: US/08/881,094A
; CURRENT FILING DATE: 1997-07-09
; EARLIER APPLICATION NUMBER: 08/308,887
; EARLIER FILING DATE: 1994-09-19
; EARLIER APPLICATION NUMBER: PCT/US93/02428
; EARLIER FILING DATE: 1993-03-18
; EARLIER APPLICATION NUMBER: 07/885,412
; EARLIER FILING DATE: 1992-03-19
; EARLIER APPLICATION NUMBER: 07/528,956
; EARLIER FILING DATE: 1990-05-25
; EARLIER APPLICATION NUMBER: PCT/US91/03685
; EARLIER FILING DATE: 1991-05-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Solanum nigrum
US-08-881-094-11

Query Match      80.0%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 6 PPPK 9

RESULT 48
US-08-881-094-12
; Sequence 12, Application US/08881094A
; Patent No. 6022739
; GENERAL INFORMATION:
; APPLICANT: Ryan, Clarence A
; APPLICANT: Pearce, Gregory L
; APPLICANT: McGurl, Barry F
; TITLE OF INVENTION: Systemin
; FILE REFERENCE: 7555-000001CPB
; CURRENT APPLICATION NUMBER: US/08/881,094A
; CURRENT FILING DATE: 1997-07-09
; EARLIER APPLICATION NUMBER: 08/308,887
; EARLIER FILING DATE: 1994-09-19
; EARLIER APPLICATION NUMBER: PCT/US93/02428
; EARLIER FILING DATE: 1993-03-18
; EARLIER APPLICATION NUMBER: 07/885,412
; EARLIER FILING DATE: 1992-03-19
; EARLIER APPLICATION NUMBER: 07/528,956
; EARLIER FILING DATE: 1990-05-25
; EARLIER APPLICATION NUMBER: PCT/US91/03685
; EARLIER FILING DATE: 1991-05-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Capsicum annuum
US-08-881-094-12

Query Match      80.0%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5
Db 6 PPPK 9
```

Db 11 PPPK 14

## RESULT 49

US-08-602-999A-305  
; Sequence 305, Application US/08602999A

; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie &amp; Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Mistrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 305:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; US-08-602-999A-305

Query Match 80.0%; Score 4; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4

Db 7 FPPP 10

## RESULT 50

US-08-630-915A-165

; Sequence 165, Application US/08630915A

; Patent No. 6309820

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: HOFFMAN, No. 6309820h

; APPLICANT: KAY, Brian K.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: MCCONNELL, Stephen J.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

; TITLE OF INVENTION: USING SAME

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie &amp; Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,915A

; FILING DATE: 03-APR-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Mistrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-174

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 165:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; US-08-630-915A-165

Query Match

Best Local Similarity 80.0%; Score 4; DB 4; Length 18;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4

Db 10 FPPP 13

## RESULT 51

US-09-500-124-305

; Sequence 305, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie &amp; Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124

; FILING DATE:

; CLASSIFICATION:

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/602,999  
;; FILING DATE: 16-FEB-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MISROCK, S. LESLIE  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-202  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 305:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-09-500-124-305

Query Match 80.0%; Score 4; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 7 FPPP 10

RESULT 52  
US-08-630-916A-106  
; Sequence 106, Application US/08630916A  
; Patent No. 601137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; APPLICANT: Kay, Brian K.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,916A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-203  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; INFORMATION FOR SEQ ID NO: 106:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-916A-106

Query Match 80.0%; Score 4; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 50;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FPPP 4  
DB 8 FPPP 11

RESULT 53  
US-08-630-915A-162  
; Sequence 162, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6309820h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: McCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,915A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 162:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-915A-162

Query Match 80.0%; Score 4; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
DB 8 FPPP 11

RESULT 54  
US-08-103-742-36  
; Sequence 36, Application 08/103742  
; Patent No. 5420244  
; GENERAL INFORMATION:  
; APPLICANT: RUDOLPH, DONNA L.  
; APPLICANT: LAL, RENU B.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; DIAGNOSING HTLV-I ASSOCIATED MYELOPATHY AND ADULT T-CELL LEUK  
; NUMBER OF SEQUENCES: 40

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
;; STREET: Suite 1200, 127 Peachtree Street  
;; CITY: Atlanta  
;; STATE: Georgia  
;; COUNTRY: USA  
;; ZIP: 30303  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: 08/103,742  
;; FILING DATE: 06 AUG 1993  
;; CLASSIFICATION: 436  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SPRATT, GWENDOLYN D.  
;; REGISTRATION NUMBER: 36,016  
;; REFERENCE/DOCKET NUMBER: 1414.080  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 404/688-0770  
;; TELEFAX: 404/688-9880  
;; INFORMATION FOR SEQ ID NO: 36:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-103-742-36

Query Match 80.0%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPPP 4  
Db 13 FPPP 16

RESULT 55  
US-08-466-975A-20  
; Sequence 20, Application US/08466975A  
; Patent No. 5910404  
; GENERAL INFORMATION:  
; APPLICANT: DELEYS, ROBERT J  
; APPLICANT: POLLET, DIRK  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: VAN HEUVERSWUN, HUGO  
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,975A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,671  
; FILING DATE:  
; APPLICATION NUMBER: US 07/920,286

;; FILING DATE: 14-OCT-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/EP91/02409  
;; FILING DATE: 13-DEC-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 90124241.2  
;; FILING DATE: 14-DEC-1990  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SADOFF, B.J.  
;; REGISTRATION NUMBER: 36,663  
;; REFERENCE/DOCKET NUMBER: 1487-5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 7038164000  
;; TELEFAX: 7038164100  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-466-975A-20

Query Match 80.0%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 7 PPPK 10

RESULT 56  
US-08-391-671A-20  
; Sequence 20, Application US/08391671A  
; Patent No. 5922532  
; GENERAL INFORMATION:  
; APPLICANT: DELEYS, ROBERT J  
; APPLICANT: POLLET, DIRK  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: VAN HEUVERSWUN, HUGO  
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/391,671A  
; FILING DATE: 21-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/920,286  
; FILING DATE: 14-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP91/02409  
; FILING DATE: 13-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 90124241.2  
; FILING DATE: 14-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 1487-5

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-391-671A-20

Query Match 80.0%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 7 PPPK 10

## RESULT 57

US-08-467-902A-20  
Sequence 20, Application US/08467902A  
Patent No. 6007982

GENERAL INFORMATION:  
APPLICANT: DELEYS, ROBERT J  
APPLICANT: POLLET, DIRK  
APPLICANT: MAERTENS, GEERT  
APPLICANT: VAN HEUVERSWUN, HUGO  
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,902A  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/391,671  
FILING DATE:  
APPLICATION NUMBER: US 07/920,286  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP91/02409  
FILING DATE: 13-DEC-1991  
APPLICATION DATA:  
APPLICATION NUMBER: EP 90124241.2  
FILING DATE: 14-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-467-902A-20

Query Match 80.0%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 7 PPPK 10

## RESULT 58

US-09-275-265-20  
Sequence 20, Application US/09275265  
Patent No. 6287761

GENERAL INFORMATION:  
APPLICANT: DELEYS, ROBERT J  
APPLICANT: POLLET, DIRK  
APPLICANT: MAERTENS, GEERT  
APPLICANT: VAN HEUVERSWUN, HUGO  
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/275,265  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/391,671  
FILING DATE: 21-FEB-1995  
APPLICATION NUMBER: US 07/920,286  
FILING DATE: 14-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP91/02409  
FILING DATE: 13-DEC-1991  
APPLICATION DATA:  
APPLICATION NUMBER: EP 90124241.2  
FILING DATE: 14-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-275-265-20

Query Match 80.0%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPK 5  
Db 7 PPPK 10

Db 7 PPKK 10

RESULT 59  
US-08-850-328-13  
; Sequence 13, Application US/08850328  
; Patent No. 6379886  
; GENERAL INFORMATION:  
; APPLICANT: TAKAHAMA, Y.  
; APPLICANT: SHIRAIISHI, J.  
; TITLE OF INVENTION: DIAGNOSTIC REAGENT FOR HEPATITIS  
; TITLE OF INVENTION: C VIRUS INFECTION  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/850,328  
; FILING DATE: 02-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mays, Thomas D  
; REGISTRATION NUMBER: 34,524  
; REFERENCE/DOCKET NUMBER: 32273-20004.00  
; TELEPHONE: 202-887-1500  
; TELEFAX: 202-822-0168  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-850-328-13

Query Match 80.0%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPKK 5  
|||  
Db 7 PPKK 10

RESULT 60  
US-09-941-611-20  
; Sequence 20, Application US/09941611  
; Patent No. 6576417  
; GENERAL INFORMATION:  
; APPLICANT: DELEYS, ROBERT J  
; POLLET, DIRK  
; MAERTENS, GEERT  
; VAN HEUVERSKUN, HUGO  
; TITLE OF INVENTION: ANTIBODIES FOR THE DETECTION OF  
; ANTIBODIES TO HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,611  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/391,671  
FILING DATE: 1995-02-21  
APPLICATION NUMBER: WO PCT/EP91/02409  
FILING DATE: 13-DEC-1991  
APPLICATION NUMBER: EP 90124241.2  
FILING DATE: 14-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-941-611-20

Query Match 80.0%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPKK 5  
|||  
Db 7 PPKK 10

RESULT 61  
US-07-972-007-33  
; Sequence 33, Application US/07972007  
; Patent No. 5527681  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Cyclic and Substituted Immobilized  
; \* TITLE OF INVENTION: Molecular Synthesis  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/972,007  
; FILING DATE: 19921105  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5527681viel, Vernon A.

REGISTRATION NUMBER: 32,483  
REFERENCE/DOCKET NUMBER: 11509-57-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-972-007-33

Query Match 60.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
Db 1 PPP 3

## RESULT 62

US-08-351-058A-1  
Sequence 1, Application US/08351058A  
Patent No. 5550215

GENERAL INFORMATION:  
APPLICANT: Holmes, Christopher P.  
TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P. O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/351,058A  
FILING DATE: 28-NOV-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/978,940  
FILING DATE: 19-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,727  
FILING DATE: 22-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 000324-015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-7400  
TELEFAX: 415-854-8275  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-351-058A-1

Query Match 60.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
Db 1 PPP 3

## RESULT 63

US-08-647-618-33  
Sequence 33, Application US/08647618  
Patent No. 5770456  
GENERAL INFORMATION:  
APPLICANT: Holmes, Christopher P.  
TITLE OF INVENTION: Cyclic and Substituted Immobilized  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/647,618  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/972,007  
FILING DATE: 05-NOV-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,727  
FILING DATE: 22-NOV-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/805,727  
FILING DATE: 06-DEC-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/624,120  
FILING DATE: 06-DEC-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/492,462  
FILING DATE: 07-MAR-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/362,901  
FILING DATE: 07-JUN-1989  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, Matthew B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 16528J-000141US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-647-618-33

Query Match 60.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 1 PPP 3

## RESULT 64

US-08-477-509B-106  
; Sequence 106, Application US/08477509B  
; Patent No. 5770697  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W  
; APPLICANT: Dorman, Mary A  
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,509B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 106:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-477-509B-106

QY 2 PPP 4  
|||  
Db 2 PPP 4

## RESULT 65

US-08-358-556A-21

; Sequence 21, Application US/08358556A  
; Patent No. 5869643  
; GENERAL INFORMATION:  
; APPLICANT: Chatelain, Francois  
; APPLICANT: Kumarev, Viktor  
; TITLE OF INVENTION: Process for Preparing Polynucleotides on  
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its  
; TITLE OF INVENTION: Implementation  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/358,556A  
; FILING DATE: 14-DEC-1994  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9315164  
; FILING DATE: 16-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-358-556A-21

Query Match 60.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 1 PPP 3

## RESULT 66

US-08-482-085B-106  
; Sequence 106, Application US/08482085B  
; Patent No. 6018030  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Richardson, Charles  
; APPLICANT: Chambers, James  
; APPLICANT: Causey, Stuart  
; APPLICANT: Pollock, Thomas J.  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W.  
; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US

QY 2 PPP 4  
|||  
Db 2 PPP 4



```

; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,085B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-482-085B-106

Query Match 60.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 2 PPP 4

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RESULT 67
US-09-444-791A-106
; Sequence 106, Application US/09444791A
; Patent No. 6355776
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; Richardson, Charles
; Chambers, James
; Causey, Stuart
; Pollock, Thomas J.
; Cappelletto, Joseph
; Crissman, John W.
; TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive
; Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,791A
; FILING DATE: 22-No. 6355776-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,085
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /notes "X = any amino acid"
; US-09-444-791A-106

Query Match 60.0%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 2 PPP 4

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RESULT 68
US-09-295-996B-6
; Sequence 6, Application US/09295996B
; Patent No. 6413530
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking region
; US-09-295-996B-6

Query Match 60.0%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 1 PPP 3

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RESULT 69  
US-09-057-162-33  
; Sequence 33, Application US/09057162  
; Patent No. 6468740  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Cyclic and Substituted Immobilized  
; Molecular Synthesis  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,162  
; FILING DATE: 08-Apr-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/647,618  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: US 07/972,007  
; FILING DATE: 05-NOV-1992  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991  
; APPLICATION NUMBER: US 07/805,727  
; FILING DATE: 06-DEC-1991  
; APPLICATION NUMBER: US 07/624,120  
; FILING DATE: 06-DEC-1990  
; APPLICATION NUMBER: US 07/492,462  
; FILING DATE: 07-MAR-1990  
; APPLICATION NUMBER: US 07/362,901  
; FILING DATE: 07-JUN-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy, Matthew B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 16528J-000141US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-057-162-33  
Query Match 60.0%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db 1 PPP 3  
RESULT 70  
US-09-295-846B-9  
; Sequence 9, Application US/09295846B  
; Patent No. 6562590  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UF-223  
; CURRENT APPLICATION NUMBER: US/09/295,846B  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: flanking  
; OTHER INFORMATION: region  
; US-09-295-846B-9  
Query Match 60.0%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db 1 PPP 3  
RESULT 71  
US-09-551-737C-9  
; Sequence 9, Application US/09551737C  
; Patent No. 6566129  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; APPLICANT: Schlesinger, Yaagov  
; APPLICANT: Nauwelaers, Sabine M. I.  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UF-223C1  
; CURRENT APPLICATION NUMBER: US/09/551,737C  
; CURRENT FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 09/295,846  
; PRIOR FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flanking region  
; US-09-551-737C-9  
Query Match 60.0%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db 1 PPP 3  
RESULT 72  
PCT-US92-09964-1  
; Sequence 1, Application PC/TUS9209964  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; PCT-US92-09964-1  
; Sequence 1, Application PC/TUS9209964  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:

US-09-295-846B-9  
; Sequence 9, Application US/09295846B  
; Patent No. 6562590  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UF-223  
; CURRENT APPLICATION NUMBER: US/09/295,846B  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: flanking  
; OTHER INFORMATION: region  
; US-09-295-846B-9  
Query Match 60.0%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db 1 PPP 3  
RESULT 70  
US-09-295-846B-9  
; Sequence 9, Application US/09295846B  
; Patent No. 6562590  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UF-223  
; CURRENT APPLICATION NUMBER: US/09/295,846B  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: flanking  
; OTHER INFORMATION: region  
; US-09-295-846B-9  
Query Match 60.0%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db 1 PPP 3  
RESULT 71  
US-09-551-737C-9  
; Sequence 9, Application US/09551737C  
; Patent No. 6566129  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; APPLICANT: Schlesinger, Yaagov  
; APPLICANT: Nauwelaers, Sabine M. I.  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UF-223C1  
; CURRENT APPLICATION NUMBER: US/09/551,737C  
; CURRENT FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 09/295,846  
; PRIOR FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flanking region  
; US-09-551-737C-9  
Query Match 60.0%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPP 4  
Db 1 PPP 3  
RESULT 72  
PCT-US92-09964-1  
; Sequence 1, Application PC/TUS9209964  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/09964  
; FILING DATE: 19921119  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11509-51-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; PCT-US92-09964-1

Query Match 60.0%; Score 3; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
Db 1 PPP 3

RESULT 73  
US-08-351-058A-5  
; Sequence 5, Application US/08351058A  
; Patent No. 5550215  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/351,058A  
; FILING DATE: 28-NOV-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,940  
; FILING DATE: 19-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275

; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-351-058A-5

Query Match 60.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
Db 1 PPP 3

RESULT 74  
US-08-240-514-31  
; Sequence 31, Application US/08240514  
; Patent No. 5670347  
; GENERAL INFORMATION:  
; APPLICANT: GOPAL, T. Venkat  
; TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/240,514  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 73521/102/CLIN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-240-514-31

Query Match 60.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPK 5  
Db 1 PPK 3

RESULT 75  
US-08-477-5098-9  
; Sequence 9, Application US/08477509B  
; Patent No. 5770697  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A

APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W  
APPLICANT: Dornan, Mary A  
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,509B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-509B-9

Query Match 60.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPP 4  
Db 2 PPP 4

Search completed: November 25, 2003, 20:16:09  
Job time : 6.45213'secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 5.52128 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-13

Perfect score: 6  
Sequence: 1 DSQPPV 6

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR\_76.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3	50.0	7	2 S71299	ICL2 protein - Par
3	3	50.0	7	2 PC1316	large granule L3 c
4	3	50.0	7	2 PT0283	Ig heavy chain CRD
5	3	50.0	9	2 A60427	macrophage cytotox
6	3	50.0	10	2 S18396	probable glucose-6
7	3	50.0	11	2 YHRT	morphogenetic neur
8	3	50.0	11	2 YHHU	morphogenetic neur
9	3	50.0	11	2 YHBO	morphogenetic neur
10	3	50.0	11	2 YHAE	morphogenetic neur
11	3	50.0	11	2 YHJFHY	morphogenetic neur
12	3	50.0	11	2 C61497	seed protein ws-18
13	3	50.0	12	2 S43013	hypothetical prote
14	3	50.0	12	2 PA0098	ribosomal protein
15	3	50.0	13	2 B35245	histone H1.c - mou
16	3	50.0	13	2 A35245	histone H1a - mou
17	3	50.0	13	2 G61458	Ig lambda chain V-
18	3	50.0	14	2 PH1627	Ig H chain V-D-J r
19	3	50.0	14	2 PH0753	T-cell receptor be
20	3	50.0	14	2 I52618	hemoglobin beta ch
21	3	50.0	15	2 B39109	hypothetical 1.5K
22	3	50.0	15	2 A60221	apolipoprotein A-I
23	3	50.0	16	2 C61414	chymotrypsin (EC 3
24	3	50.0	17	2 A49237	45/47K antigen - M
25	3	50.0	17	2 S59481	hydroxyproline-ric
26	3	50.0	17	2 B61414	chymotrypsin (EC 3
27	3	50.0	17	2 S10786	enamelin, 26K - bo
28	3	50.0	18	2 S09026	carboxylesterase (
29	3	50.0	18	2 S19914	choline O-acetyltr

T-cell receptor al  
hydroxyproline-rich  
genome polypeptide  
cell wall protein,  
glutathione S-tran  
notch1b 11-5b non  
carboxylesterase (   
carboxylesterase (   
carboxylesterase (   
ribonuclease RCL2  
T-cell receptor be  
peptidyl-dipeptida  
mitosis inhibiting  
major protein anti  
angiotensin-conver  
acid proteinase li  
phosphoprotein, bo  
T-cell receptor be  
tryptophyllin, bas  
endospem protein,  
neural cell adhesi  
carnocin U149 - Ca  
peptidyl-dipeptida  
neuropeptide B - b  
tumor-associated a  
glycine reductase  
endoglycosylcerami  
hypothetical prote  
lectin . potato (f  
unidentified 6.5/3  
glucose-6-phosphat  
ribosomal protein  
inulinase (EC 3.2.  
neuropeptide calla  
aspartate transami  
enamelin f - bovin  
T-cell receptor be  
T-cell receptor ga  
gene Cfr protein  
neural cell adhesi  
thymic factor - pi  
thymocyte growth p  
sperm-activating p  
bradykinin-like pe  
Thr-6 bradykinin -  
bradykinin-like pe  
bradykinin-like pe  
bradykinin-like pe  
ornitho-kinin - ch  
carbon-monoxide de  
orf downstream to b  
hutu protein - Kle  
sucrose 3-glucosyl  
exotoxin A - Strept  
phosphoenolpyruvat  
locustamyotropin I  
bradykinin - horn  
calliFMRamide 2 -  
calliFMRamide 3 -  
[phe-6]-mosact - s  
cytochrome-c oxida  
118K stomach cance  
Ig heavy chain CRD  
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collagen alpha 2(V  
collagen alpha 2(V  
pyrimidine synthes  
3-oxoacid CoA-tran  
T-cell receptor be  
hydroxyproline-3-b  
angiotensin-conver

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31 3 50.0 19 2 S59485  
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33 3 50.0 19 2 S59486  
34 3 50.0 20 2 S63602  
35 3 50.0 20 2 A39328  
36 3 50.0 20 2 S09022  
37 3 50.0 20 2 S09025  
38 3 50.0 20 2 S09023  
39 3 50.0 20 2 JC5589  
40 3 50.0 20 2 C49404  
41 3 50.0 20 2 JN0862  
42 3 50.0 20 2 A26830  
43 3 50.0 20 2 D60274  
44 3 50.0 20 2 PQ0009  
45 3 50.0 20 2 B37988  
46 3 50.0 20 2 S11127  
47 3 50.0 20 2 PT0600  
48 3 50.0 20 2 A61081  
49 3 50.0 20 2 S70335  
50 3 50.0 20 2 A39690  
51 3 50.0 20 2 A58718  
52 3 50.0 20 2 A32523  
53 3 50.0 20 2 B24749  
54 3 50.0 20 2 S43971  
55 3 50.0 20 2 A39308  
56 3 50.0 20 2 B39745  
57 3 50.0 20 2 S16324  
58 3 50.0 20 2 S21288  
59 3 50.0 20 2 PQ0701  
60 3 50.0 20 2 S11078  
61 3 50.0 20 2 S78036  
62 3 50.0 20 2 PT0030  
63 3 50.0 20 2 E47393  
64 3 50.0 20 2 A14683  
65 3 50.0 20 2 S10783  
66 3 50.0 20 2 PT0559  
67 3 50.0 20 2 A38887  
68 3 50.0 20 2 I57018  
69 3 50.0 20 2 C39690  
70 3 50.0 20 2 YFPG  
71 3 50.0 20 2 A60957  
72 3 50.0 20 2 JN0026  
73 3 50.0 20 2 A61358  
74 3 50.0 20 2 A61057  
75 3 50.0 20 2 A26744  
76 3 50.0 20 2 A61363  
77 3 50.0 20 2 A60579  
78 3 50.0 20 2 B60246  
79 3 50.0 20 2 PL0139  
80 3 50.0 20 2 B41983  
81 3 50.0 20 2 C36730  
82 3 50.0 20 2 A39841  
83 3 50.0 20 2 A60108  
84 3 50.0 20 2 S55696  
85 3 50.0 20 2 A61620  
86 3 50.0 20 2 S65433  
87 3 50.0 20 2 B41978  
88 3 50.0 20 2 C41978  
89 3 50.0 20 2 JN0027  
90 3 50.0 20 2 S77984  
91 3 50.0 20 2 A60356  
92 3 50.0 20 2 PT0247  
93 3 50.0 20 2 PT0270  
94 3 50.0 20 2 S65865  
95 3 50.0 20 2 S26508  
96 3 50.0 20 2 S65913  
97 3 50.0 20 2 PD0443  
98 3 50.0 20 2 B30572  
99 3 50.0 20 2 A43065  
100 3 50.0 20 2 XAVI6B

## ALIGNMENTS

RESULT 1  
A37968  
neural surface protein Bravo - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 15-Aug-1997  
C;Accession: A37968; A36345  
R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.  
J. Cell Biol. 112, 1049, 1991  
A;Reference number: A37968; MUID:91154309; PMID:1999455  
A;Contents: extratum  
A;Accession: A37968  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <DEL>  
R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.  
J. Cell Biol. 111, 3087-3096, 1990  
A;Title: Topologically restricted appearance in the developing chick retinotectal system  
A;Reference number: A36345; MUID:91100421; PMID:2269667  
A;Accession: A36345  
A;Molecule type: protein  
A;Residues: 1-7,9-19 <DE2>

Query Match 66.7%; Score 4; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
DB 14 SQPP 17

RESULT 2  
S71299  
ICL2 protein - Paramecium tetraurelia (fragment)  
C;Species: Paramecium tetraurelia  
C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999  
C;Accession: S71299  
R;Wadeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.  
Eur. J. Biochem. 238, 121-128, 1996  
A;Title: Characterization of centrin genes in Paramecium.  
A;Reference number: S71298; MUID:96248429; PMID:8665928  
A;Accession: S71299  
A;Molecule type: protein  
A;Residues: 1-7 <MAD>  
A;Experimental source: strain d4-2  
C;Genetics:  
A;Genetic code: SGC5

Query Match 50.0%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
DB 2 QPP 4

RESULT 3  
PC1316  
large granule L3 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)  
C;Species: Tachyplesus tridentatus  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C;Accession: PC1316  
R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa  
J. Biochem. 114, 307-315, 1993  
A;Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentatus)  
A;Reference number: PC1309; MUID:94110249; PMID:8282718  
A;Accession: PC1316  
A;Molecule type: protein  
A;Residues: 1-7 <SHI>

Query Match 50.0%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
DB 2 QPP 4

RESULT 4  
PT0283  
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0283  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0283  
A;Molecule type: DNA  
A;Residues: 1-7 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 50.0%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
DB 5 QPP 7

RESULT 5  
A60427  
macrophage cytotoxicity-inducing factor, 29K - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Jun-1993  
C;Accession: A60427  
R;Jones, C.M.; Prince, C.A.; Williams, J.S.  
Exp. Hematol. 19, 704-709, 1991  
A;Title: Purification and amino acid analysis of a human macrophage cytotoxicity-induc  
A;Reference number: A60427; MUID:91372335; PMID:1909970  
A;Accession: A60427  
A;Molecule type: protein  
A;Residues: 1-9 <JON>  
A;Note: the sequence from the text on page 706 is inconsistent with that from page 708  
C;Keywords: cytokine

Query Match 50.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3  
DB 7 DSQ 9

RESULT 6  
S18396  
probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Acetobacter hansenii (frag  
C;Species: Acetobacter hansenii  
C;Date: 19-Mar-1997 #sequence\_revision 01-Feb-1999 #text\_change 01-Feb-1999  
C;Accession: S18396  
R;Levy, H.R.; Cook, C.  
Arch. Biochem. Biophys. 291, 161-167, 1991  
A;Title: Purification and properties of NADP-linked glucose-6-phosphate dehydrogenase f  
A;Reference number: S18396; MUID:92027789; PMID:1929428  
A;Accession: S18396  
A;Molecule type: protein

Query Match 50.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3  
DB 7 DSQ 9

A;Residues: 1-10 <LEV>  
A;Experimental source: ATCC 23769  
C;Function:  
A;Description: catalyzes reduction of glucose-6-phosphate to gluconolactone 6-phosphate  
A;Pathway: pentose phosphate pathway  
C;Keywords: oxidoreductase; homotetramer; NADP; pentose phosphate pathway

Query Match 50.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6  
Db 4 PPV 6

RESULT 7  
YHRT  
morphogenetic neuropeptide - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: A01427  
R;Bodenmuller, H.; Schaller, H.C.  
Nature 293, 579-580, 1981  
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelomocytes of the rat.  
A;Reference number: A93266; PMID:82035850; PMID:7290191  
A;Accession: A01427  
A;Molecule type: protein  
A;Residues: 1-11 <BOD>  
R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; PMID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator.  
C;Superfamily: unassigned animal peptides  
C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 50.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
Db 1 QPP 3

RESULT 8  
YHUU  
morphogenetic neuropeptide - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: B01427  
R;Bodenmuller, H.; Schaller, H.C.  
Nature 293, 579-580, 1981  
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelomocytes of the human.  
A;Reference number: A93266; PMID:82035850; PMID:7290191  
A;Accession: B01427  
A;Molecule type: protein  
A;Residues: 1-11 <BOD>  
R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; PMID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator.  
C;Superfamily: unassigned animal peptides  
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 50.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
Db 1 QPP 3

RESULT 9  
YHBO  
morphogenetic neuropeptide - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: C01427; A01427  
R;Bodenmuller, H.; Schaller, H.C.  
Nature 293, 579-580, 1981  
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelomocytes of the bovine.  
A;Reference number: A93266; PMID:82035850; PMID:7290191  
A;Accession: C01427  
A;Molecule type: protein  
A;Residues: 1-11 <BOD>  
R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; PMID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator.  
C;Superfamily: unassigned animal peptides  
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide  
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 50.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
Db 1 QPP 3

RESULT 10  
YHXA  
morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)  
N;Alternate names: head activator  
C;Species: Anthopleura elegantissima  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: A93900; A01427  
R;Schaller, H.C.; Bodenmuller, H.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
A;Reference number: A93900  
A;Accession: A93900  
A;Molecule type: protein  
A;Residues: 1-11 <SCH>  
R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; PMID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator.  
C;Superfamily: unassigned animal peptides  
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 50.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 OPP 5  
 ||||  
 Db 1 OPP 3

## RESULT 11

YHUFHY  
 morphogenetic neuropeptide - Hydra attenuata  
 N;Alternate names: head activator  
 C;Species: Hydra attenuata  
 C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
 C;Accession: B93900; A01427  
 R;Schaller, H.C.; Bodenmuller, H. 7000-7004, 1981  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
 A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
 A;Reference number: A93900

A;Accession: B93900  
 A;Molecule type: protein  
 A;Residues: 1-11 <SCH>  
 R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A;Reference number: A91296; MUID:82050803; PMID:7297679  
 C;Accession: C61497  
 A;Contents: annotation; synthesis  
 A;Note: The synthetic peptide was identical with the natural peptide in chemical structure  
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head  
 n mammalian intestine and hypothalamus.  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 50.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 OPP 5  
 ||||  
 Db 1 OPP 3

## RESULT 12

C61497  
 seed protein ws-18 - winged bean (fragment)  
 C;Species: Psophocarpus tetragonolobus (winged bean)  
 C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
 C;Accession: C61497  
 R;Hirano, H.  
 J. Protein Chem. 8, 115-130, 1989  
 A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis  
 A;Reference number: A61491; MUID:89351606; PMID:2785119

A;Accession: C61497  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-11 <HIR>  
 C;Keywords: glycoprotein; seed

Query Match 50.0%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 ||||  
 Db 6 PPV 8

## RESULT 13

S43013  
 hypothetical protein URF-2X - Yersinia enterocolitica transposon TN3926  
 C;Species: Yersinia enterocolitica  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
 C;Accession: S43013

R;Osborn, S.E.V.; Turner, A.K.; Grinstead, J.  
 submitted to the EMBL Data Library, March 1994  
 A;Description: The structure of the bacterial transposable element, TN3926.  
 A;Reference number: S43011  
 A;Accession: S43013  
 A;Molecule type: DNA  
 A;Residues: 1-12 <OSB>  
 A;Cross-references: EMBL:X78059; NID:G460067; PIDN:CAAS4979.1; PID:G460070  
 C;Genetics:

A;Mobile element: transposon TN3926

Query Match 50.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
 ||||  
 Db 4 SQP 6

## RESULT 14

PA0098  
 ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)  
 C;Species: Fusarium sporotrichioides  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C;Accession: PA0098  
 R;Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JFIPD, October 1994  
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
 A;Reference number: PA0051  
 A;Accession: PA0098  
 A;Molecule type: protein  
 A;Residues: 1-12 <CHO>

Query Match 50.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 ||||  
 Db 4 PPV 6

## RESULT 15

B35245  
 histone H1.c - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997  
 C;Accession: B35245  
 R;Atjro, K.; Shibata, K.; Nishikawa, Y.  
 J. Biol. Chem. 265, 6494-6500, 1990  
 A;Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differentially phosphorylated serines  
 A;Reference number: A35245; MUID:90202935; PMID:1690730

A;Accession: B35245  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-13 <AJI>  
 C;Superfamily: histone H1  
 C;Keywords: chromosomal protein; nucleosome

Query Match 50.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 ||||  
 Db 5 PPV 7

## RESULT 16

A35245  
 histone H1a - mouse (fragment)  
 C;Species: Mus musculus (house mouse)



C;Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997  
 C;Accession: A35245  
 R;Ajiro, K.; Shibata, K.; Nishikawa, Y.  
 J. Biol. Chem. 265, 6494-6500, 1990  
 A;Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the differentially phosphorylated serines  
 A;Reference number: A35245; MUID:90202935; PMID:1690730  
 A;Accession: A35245  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-13 <AZI>  
 C;Superfamily: histone H1  
 C;Keywords: chromosomal protein; nucleosome

Query Match 50.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 DB 5 PPV 7

RESULT 17  
 G61458  
 Ig lambda chain V-II region (AZI) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
 C;Accession: G61458; PLO159  
 R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
 J. Exp. Med. 170, 1551-1558, 1989  
 A;Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein  
 A;Reference number: A61458; MUID:90039128; PMID:2478651  
 A;Accession: G61458  
 A;Molecule type: protein  
 A;Residues: 1-13 <BRO>  
 C;Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 50.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
 DB 6 QPP 8

RESULT 18  
 PH1627  
 Ig H chain V-D-J region (clone B-less 120) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C;Accession: PH1627  
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A;Reference number: PH1580; MUID:93301609; PMID:8315387  
 A;Accession: PH1627  
 A;Molecule type: DNA  
 A;Residues: 1-14 <LEV>  
 A;Experimental source: bone marrow pre-B lymphocyte  
 C;Keywords: immunoglobulin

Query Match 50.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 DB 3 PPV 5

RESULT 19

PH0753  
 T-cell receptor beta chain (H3) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
 C;Accession: PH0753  
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex alleles: exclusion and antigen-specific repertoire.  
 A;Reference number: PH0745; MUID:92078846; PMID:1836010  
 A;Accession: PH0753  
 A;Molecule type: mRNA  
 A;Residues: 1-14 <CAS>  
 A;Cross-references: EMBL:X60846; NID:G51199; PIDN:CAA43237.1; PID:G51200  
 A;Experimental source: T lymphocyte  
 C;Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3  
 DB 5 DSQ 7

RESULT 20  
 IS2618  
 hemoglobin beta chain thalassemia mutant Portuguese - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 02-Jul-1996 #sequence\_revision 11-Jul-1996 #text\_change 20-Apr-2000  
 C;Accession: IS2618  
 R;Oner, R.; Oner, C.; Wilson, J.B.; Tamagnini, G.P.; Ribeiro, L.M.; Huismann, T.H.  
 Br. J. Haematol. 79, 306-310, 1991  
 A;Title: Dominant beta-thalassemia trait in a Portuguese family is caused by a deletion  
 A;Reference number: IS2618; MUID:92068764; PMID:1659862  
 A;Accession: IS2618  
 A;Status: translated from GB/EMBL/DBDJ  
 A;Molecule type: DNA  
 A;Residues: 1-14 <ONE>  
 A;Cross-references: GB:S68042; NID:G239717; PIDN:AAB20440.1; PID:G239718  
 A;Gene: GDB:HBB  
 A;Cross-references: GDB:119297; OMIM:141900  
 A;Map position: 11p15.4-11p15.4

Query Match 50.0%; Score 3; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 DB 1 PPV 3

RESULT 21  
 B39109  
 hypothetical 1.5K protein - hepatitis C virus  
 N;Alternate names: hypothetical protein 2  
 C;Species: hepatitis C virus  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
 C;Accession: B39109; J01585  
 R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp  
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
 A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification  
 A;Reference number: A39109; MUID:91156678; PMID:1705704  
 A;Accession: B39109  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-15 <HAN>  
 A;Cross-references: GB:M58406  
 R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
 J. Gen. Virol. 73, 1521-1525, 1992

A:Title: Cloning and sequencing of the structural region and expression of putative core  
A:Reference number: JQ1584; MUID:92300349; PMID:1318944  
A:Accession: JQ1585  
A:Molecule type: genomic RNA  
A:Residues: 1-15 <KUM>  
A:Experimental source: strain U.K.

Query Match 50.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 3 QPP 5  
|||  
Db 5 QPP 7

## RESULT 22

A60221  
apolipoprotein A-I - common carp (fragment)  
C:Species: Cyprinus carpio (common carp)  
C:Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 31-Dec-1993  
A:Accession: A60221  
R:Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.  
J. Neurochem. 55, 1237-1243, 1990  
A:Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve reg  
A:Reference number: A60221; MUID:90376100; PMID:2118944  
A:Accession: A60221  
A:Molecule type: protein  
A:Residues: 1-15 <HAR>  
A:Note: protein from plasma and from optic nerve yielded the same sequence  
C:Keywords: lipid binding; lipoprotein

Query Match 50.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 3 QPP 5  
|||  
Db 2 QPP 4

## RESULT 23

C61414  
chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)  
C:Species: Pseudemys scripta (slider)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 07-May-1999  
A:Accession: C61414  
R:Bhargava, A.K.; Barnard, E.A.  
J. Mol. Evol. 2, 187-198, 1973  
A:Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determ  
A:Reference number: A61414; MUID:76146602; PMID:4807189  
A:Accession: C61414  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <BHA>  
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 50.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 4 PPV 6  
|||  
Db 7 PPV 9

## RESULT 24

A49237  
45/47K antigen - Mycobacterium bovis (fragment)  
C:Species: Mycobacterium bovis  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Feb-1995  
A:Accession: A49237  
R:Romain, F.; Laqueyrie, A.; Millitzer, P.; Pescher, P.; Chavarot, P.; Lagrandier, M.

Infect. Immun. 61, 742-750, 1993  
A:Title: Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen complex,  
A:Reference number: A49237; MUID:93138802; PMID:8423100  
A:Contents: BCG  
A:Accession: A49237  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-17 <ROM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:123246)

Query Match 50.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 4 PPV 6  
|||  
Db 6 PPV 8

## RESULT 25

S59481  
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)  
C:Species: Phaseolus vulgaris (kidney bean)  
C:Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998  
A:Accession: S59481  
R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
Plant Mol. Biol. 28, 1075-1087, 1995  
A:Title: Specificity in the immobilisation of cell wall proteins in response to differ  
A:Reference number: S59481; MUID:96011753; PMID:7548825  
A:Accession: S59481  
A:Molecule type: protein  
A:Residues: 1-17 <WOJ>  
C:Keywords: glycoprotein; hydroxyproline  
F:6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 50.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 4 PPV 6  
|||  
Db 5 PPV 7

## RESULT 26

B61414  
chymotrypsin (EC 3.4.21.1) - painted turtle (fragment)  
C:Species: Chrysemys picta (painted turtle)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 07-May-1999  
A:Accession: B61414  
R:Bhargava, A.K.; Barnard, E.A.  
J. Mol. Evol. 2, 187-198, 1973  
A:Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determ  
A:Reference number: A61414; MUID:76146602; PMID:4807189  
A:Accession: B61414  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-17 <BHA>  
C:Keywords: hydrolase; serine proteinase

Query Match 50.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 4 PPV 6  
|||  
Db 7 PPV 9

## RESULT 27

S10786  
enamelin, 26K - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998

C;Accession: S10786  
R;Strawich, E.; Glincher, M.J.  
Eur. J. Biochem. 191, 47-56, 1990  
A;Title: Tooth 'enameling', identified mainly as serum proteins. Major 'enamelin' is abundant in tooth enamel.  
A;Reference number: S10780; MUID:90336641; PMID:2379503  
A;Accession: S10786  
A;Molecule type: protein  
A;Residues: 1-17 <STR>  
C;Keywords: enamel; phosphoprotein

Query Match 50.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 3 QPP 5

#### RESULT 28

S03026  
carboxylesterase (EC 3.1.1.1) MK1, microsomal - crab-eating macaque (fragment)

C;Species: Macaca fascicularis (crab-eating macaque)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 28-Apr-1993  
C;Accession: S09026  
R;Hosokawa, M.; Maki, T.; Satoh, T.  
Arch. Biochem. Biophys. 277, 219-227, 1990  
A;Title: Characterization of molecular species of liver microsomal carboxylesterases of *Macaca fascicularis*.  
A;Reference number: S09021; MUID:9019180; PMID:2310190  
A;Accession: S09026  
A;Molecule type: protein  
A;Residues: 1-18 <HOS>  
C;Keywords: carboxylic ester hydrolase

Query Match 50.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 5 PPV 7

#### RESULT 29

S19914  
choline O-acetyltransferase (EC 2.3.1.6) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 05-May-2000  
C;Accession: S19914  
R;Toussaint, J.L.; Bausero, P.; Stricker, C.; Geoffroy, V.; Simoni, P.; Kempf, J.; Schmidt, J.  
submitted to the EMBL Data Library, March 1992  
A;Description: Human choline acetyltransferase gene: analysis of transcription control region.  
A;Reference number: S19914  
A;Accession: S19914  
A;Molecule type: DNA  
A;Residues: 1-18 <TOU>  
A;Cross-references: EMBL:X65023  
C;Keywords: acyltransferase; coenzyme A

Query Match 50.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
|||  
Db 3 SQP 5

#### RESULT 30

A41299  
T-cell receptor alpha chain precursor V region (17.2) - human (fragment)  
C;Species: Homo sapiens (man)

C;Date: 28-May-1992 #sequence\_revision 28-May-1992 #text\_change 23-Jul-1999

C;Accession: A41299  
R;Uematsu, Y.; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G.; Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991  
A;Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheumatoid arthritis.  
A;Reference number: A41299; MUID:92020887; PMID:1656449  
A;Accession: A41299  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-19 <UEM>  
A;Cross-references: GB:S57433; NID:9236318; PIDN:AAB19956.1; PID:9236319  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
|||  
Db 8 SQP 10

#### RESULT 31

S59485  
hydroxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)  
C;Species: Phaseolus vulgaris (kidney bean)  
C;Date: 27-Apr-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Dec-1998  
C;Accession: S59485; S59484; S59483  
R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
Plant Mol. Biol. 28, 1075-1087, 1995  
A;Title: Specificity in the immobilisation of cell wall proteins in response to different pH values.  
A;Reference number: S59481; MUID:96011753; PMID:7548825  
A;Accession: S59485  
A;Molecule type: protein

A;Residues: 1-19 <WOJ>  
A;Note: Hydroxyproline-rich cell wall glycoprotein, 42K  
A;Accession: S59484  
A;Molecule type: protein  
A;Residues: 1-15 <WOM>  
A;Note: Hydroxyproline-rich cell wall glycoprotein, 84K  
A;Accession: S59483  
A;Molecule type: protein  
A;Residues: 1-14 <WOP>  
A;Note: Hydroxyproline-rich cell wall glycoprotein, 136K, minor component  
C;Superfamily: proline-rich protein 3  
C;Keywords: glycoprotein; hydroxyproline  
F;6,11,16/Modified site: hydroxyproline (Pro) #status experimental

Query Match 50.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 5 PPV 7

#### RESULT 32

B61409  
genome polyprotein (clone L3/S2) - Skalka virus (fragment)  
C;Species: Skalka virus  
C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Nov-2000  
C;Accession: B61409  
R;Guirakhoo, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Griesikova, M.  
J. Gen. Virol. 72, 333-338, 1991  
A;Title: The relationship between the flaviviruses Skalka and Langat as revealed by molecular biology.  
A;Reference number: A61409; MUID:91132129; PMID:1847173  
A;Accession: B61409  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: Genomic RNA  
A;Residues: 1-19 <GUI>  
C;Superfamily: yellow fever virus genome polyprotein

Query Match 50.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
DB 2 PPV 4

## RESULT 33

S59486  
cell wall protein, 22K - kidney bean (fragment)  
C;Species: Phaseolus vulgaris (kidney bean)  
C;Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C;Accession: S59486  
R;Wojtaszek, P.; Trethowan, J.; Bolwell, G. P.  
Plant Mol. Biol. 28, 1075-1087, 1995  
A;Title: Specificity in the immobilisation of cell wall proteins in response to different  
A;Reference number: S59481; MUID:96011753; PMID:7548825  
A;Accession: S59486  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <WOJ>

Query Match 50.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
DB 3 QPP 5

## RESULT 34

S63602  
glutathione S-transferase chain T2-2 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C;Accession: S63602  
R;Mainwaring, G.W.; Nash, J.; Davidson, M.; Green, T.  
Biochem. J. 314, 445-448, 1996  
A;Title: Isolation of a mouse Theta Glutathione S-transferase active with methylene chloride  
A;Reference number: S63601; MUID:96239100; PMID:8670055  
A;Accession: S63602  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <MAI>  
C;Superfamily: glutathione transferase

Query Match 50.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
|||  
DB 10 SQP 12

## RESULT 35

A39328  
notechis II-5b nontoxic venom protein - common tiger snake (fragment)  
C;Species: Notechis scutatus (common tiger snake, mainland tiger snake)  
C;Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 30-Sep-1993  
C;Accession: A39328  
R;Yang, C.C.; Chang, L.S.; Wu, F.S.  
Toxicol. 29, 1337-1344, 1991  
A;Title: Venom constituents of Notechis scutatus (Australian tiger snake) from  
A;Reference number: A39328; MUID:92263371; PMID:1814009  
A;Accession: A39328  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <YAN>

C;Superfamily: phospholipase A2

Query Match 50.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
|||  
DB 16 SQP 18

## RESULT 36

S09022  
carboxylesterase (EC 3.1.1.1) RL1, microsomal - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Aug-1998  
C;Accession: S09022  
R;Hosokawa, M.; Maki, T.; Satoh, T.  
Arch. Biochem. Biophys. 277, 219-227, 1990  
A;Title: Characterization of molecular species of liver microsomal carboxylesterases of  
A;Reference number: S09021; MUID:90179180; PMID:2310190  
A;Accession: S09022  
A;Molecule type: protein  
A;Residues: 1-20 <HOS>  
C;Superfamily: cholinesterase; cholinesterase homology  
C;Keywords: carboxylic ester hydrolase

Query Match 50.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
DB 5 PPV 7

## RESULT 37

S09025  
carboxylesterase (EC 3.1.1.1), microsomal - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Aug-1998  
C;Accession: S09025  
R;Hosokawa, M.; Maki, T.; Satoh, T.  
Arch. Biochem. Biophys. 277, 219-227, 1990  
A;Title: Characterization of molecular species of liver microsomal carboxylesterases of  
A;Reference number: S09021; MUID:90179180; PMID:2310190  
A;Accession: S09025  
A;Molecule type: protein  
A;Residues: 1-20 <HOS>  
C;Superfamily: cholinesterase; cholinesterase homology  
C;Keywords: carboxylic ester hydrolase

Query Match 50.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
DB 5 PPV 7

## RESULT 38

S09023  
carboxylesterase (EC 3.1.1.1) RL2, microsomal - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Aug-1998  
C;Accession: S09023  
R;Hosokawa, M.; Maki, T.; Satoh, T.  
Arch. Biochem. Biophys. 277, 219-227, 1990  
A;Title: Characterization of molecular species of liver microsomal carboxylesterases of  
A;Reference number: S09021; MUID:90179180; PMID:2310190  
A;Accession: S09023  
A;Molecule type: protein

A;Residues: 1-20 <HOS>  
 C;Superfamily: cholinesterase; cholinesterase homology  
 C;Keywords: carboxylic ester hydrolase

Query Match 50.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 ||||  
 Db 5 PPV 7

## RESULT 39

JC5589  
 ribonuclease RCL2 (EC 3.1.27.-) peptide 2 - bullfrog  
 N;Alternate names: ribonuclease RCL2 peptide 1  
 C;Species: Rana catesbeiana (bullfrog)  
 C;Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 07-May-1999  
 C;Accession: JC5589  
 R;Inokuchi, N.; Kobayashi, H.; Miyamoto, M.; Koyama, T.; Iwama, M.; Ohgi, K.; Irie, M.  
 Biol. Pharm. Bull. 20, 471-478, 1997  
 A;Title: Primary structure of base non-specific and acid ribonuclease from bullfrog (Rana catesbeiana)  
 A;Reference number: JC5589; MUID:9732289; PMID:9178923  
 A;Accession: JC5589  
 A;Molecule type: protein  
 A;Residues: 1-20 <IN2>  
 C;Comment: This enzyme belongs to ribonuclease T2 family. This peptide 2 or peptide 1 corresponds to the mature form of the enzyme.  
 C;Keywords: hydrolase  
 F;4-20/Product: peptide 1 #status experimental <PPI>

Query Match 50.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 ||||  
 Db 16 PPV 18

## RESULT 40

C49404  
 T-cell receptor beta chain VDJ region - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C;Accession: C49404  
 R;Brooks, E.G.; Balk, S.P.; Aupeix, K.; Colonna, M.; Strominger, J.L.; Groh-Spies, V.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 11787-11791, 1993  
 A;Title: Human T-cell receptor (TCR) alpha/beta + CD4-CD8- T cells  
 A;Reference number: A49404; MUID:94089717; PMID:7505446  
 A;Accession: C49404  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-20 <BR0>  
 A;Cross-references: GB:S67401; NID:G455870; PIDN:AA229276.1; PID:G455871  
 A;Experimental source: alpha/beta + CD4-CD8- T cells  
 A;Note: sequence extracted from NCBI backbone (NCBIN:141026, NCBIP:141027)  
 C;Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 ||||  
 Db 5 PPV 7

## RESULT 41

JN0862  
 peptidyl-dipeptidase A inhibitory peptide C112 - striped bonito  
 C;Species: Sarda orientalis (striped bonito)  
 C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999

C;Accession: JN0862  
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide  
 A;Reference number: JN0859; MUID:94080036; PMID:7764272  
 A;Accession: JN0862  
 A;Molecule type: protein  
 A;Residues: 1-5 <MAT>  
 A;Experimental source: intestine  
 C;Comment: The amino terminal tripeptide of this protein inhibits angiotensin I-converting enzyme  
 C;Superfamily: bradykinin-potentiating peptide  
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 33.3%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PV 6  
 ||||  
 Db 3 PV 4

## RESULT 42

A26830  
 mitosis inhibiting peptide - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 19-Nov-1988 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
 C;Accession: A26830  
 R;Reichelt, K.; Elgjo, K.; Edmison, P.D.  
 Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987  
 A;Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.  
 A;Reference number: A26830; MUID:87298602; PMID:3619940  
 A;Accession: A26830  
 A;Molecule type: protein  
 A;Residues: 1-5 <REI>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: blocked amino end; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DS 2  
 ||||  
 Db 3 DS 4

## RESULT 43

D60274  
 major protein antigen MPT46 - Mycobacterium tuberculosis (fragment)  
 C;Species: Mycobacterium tuberculosis  
 C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993  
 C;Accession: D60274  
 R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.  
 Infect. Immun. 59, 372-382, 1991  
 A;Title: Isolation and partial characterization of major protein antigens in the culture supernatant of Mycobacterium tuberculosis  
 A;Reference number: A60274; MUID:91099899; PMID:1898899  
 A;Accession: D60274  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-5 <NAG>

Query Match 33.3%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DS 2  
 ||||  
 Db 2 DS 3

## RESULT 44

PQ0009  
 angiotensin-converting enzyme inhibitor (FLP-2) - common fig  
 N:Alternate names: ficus latex peptide 2  
 C:Species: Ficus carica (common fig)  
 C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995  
 C:Accession: PQ0009  
 R:Matuyama, S.; Miyoshi, S.; Tanaka, H.  
 Agric. Biol. Chem. 53: 2763-2767, 1989  
 A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.  
 A:Reference number: PQ0008  
 A:Accession: PQ0009  
 A:Molecule type: protein  
 A:Residues: 1-5 <MAR>  
 A:Experimental source: latex  
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 33.3%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PV 6  
 ||  
 Db 3 PV 4

RESULT 45  
 B37988  
 acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
 C:Species: Physarum polycephalum  
 C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
 C:Accession: B37988  
 R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og  
 J. Biol. Chem. 265, 19898-19903, 1990  
 A:Title: Purification and characterization of a novel intracellular acid proteinase from  
 A:Reference number: A37988; MUID:91060608; PMID:2246266  
 A:Accession: B37988  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <MUR>

Query Match 33.3%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5  
 ||  
 Db 3 PP 4

RESULT 46  
 S11127  
 phosphoprotein, bone - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 04-Mar-2000  
 C:Accession: S11127; S11128  
 R:Mikuni-Takagaki, Y.; Glimcher, M.J.  
 Biochem. J. 268, 585-591, 1990  
 A:Title: Post-translational processing of chicken bone phosphoproteins. Identification o  
 A:Reference number: S11127; MUID:90303246; PMID:2363696  
 A:Accession: S11127  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <MIK1>  
 A:Accession: S11128  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 'X', 2-5 <MIK2>  
 C:Keywords: phosphoprotein

Query Match 33.3%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PV 6  
 ||  
 Db 3 PV 4

Qy 5 PV 6  
 ||  
 Db 2 PV 3

RESULT 47  
 PT0600  
 T-cell receptor beta chain V-D-J region (120-1C) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0600  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0600  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <PFE>  
 A:Experimental source: newborn thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 33.3%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DS 2  
 ||  
 Db 4 DS 5

RESULT 48  
 A61081  
 tryptophyllin, basic - Rohde's leaf frog  
 C:Species: Phyllomedusa rohdei (Rohde's leaf frog)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000  
 C:Accession: A61081  
 R:Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.  
 Int. J. Pept. Protein Res. 33, 391-395, 1989  
 A:Title: Isolation, structure determination and synthesis of a novel tryptophan-contain  
 A:Reference number: A61081  
 A:Accession: A61081  
 A:Molecule type: protein  
 A:Residues: 1-7 <MON>  
 C:Comment: The biological activity of this peptide was not determined.  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end; hydroxyproline; skin  
 F:3/Modified site: 4-hydroxyproline (Pro) #status experimental  
 F:7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5  
 ||  
 Db 2 PP 3

RESULT 49  
 S70335  
 endosperm protein, 40K - rye (fragment)  
 C:Species: Secale cereale (rye)  
 C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
 C:Accession: S70335  
 R:Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.  
 Biochim. Biophys. Acta 1295, 13-22, 1996  
 A:Title: Identification of major rye secalins as coeliac immunoreactive proteins.  
 A:Reference number: S70327; MUID:96283789; PMID:8679669  
 A:Accession: S70335  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <ROC>

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3  
||  
6 SQ 7

Db

RESULT 50

A39690

neural cell adhesion molecule, cardiac splice form -, -, - - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999

C;Accession: A39690

R;Reyes, A.A.; Small, S.J.; Akeson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991

A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA

A;Reference number: A39690; MUID:91141516; PMID:1996115

A;Accession: A39690

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-7 <REV>

A;Cross-references: GB:M63970

C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
1 QP 2

Db

RESULT 51

A58718

carnocin U149 - Carnobacterium sp. (fragment)

C;Species: Carnobacterium sp.

C;Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998

C;Accession: A58718

R;Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.

Appl. Environ. Microbiol. 58, 1417-1422, 1992

A;Title: Purification and characterization of a new bacteriocin isolated from a Carnobacterium

A;Reference number: A58718; MUID:92321768; PMID:1622206

A;Accession: A58718

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <STO>

C;Keywords: antibiotic; lanthionine

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
5 QP 6

Db

RESULT 52

A32523

peptidyl-dipeptidase A (EC 3.4.15.1) - bovine (fragment)

N;Alternate names: angiotensin I-converting enzyme; peptidyl-dipeptidase I

C;Species: Bos primigenius taurus (cattle)

C;Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 11-May-2000

C;Accession: A32523

R;Harris, R.B.

Adv. Exp. Med. Biol. 198, 513-521, 1986

A;Title: Isolation and sequencing of an active-site peptide from angiotensin I-converting

A;Reference number: A32523; MUID:87123961; PMID:3028071

A;Accession: A32523

A;Molecule type: protein

A;Residues: 1-8 <HAR>

C;Superfamily: mammalian peptidyl-dipeptidase A

C;Keywords: alternative splicing; blood pressure control; peptidyl-dipeptide hydrolase;

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DS 2  
||  
6 DS 7

Db

RESULT 53

B24749

neuropeptide B - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Aug-2000

C;Accession: B24749

R;Yang, H.Y.T.; Pratta, W.; Majane, E.A.; Costa, E.

Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985

A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two

A;Reference number: A94074; MUID:86067985; PMID:3865193

A;Accession: B24749

A;Molecule type: protein

A;Residues: 1-8 <YAN>

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
4 QP 5

Db

RESULT 54

S43971

tumor-associated antigen MUT1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000

C;Accession: S43971

R;Handelboim, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.

Nature 369, 67-71, 1994

A;Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine

A;Reference number: S43971; MUID:94217811; PMID:8164742

A;Accession: S43971

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <MAN>

C;Superfamily: unassigned animal peptides

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
||  
7 QP 8

Db

RESULT 55

A39308

glycine reductase (EC 1.4.99.-) sulphydryl protein C, alpha chain - Clostridium sticklandii

C;Species: Clostridium sticklandii

C;Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 15-Aug-1997

C;Accession: A39308

R;Stadtman, T.C.; Davis, J.N.

J. Biol. Chem. 266, 22147-22153, 1991

A;Title: Glycine reductase protein C. Properties and characterization of its role in the

A;Reference number: A39308; MUID:92042141; PMID:1939235

A;Accession: A39308

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <STA>

C;Function:

A;Description: glycine reductase complex catalyzes the reductive deamination of glycine

C;Keywords: ATP; oxidoreductase

Query Match 33.3%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PV 6

DB 3 PV 4

RESULT 56

B39745

endoglycosylceramidase (EC 3.2.1.123) I - Rhodococcus sp. (fragment)

C;Species: Rhodococcus sp.

C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 31-Dec-1993

C;Accession: B39745

R;Ito, M.; Ikegami, Y.; Yamagata, T.

J. Biol. Chem. 266, 7919-7926, 1991

A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosylceramidases. Bl

ble using these activator proteins.

A;Reference number: A39745; MUID:91210321; PMID:1850427

A;Accession: B39745

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <ITO>

C;Keywords: glycosidase; hydrolase

Query Match 33.3%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5

DB 2 PP 3

RESULT 57

S16324

hypothetical protein 2 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000

C;Accession: S16324

R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.

EMBO J. 10, 1787-1791, 1991

A;Title: A novel class of plant proteins containing a homeodomain with a closely linked

A;Reference number: S16323; MUID:91266907; PMID:1675603

A;Accession: S16324

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-8 <RUB>

A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA1624.1; PID:g579259

Query Match 33.3%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5

DB 7 PP 8

RESULT 58

S21288

lectin - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 05-Dec-1998

C;Accession: S21288

R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.

Biochem. J. 283, 813-821, 1992

A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizati

A;Reference number: S21288; MUID:92272683; PMID:1590771

A;Accession: S21288

A;Molecule type: protein

A;Residues: 1-8 <MIL>

A;Experimental source: var. Ulster Sceptre

C;Function:

A;Description: may be involved in defence mechanism of the plant

C;Keywords: hydroxyproline; lectin

Query Match 33.3%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5

DB 7 PP 8

RESULT 59

PQ0701

unidentified 6.5/31K protein [imported] - rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C;Accession: PQ0701

R;Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensio

A;Reference number: PQ0696

A;Accession: PQ0701

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <KOM>

Query Match 33.3%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PV 6

DB 4 PV 5

RESULT 60

S11078

glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - yeast (Pichia jadinii) (fragment)

C;Species: Pichia jadinii, Candida utilis

C;Date: 30-Jun-1991 #sequence\_revision 30-Sep-1991 #text\_change 05-Aug-1994

C;Accession: S11078

R;Egestad, B.; Estenius, M.; Danielsson, O.; Persson, B.; Cederlund, E.; Kaiser, R.; Ho

FEBS Lett. 269, 194-196, 1990

A;Title: Fast atom bombardment mass spectrometry and chemical analysis in determination

A;Reference number: S11074; MUID:90353571; PMID:2387402

A;Accession: S11078

A;Molecule type: protein

A;Residues: 1-8 <EGE>

A;Note: the source is designated as Pichia jadinii

C;Keywords: acetylated amino end; oxidoreductase; pentose phosphate pathway

F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DS 2

DB 3 DS 4



## RESULT 61

S78036  
ribosomal protein Yms-B, mitochondrial - yeast (*Saccharomyces cerevisiae*) (fragment)  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 14-Nov-1997  
C;Accession: S78036  
R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma  
Eur. J. Biochem. 245, 449-456, 1997  
A;Title: Identification and characterization of the genes for mitochondrial ribosomal pr  
A;Reference number: S78018; MUID:97296414; PMID:9151978  
A;Accession: S78036  
A;Molecule type: protein  
A;Residues: 1-8 <KIT>  
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DS 2  
||  
Db 6 DS 7

## RESULT 62

PT0030  
inulinase (EC 3.2.1.7) - *Aspergillus ficuum* (fragment)  
N;Alternate names: inulase  
C;Species: *Aspergillus ficuum*  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 07-May-1999  
C;Accession: PT0030  
R;Ettaibbi, M.; Baratti, J.C.  
Agric. Biol. Chem. 54, 61-68, 1990  
A;Title: Molecular and kinetic properties of *Aspergillus ficuum* inulinases.  
A;Reference number: PT0030; MUID:90344234; PMID:1368526  
A;Accession: PT0030  
A;Molecule type: protein  
A;Residues: 1-8 <ETT>  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4  
||  
Db 5 QP 6

## RESULT 63

E47393  
neuropeptide callatostatin 5 - bluebottle fly (*Calliphora vomitoria*)  
C;Species: *Calliphora vomitoria*  
C;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 03-Mar-1995  
C;Accession: E47393  
R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993  
A;Title: Callatostatins: neuropeptides from the blowfly *Calliphora vomitoria* with sequen  
A;Reference number: A47393; MUID:93211980; PMID:8460157  
A;Accession: E47393  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <DUV>  
A;Experimental source: whole flies  
A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5  
||  
Db 2 PP 3

## RESULT 64

Al4683  
aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (frag  
N;Alternate names: aspartate aminotransferase, mitochondrial  
C;Species: *Gallus gallus* (chicken)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000  
C;Accession: Al4683  
R;Wilson, K.J.; Hunziker, P.; Hughes, G.J.  
FEBS Lett. 108, 98-102, 1979  
A;Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.  
A;Reference number: Al4683; MUID:80092116; PMID:520566  
A;Accession: Al4683  
A;Molecule type: protein  
A;Residues: 1-8 <WIL>  
C;Keywords: aminotransferase; mitochondrion

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4  
||  
Db 6 QP 7

## RESULT 65

S10783  
enamelin f - bovine (fragment)  
C;Species: *Bos primigenius taurus* (cattle)  
C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
C;Accession: S10783  
R;Strawich, E.; Glimcher, M.J.  
Eur. J. Biochem. 191, 47-56, 1990  
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is al  
A;Reference number: S10780; MUID:90336641; PMID:2379503  
A;Accession: S10783  
A;Molecule type: protein  
A;Residues: 1-8 <STR>  
C;Keywords: enamel; phosphoprotein

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5  
||  
Db 4 PP 5

## RESULT 66

PT0559  
T-cell receptor beta chain V-D-J region (126-1BH) - mouse (fragment)  
C;Species: *Mus musculus* (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0559  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0559  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-8 <FEE>  
A;Experimental source: day 18 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5

Db 4 PP 5

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 67

A38887  
T-cell receptor gamma chain (St.2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C:Accession: A38887  
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene  
A:Reference number: A41946; MUID:92049316; PMID:1658619  
C:Accession: A38887  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-8 <WHE>  
C:Keywords: T-cell receptor

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DS 2  
DB 4 DS 5

## RESULT 68

I57018  
Gene Ctrr protein - mouse (fragment)  
C:Species: Mus sp. (mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
C:Accession: I57018  
R:Dorin, J.R.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D.J.  
Mamm. Genome 5, 465-472, 1994  
A:Title: Long-term survival of the exon 10 insertional cystic fibrosis mutant mouse is a  
A:Reference number: I57018; MUID:95037043; PMID:7949729  
C:Accession: I57018  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-8 <RES>  
A:Cross-references: GB:S74246; NID:G710482  
C:Genetics:  
A:Gene: Ctrr

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DS 2  
DB 3 DS 4

## RESULT 69

C39690  
neural cell adhesion molecule, cardiac splice form -, -, + - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
C:Accession: C39690  
R:Reyes, A.A.; Small, S.J.; Akesson, R.  
Mol. Cell. Biol. 11, 1654-1661, 1991  
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA  
A:Reference number: A39690; MUID:91141516; PMID:1996115  
C:Accession: C39690  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-8 <REY>  
A:Cross-references: GB:M63790  
C:Keywords: cardiac muscle; cell adhesion; heart

QY 3 QP 4  
DB 1 QP 2

## RESULT 70

YFPG  
thymic factor - pig  
N:Alternate names: FTS (facteur thymique serique)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 07-May-1999  
C:Accession: A01523; A60983  
R:Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.  
J. Biol. Chem. 252, 8045-8047, 1977  
A:Title: Structural study of circulating thymic factor: a peptide isolated from pig ser  
A:Reference number: A01523; MUID:78026571; PMID:914862  
C:Accession: A01523  
A:Molecule type: protein  
A:Residues: 1-9 <PUE>  
R:Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.  
Nature 266, 55-57, 1977  
A:Title: Biochemical characterisation of a serum thymic factor.  
A:Reference number: A60983; MUID:77123829; PMID:300146  
C:Accession: A60983  
A:Molecule type: protein  
A:Residues: 'Z', '2', '4', 'Z', '6', '9' <BAC>  
C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not periph  
in a variety of immunoassays.  
C:Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modifi  
C:Superfamily: thymic factor  
C:Keywords: Pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3  
DB 4 SQ 5

## RESULT 71

A60957  
thymocyte growth peptide - sheep  
N:Contains: FTS (facteur thymique serique)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 24-Nov-1999  
C:Accession: A60957  
R:Ernstroem, U.; Gafvelin, G.; Rudja, J.M.  
Bioosci. Rep. 10, 403-412, 1990  
A:Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship  
A:Reference number: A60957; MUID:91064427; PMID:2249004  
C:Accession: A60957  
A:Molecule type: protein  
A:Residues: 1-9 <ERN>  
C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not periph  
in a variety of immunoassays.  
C:Comment: This peptide was isolated in two forms. One form contained the pyrrolidone c  
r form (thymocyte growth peptide) contains a large, non-peptide blocking group with a h  
C:Superfamily: thymic factor  
C:Keywords: blocked amino end; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Glx) (in FTS) #status experimental  
F:1/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) #status experi.

Query Match 33.3%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQ 3  
||  
Db 4 SQ 5

## RESULT 72

JN0026  
sperm-activating peptide SAP-b - sea urchin (Clypeaster japonicus)  
N;Alternate names: [His-6]-mosact  
C;Species: Clypeaster japonicus  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 18-Aug-2000  
C;Accession: JN0026; B60973  
R;Suzuki, N.; Kurita, M.; Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Yamaguchi, M.  
Zool. Sci. 4, 649-656, 1987  
A;Title: Purification and structure of mosact and its derivatives from the egg jelly of  
A;Reference number: JN0025  
A;Accession: JN0026  
A;Molecule type: protein  
A;Residues: 1-9 <SUZ>  
R;Takao, T.; Yoshino, K.; Suzuki, N.; Shimonishi, Y.  
Biomed. Environ. Mass Spectrom. 19, 705-712, 1990  
A;Title: Analysis of post-translational modifications of proteins by accurate mass measu  
A;Reference number: A60973; MUID:91167743; PMID:2076468  
A;Accession: B60973  
A;Molecule type: protein  
A;Residues: 1-9 <TAK>  
C;Comment: SAP-b (mosact), one of several sperm activating peptides located in egg jelly  
C;Comment: Forms with and without the bromohistidine moiety were purified separately.  
C;Superfamily: unassigned animal peptides  
C;Keywords: bromine  
F;6/Modified site: bromohistidine (His) (partial) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DS 2  
||  
Db 1 DS 2

## RESULT 73

A61358  
bradykinin-like peptide I - Japanese pond frog  
C;Species: Rana nigromaculata (Japanese pond frog)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 02-Sep-2000  
C;Accession: A61358  
R;Nakajima, T.  
Chem. Pharm. Bull. 16, 769-770, 1968  
A;Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin  
A;Reference number: A61358; MUID:68412013; PMID:5677638  
A;Accession: A61358  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <NAK>  
C;Superfamily: unassigned animal peptides  
C;Keywords: skin

Query Match 33.3%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5  
||  
Db 2 PP 3

## RESULT 74

A61057  
Thr-6 bradykinin - scoliid wasp (Colpa interrupta)  
C;Species: Colpa interrupta  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Aug-2000  
C;Accession: A61057

R;Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.  
Comp. Biochem. Physiol. C 96, 157-162, 1990  
A;Title: Threonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presyna  
A;Reference number: A61057; MUID:91130217; PMID:1980872  
A;Accession: A61057  
A;Molecule type: protein  
A;Residues: 1-9 <PIE>  
C;Superfamily: unassigned animal peptides  
C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 33.3%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5  
||  
Db 2 PP 3

## RESULT 75

A26744  
bradykinin-like peptide - garden dagger wasp  
N;Alternate names: Thr-6-bradykinin  
C;Species: Megascollia Flavifrons (Garden dagger wasp)  
C;Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 18-Aug-2000  
C;Accession: A26744  
R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.  
Toxicon 25, 527-535, 1987  
A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wa  
A;Reference number: A94322; MUID:87293024; PMID:3617088  
A;Accession: A26744  
A;Molecule type: protein  
A;Residues: 1-9 <YAS>  
C;Superfamily: unassigned animal peptides

Query Match 33.3%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5  
||  
Db 2 PP 3

Search completed: November 25, 2003, 18:28:22  
Job time : 5.52128 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 2.90426 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-13

Perfect score: 6  
Sequence: 1 DSQPPV 6

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	50.0	9	FAR4_PENMO	P83319 penaeus mon
2	3	50.0	10	UH05_RAT	P56573 rattus norv
3	3	50.0	11	MORN_HUMAN	P01163 homo sapien
4	3	50.0	13	EP65_HUMAN	P54963 homo sapien
5	3	50.0	13	MP1_MICOC	P81532 microplitis
6	3	50.0	14	GLGS_SPIOL	P55235 spinacia ol
7	3	50.0	14	PH1_PRUSE	P29283 prunus sero
8	3	50.0	14	TAT_HV1W2	P12509 human immun
9	3	50.0	14	TAT_HV1Z8	P12511 human immun
10	3	50.0	15	PH3_PRUSE	P29265 prunus sero
11	3	50.0	15	UC15_MAIZE	P80625 zea mays (m
12	3	50.0	15	UP01_METAN	P83440 metarhizium
13	3	50.0	16	PH2_PRUSE	P29284 prunus sero
14	3	50.0	17	A45K_MYCBO	P80069 mycobacteri
15	3	50.0	18	LCTN_LAMGL	P83315 lama glama
16	2	33.3	5	UKA4_CHLTR	P38005 chlamydia t
17	2	33.3	7	LANC_CARUI	P36960 carnobacter
18	2	33.3	7	TFPV_PACDA	P83455 pachymedusa
19	2	33.3	7	UF04_MOUSE	P38642 mus musculu
20	2	33.3	8	ALL5_CALVO	P41841 calliphora
21	2	33.3	8	CLP_THICU	P80488 thiobacillu
22	2	33.3	8	NPB_BOVIN	P15507 bos taurus
23	2	33.3	8	PPK2_PERAM	P82692 periplaneta
24	2	33.3	9	AL10_CARMA	P81813 carcinus ma
25	2	33.3	9	COXE_THUOB	P80975 thunnus obe
26	2	33.3	9	FAR2_CALVO	P41857 calliphora
27	2	33.3	9	FAR3_CALVO	P41858 calliphora
28	2	33.3	9	FAR3_PENMO	P83318 penaeus mon
29	2	33.3	9	FRF1_SARBU	P83350 sarcophaga
30	2	33.3	9	HUTU_KLEAE	P12381 klebsiella
31	2	33.3	9	KNL3_BOMVA	P83058 bomina var
32	2	33.3	9	LMT3_LOCMI	P41489 locusta mig
33	2	33.3	9	MOSF_CLYJA	P19853 clypeaster

#### ALIGNMENTS

RESULT 1

34	2	33.3	9	1	MOSH_CLYJA	P19852 clypeaster
35	2	33.3	9	1	OXVA_SCYCA	P42996 scylliorhinu
36	2	33.3	9	1	OXVF_SCYCA	P42997 scylliorhinu
37	2	33.3	9	1	OXVV_SOUAC	P43000 squalus aca
38	2	33.3	9	1	RT33_BOVIN	P82926 bos taurus
39	2	33.3	9	1	THYF_PIG	P01255 sus scrofa
40	2	33.3	9	1	YBFR_AZOVI	P25825 azotobacter
41	2	33.3	10	1	AH3_PRUSE	P29261 prunus sero
42	2	33.3	10	1	BPP2_BOTIN	P30422 bothrops ja
43	2	33.3	10	1	BPP8_BOTIN	P30426 bothrops in
44	2	33.3	10	1	BPP8_BOTIN	P30426 bothrops in
45	2	33.3	10	1	BPP8_BOTIN	P30426 bothrops in
46	2	33.3	10	1	BRK_ONCMY	P93151 vipera aspi
47	2	33.3	10	1	BRK_ONCMY	P93151 vipera aspi
48	2	33.3	10	1	CATB_SHEEP	P83205 ovis aries
49	2	33.3	10	1	FAR6_PANRE	P82660 panagrellus
50	2	33.3	10	1	GAJU_HUMAN	P01358 homo sapien
51	2	33.3	10	1	GONI_ALLMI	P37041 alligator m
52	2	33.3	10	1	MOSQ_CLYJA	P19962 clypeaster
53	2	33.3	10	1	RRPL_PHODV	P35946 phocine dis
54	2	33.3	10	1	TKNB_CHICK	P19851 gallus gall
55	2	33.3	10	1	TKNB_RANCA	P22689 rana catesb
56	2	33.3	10	1	TKNB_RANRI	P29135 rana ridibu
57	2	33.3	10	1	TKUI_UREUN	P40751 urechis uni
58	2	33.3	10	1	TMOF_AEDAE	P19425 aedes aegypt
59	2	33.3	10	1	UPA2_HUMAN	P30088 homo sapien
60	2	33.3	10	1	UPA5_HUMAN	P30091 homo sapien
61	2	33.3	10	1	URE3_MORMO	P17339 morganella
62	2	33.3	10	1	UXB1_YEAST	P99012 saccharomyc
63	2	33.3	11	1	BPP4_BOTIN	P30423 bothrops in
64	2	33.3	11	1	BPPB_AGKHA	P01021 agkistrodon
65	2	33.3	11	1	BPP_AGKHP	P04562 agkistrodon
66	2	33.3	11	1	BRK_MEGFL	P12797 megascolia
67	2	33.3	11	1	CXSE_CONAL	P58849 conus aulic
68	2	33.3	11	1	LADD_ONCMY	P81018 oncorhynch
69	2	33.3	11	1	PVK1_PERAM	P41837 periplaneta
70	2	33.3	11	1	RRPL_CHAV	P13179 chandipura
71	2	33.3	11	1	TKN1_PSEGU	P42986 pseudophryn
72	2	33.3	11	1	TKN1_PSEGU	P08612 urotoleia r
73	2	33.3	11	1	TKN2_PSEGU	P42987 pseudophryn
74	2	33.3	11	1	TKN3_PSEGU	P42988 pseudophryn
75	2	33.3	11	1	TKN4_PSEGU	P42989 pseudophryn
76	2	33.3	11	1	TKN5_PSEGU	P42990 pseudophryn
77	2	33.3	11	1	TKN_ELEMO	P01293 eledone mos
78	2	33.3	12	1	FAR7_PENMO	P83332 penaeus mon
79	2	33.3	12	1	FARI_CALVO	P41859 calliphora
80	2	33.3	12	1	FIFI_SARBU	P83349 sarcophaga
81	2	33.3	12	1	H2AX_ONCMY	P83337 oncorhynch
82	2	33.3	12	1	HCYB_MEGCR	Q10584 megathura c
83	2	33.3	12	1	HS9A_RAT	P82995 rattus norv
84	2	33.3	12	1	RF1_CONSP	P58805 conus apuri
85	2	33.3	12	1	TKN2_KASMA	P08614 kassina mac
86	2	33.3	12	1	TMZA_METMA	P80852 methanosarc
87	2	33.3	12	1	ULAL_MOUSE	P99032 mus musculu
88	2	33.3	13	1	ACT7_SOYBN	P15987 glycine max
89	2	33.3	13	1	AH4_PRUSE	P29262 prunus sero
90	2	33.3	13	1	BPPI_BOTJA	P01020 bothrops ja
91	2	33.3	13	1	BRK_FARID	P42717 parapolybia
92	2	33.3	13	1	ECDE_LYMDI	P80941 lymantria d
93	2	33.3	13	1	E122_LITRU	P82998 litoria rub
94	2	33.3	13	1	FR12_PEA	P83445 pisum sativ
95	2	33.3	13	1	HPA1_RANES	P32415 rana esculu
96	2	33.3	13	1	MLA_ANOCA	P41589 anolis caro
97	2	33.3	13	1	MLA_CAMDR	P01198 camelus dro
98	2	33.3	13	1	PSAJ_PEA	P17229 pisum sativ
99	2	33.3	13	1	SA2A_ONCMY	P82238 oncorhynch
100	2	33.3	13	1	SA2B_ONCMY	P82239 oncorhynch

```

FAR4 PENMO
ID FAR4 PENMO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP4 (SQPSMRLRF-amide).
OS Pnaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkasee C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
DB 1 SQP 3

RESULT 2
UH05 RAT
ID UH05 RAT STANDARD; PRT; 10 AA.
AC P56573;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2b-page of heart tissue (Spot P5) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=WiStar; TISSUE=Heart;
RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RA Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.3, ITS MW IS: 30 KDa.
FT UNSURE 9 OR P.
FT NON TER 10
SQ SEQUENCE 10 AA; 1269 MW; 00CBA4BB46C5BABB CRC64;

Query Match 50.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3
DB 4 DSQ 6

RESULT 3
MORN_HUMAN
ID FAR4 PENMO STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
from coelenterates to humans."
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
hydra."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuropeptide, the head activator from hydra."
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
in the G2/mitosis transition."
RL EMBO J. 8:3311-3318(1989).
CC -1- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
IN THE G2/MITOSIS TRANSITION.
CC -1- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS. BECAUSE IT INDUCED
HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHXAE.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJPHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
DB 1 QPP 3

RESULT 4
EP65 HUMAN
ID EP65 HUMAN STANDARD; PRT; 13 AA.
AC P54963;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

```

DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Erythrocyte 65 kDa protein (P65) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RP SEQUENCE.  
 RX MEDLINE=90004678; PubMed=2507249;  
 RA Hart G.W., Haltiwanger R.S., Holt G.D., Kelly W.G.;  
 RT "Nucleoplasmic and cytoplasmic glycoproteins";  
 RL Ciba Found. Symp. 145:102-118(1989).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 DR GO: GO:0005737; C:cytoplasm; NAS.  
 KM Glycoprotein.  
 FT NON TER 1 1  
 FT CARBOHYD 2 2 O-LINKED (GLCNAC).  
 FT NON TER 13 13  
 FT SEQUENCE 13 AA; 1300 MW; D0B873344C61A776 CRC64;  
 SQ SEQUENCE 13 AA; 1300 MW; D0B873344C61A776 CRC64;  
 Query Match 50.0%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 SOP 4  
 Db 5 SOP 7  
 RESULT 5  
 MP1 MICOC STANDARD; PRT; 13 AA.  
 AC P81532;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE MPI protein (Fragments).  
 OS Microplitis ocellatae (Braconidae; Insecta; Preygota;  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;  
 OC Braconidae; Microgasterinae; Microplitis.  
 NCBI\_TaxID=99573;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RA Takahashi M., Quicke D.L.J.;  
 RL Submitted (OCT-1998) to the SWISS-PROT data bank.  
 CC -1- TISSUE SPECIFICITY: SALIVARY GLANDS.  
 CC -1- DEVELOPMENTAL STAGE: LARVAL.  
 FT NON CONS 10 11  
 FT SEQUENCE 13 AA; 1595 MW; 0C0786C9DB82777B CRC64;  
 SQ SEQUENCE 13 AA; 1595 MW; 0C0786C9DB82777B CRC64;  
 Query Match 50.0%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4 PPV 6  
 Db 7 PPV 9  
 RESULT 6  
 GLGS\_SPTOL STANDARD; PRT; 14 AA.  
 ID GLGS\_SPTOL  
 AC P55235;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucose-1-phosphate adenylyltransferase small subunit (EC 2.7.7.27)  
 DE (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase B)  
 DE (Alpha-D-glucose-1-phosphate adenylyl transferase) (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.  
 NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Leaf;  
 RA Morell M.K., Bloom M., Knowles V., Preiss J.;  
 RT "Subunit structure of spinach leaf ADPglucose pyrophosphorylase";  
 RL Plant Physiol. 85:182-187(1987).  
 CC -1- FUNCTION: This protein plays a role in synthesis of starch. It  
 catalyzes the synthesis of the activated glycosyl donor, ADP-  
 glucose from Glc-1-P and ATP.  
 CC -1- CATALYTIC ACTIVITY: ATP + alpha-D-glucose 1-phosphate =  
 ADP + glucose.  
 CC -1- ENZYME REGULATION: ACTIVATED BY 3'-PHOSPHOGLYCERATE, INHIBITED  
 BY ORTHOPHOSPHATE. ALLOSTERIC REGULATION.  
 CC -1- PATHWAY: Starch biosynthesis.  
 CC -1- SUBUNIT: Heterotrimer.  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLASTS OF LEAVES AND AMYLOPLASTS  
 OF DEVELOPING ENDOSPERM.  
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-  
 PHOSPHATE ADENYLYLTRANSFERASE FAMILY.  
 DR InterPro: IPR005836; ADP\_Glu\_Pyrop.  
 DR PROSITE: PS00808; ADP\_GLC\_PYROPHOSPH\_1; PARTIAL.  
 DR PROSITE: PS00809; ADP\_GLC\_PYROPHOSPH\_2; PARTIAL.  
 DR PROSITE: PS00810; ADP\_GLC\_PYROPHOSPH\_3; PARTIAL.  
 KM Glycogen biosynthesis; Transferase; Nucleotidyltransferase;  
 KM Multigene family; Starch biosynthesis; Allosteric enzyme;  
 KM Amyloplast; Chloroplast.  
 FT NON TER 14 14  
 FT SEQUENCE 14 AA; 1490 MW; 98B57923AE738C5 CRC64;  
 SQ SEQUENCE 14 AA; 1490 MW; 98B57923AE738C5 CRC64;  
 Query Match 50.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DSQ 3  
 Db 3 DSQ 5  
 RESULT 7  
 PH1\_PRUSE STANDARD; PRT; 14 AA.  
 ID PH1\_PRUSE  
 AC P29263;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Prunasin beta-glucosidase I (EC 3.2.1.118) (Prunasin hydrolase  
 isoenzyme I) (PH I) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-  
 glucose.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 EMBRYONAL TISSUES.  
 CC -1- PTM: GLYCOSYLATED.  
 CC -1- PFM: GLYCOSYLATED.  
 KM Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON TER 14 14  
 FT SEQUENCE 14 AA; 1575 MW; FB3D7FAFB90CA9CA CRC64;  
 SQ SEQUENCE 14 AA; 1575 MW; FB3D7FAFB90CA9CA CRC64;

Query Match 50.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 |||  
 Db 3 PPV 5

RESULT 8  
 TAT\_HV1W2 STANDARD; PRT; 14 AA.  
 ID\_TAT\_HV1W2  
 AC P12509;  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE TAT protein (Transactivating regulatory protein) (Fragment).  
 GN TAT.  
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11705;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86235450; PubMed=3012778;  
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,  
 RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;  
 RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or  
 at risk for AIDS."  
 RL Science 232:1548-1553(1986).  
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
 CC PROMOTER.  
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.  
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM  
 CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO  
 CC WAS PERINATALLY INFECTED BY HER MOTHER.  
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 CC -----  
 DR EMBL; M12507; AAB1291.1; -.  
 DR HIV; M12507; TAT5WJ2.  
 KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
 KW AIDS.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1467 MW; 37CC737BFEE67AA8 CRC64;  
 Query Match 50.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SOP 4  
 |||  
 Db 3 SOP 5

RESULT 9  
 TAT\_HV1Z8 STANDARD; PRT; 14 AA.  
 ID\_TAT\_HV1Z8  
 AC P12511;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE TAT protein (Transactivating regulatory protein) (Fragment).  
 GN TAT.  
 OS Human immunodeficiency virus type 1 (2-84 isolate) (HIV-1).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11681;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86281278; PubMed=3395517;  
 RA Yourho J., Joseph S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,  
 RA Gallo R.C.;  
 RT "Nucleotide sequence analysis of the env gene of a new Zairian  
 RT isolate of HIV-1."  
 RL AIDS Res. Hum. Retroviruses 4:165-173(1988).  
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
 CC PROMOTER.  
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.  
 CC -1- MISCELLANEOUS: THE 2-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD  
 CC ZAIREAN MALE.  
 CC -----  
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 CC -----  
 DR EMBL; J03653; AAA44685.1; -.  
 DR HIV; J03653; TAT5JY1.  
 KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
 KW AIDS.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;  
 Query Match 50.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SOP 4  
 |||  
 Db 3 SOP 5

RESULT 10  
 PH3\_PRUSE STANDARD; PRT; 15 AA.  
 ID\_PH3\_PRUSE  
 AC P29265;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase  
 DE isozyme IIB) (Fr 11B) (Fragment).  
 DB Prunus serotina (Black cherry).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucosids I; Rosales; Rosaceae; Amygdaloidae; Prunus.  
 OX NCBI\_Taxid=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase."  
 RL Plant Physiol. 100:282-290(1992).  
 CC -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-  
 CC glucose.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 CC EMBRYONAL TISSUES.  
 CC -1- PTM: GLYCOSYLATED.  
 CC Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 KW NON\_TER 15 15



SQ SEQUENCE 15 AA; 1635 MW; 4F3D7F4FB90CFE4C CRC64;

Query Match 50.0%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 4 PPV 6

#### RESULT 11

UC19\_MAIZE  
ID UC19\_MAIZE STANDARD; PRT; 15 AA.  
AC P80625;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 406) (fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Fernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
RT genome analysis program."  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.6, ITS MW IS: 18.4 Kda.  
DR Maize-2DPAGE; P80625; COLEOPTILE.  
FT NON\_TER 1 15  
FT NON\_TER 1 15  
SQ SEQUENCE 15 AA; 1672 MW; 1CF69D4DA8737F9D CRC64;

Query Match 50.0%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 12 PPV 14

#### RESULT 12

UP01\_METAN  
ID UP01\_METAN STANDARD; PRT; 15 AA.  
AC P83440;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Unknown protein (fragment).  
OS Metarhizium anisopliae.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae;  
OC mitosporic Clavicipitaceae; Metarhizium.  
OX NCBI\_TaxID=5530;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=54A-1b;  
RX MEDLINE=22343006; PubMed=12455610;  
RA Kamp A.M., Bidocha M.J.;  
RT "Protein analysis in a pleomorphically deteriorated strain of the  
RT insect-pathogenic fungus Metarhizium anisopliae."  
RL Can. J. Microbiol. 48:789-792(2002).  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1651 MW; FBD76D669E1F0F4F CRC64;

Query Match 50.0%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 3 PPV 5

#### RESULT 13

PH2\_PRUSE  
ID PH2\_PRUSE STANDARD; PRT; 16 AA.  
AC P29264;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Prunasin beta-glucosidase IIA (EC 3.2.1.118) (Prunasin hydrolase  
DE isozyme IIA) (PH IIA) (fragment).  
OS Prunus serotina (Black cherry).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.  
OX NCBI\_TaxID=23207;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Seed;  
RA Li C.P., Swain E., Poulton J.E.;  
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase."  
RL Plant Physiol. 100:282-290(1992).  
CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-  
CC glucose.  
CC -!- SUBUNIT: Homodimer.  
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COYLEDON  
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
CC EMBRYONAL TISSUES.  
CC -!- PTM: GLYCOSYLATED.  
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1703 MW; FC4D7F4FB90CFE01 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 5 PPV 7

#### RESULT 14

A45K\_MYCBO  
ID A45K\_MYCBO STANDARD; PRT; 17 AA.  
AC P80069;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE 45/47 kDa antigen (fragment).  
OS Mycobacterium bovis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1765;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=BCG / Paris 1173 P2;  
RX MEDLINE=9313802; PubMed=8423100;  
RA Romain P., Laqueyrie A., Militzer P., Pescher P., Chavarot P.,  
RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;  
RT "Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen  
RT complex, an immunodominant target for antibody response after  
RT immunization with living bacteria."  
RL Infect. Immun. 61:742-750(1993).

CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: TO M. LEPRAE NL43, AND M. TUBERCULOSIS MPT32.  
 DR PIR; A49237; A49237.  
 KW Antigen.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 |||  
 Db 6 PPV 8

## RESULT 15

LANC\_CARUI STANDARD; PRT; 18 AA.  
 ID LCTN\_LAMGL  
 AC P8315;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lactophorin (Whey protein) (Fragment).  
 OS Lama glama (llama).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.  
 OX NCBI\_TaxID=9844;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=20000588; PubMed=10531593;  
 RA Kappeler S., Farah Z., Puhon Z.;  
 RT "Alternative splicing of lactophorin mRNA from lactating mammary gland  
 of the camel (Camelus dromedarius).";  
 RL J. Dairy Sci. 82:1-10(1999).  
 CC -1- SIMILARITY: BELONGS TO THE PP3 / GLYCAM-1 FAMILY.  
 DR GO; GO:0005576; C:extracellular; ISS.  
 DR Pfam; PF05242; GLYCAM-1; 1.  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2079 MW; CD596165EB236AC6 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
 |||  
 Db 16 SQP 18

## RESULT 16

UXA4\_CHLTR STANDARD; PRT; 5 AA.  
 ID UXA4\_CHLTR  
 AC P38005;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Unknown protein from 2D-page from elementary body (Fragment).  
 OS Chlamydia trachomatis.  
 CC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=L2/434/Bu;  
 RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,  
 RA Comanducci M., Christensen G., Birkelund S., Vreton E., Ratti G.,  
 RA Pallini V.;  
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.  
 DR Slena-2DPAGE; P38005; -.  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 474 MW; 75BA865AA800000 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DS 2  
 ||  
 Db 4 DS 5

## RESULT 17

LANC\_CARUI STANDARD; PRT; 7 AA.  
 ID LANC\_CARUI  
 AC P36960;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lantibiotic carnocin UI49 (Fragment).  
 OS Carnobacterium sp. (strain UI49).  
 CC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
 CC Carnobacterium  
 OX NCBI\_TaxID=35782;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92321768; PubMed=1622206;  
 RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
 RA Nes I.F.;  
 RT "Purification and characterization of a new bacteriocin isolated from  
 a Carnobacterium sp.";  
 RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
 CC -1- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).  
 CC ACTIVE ON GRAM-POSITIVE BACTERIA.  
 KW Antibiotic; Bacteriocin; Lantibiotic.  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
 ||  
 Db 5 QP 6

## RESULT 18

TPFY\_PACDA STANDARD; PRT; 7 AA.  
 ID TPFY\_PACDA  
 AC P83455;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyllin-1 (Pdt-1).  
 OS Pachymedusa dactylophora (Giant mexican leaf frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Phyllomedusinae; Pachymedusa.  
 OX NCBI\_TaxID=75986;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
 RP PRO-7.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Shaw C.;  
 RT "Pachymedusa dactylophora tryptophyllin-1 (Pdt-1): structural  
 characterization, pharmacological activity and cloning of precursor  
 cDNA";  
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
 CC smooth muscle.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 DR GO; GO:0005576; C:extracellular; NAS.

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DR GO: GO:0045986; P:negative regulation of smooth muscle contra...; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 19
UF04_MOUSE STANDARD; PRT; 7 AA.
ID UF04_MOUSE
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=75231108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
NON TER 7
FT PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

RESULT 20
ALL5_CALVO STANDARD; PRT; 8 AA.
ID ALL5_CALVO
AC F41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]_TaxID=27454;
RP SEQUENCE.
RX MEDLINE=93111980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;

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RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; E47393; E47393.
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION (20%).
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 21
CLP_THICU STANDARD; PRT; 8 AA.
ID CLP_THICU
AC P80488;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemolithotroph-specific protein (Fragment).
OS Thiobacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]_TaxID=36860;
RP SEQUENCE.
RC STRAIN=DSM 5494;
RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
RL Submitted (SEP-1995) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
CHEMOLITHOTROPHICALLY.
FT NON TER 8
SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match 33.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PV 6
DB 2 PV 3

RESULT 22
NPB_BOVIN STANDARD; PRT; 8 AA.
ID NPB_BOVIN
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.

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RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 4 QP 5

RESULT 23
PPK2_PERAM STANDARD; PRT; 8 AA.
AC P82632;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-2 (Pea-PK-2) (EXPRIL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattellidae; Periplaneta.
OX NCBI_TaxID=6978;

SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP [1]
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRILamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 24
AL10_CARMA STANDARD; PRT; 9 AA.
ID

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AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 963 MW; 372D79CDB4776C7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 3 QP 4

RESULT 25
COXE_THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottepeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 3 QP 4

RESULT 26
FAR2 CALVO
ID FAR2 CALVO STANDARD; PRT; 9 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliPMPRFamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE
RC TISSUE=thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliPMPRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMPRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; B41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3
DB 3 SQ 4

RESULT 27
FAR3 CALVO
ID FAR3 CALVO STANDARD; PRT; 9 AA.
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliPMPRFamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE
RC TISSUE=thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliPMPRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 3 QP 4

RESULT 28
FAR3 PENMO
ID FAR3 PENMO STANDARD; PRT; 9 AA.
AC P8318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMPRFamide-like neuropeptide FLP3 (AQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eveastalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivithangkura P., Sithigorngul W., Patson A.;
RT "Seven novel FMPRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMPRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 2 QP 3

RESULT 29
FRF1 SARBU
ID FRF1 SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMPRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
```



DR PIR; A61620; A61620.  
 DR InterPro: IPR001484; Pyrokinin.  
 DR PROSITE: PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QP 4  
 DB 3 QP 4  
 RESULT 33  
 MOSF\_CLYJA STANDARD; PRT; 9 AA.  
 AC P19853;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE [Phe-6]-mosact.  
 OS Clypeaster japonicus (Sand dollar).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;  
 OC Clypeasteridae; Clypeaster.  
 OX NCBI\_TaxID=7644;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Egg jelly;  
 RA Suzuki N., Kurita M., Yoshino K.I., Kajiuira H., Nomura K.,  
 RA Yamaguchi M.;  
 RT "Purification and structure of mosact and its derivatives from the  
 RT egg jelly of the sea urchin Clypeaster japonicus.";  
 RL Zool. Sci. 4:649-656(1987).  
 CC -!- FUNCTION: Stimulates sperm respiration and motility.  
 DR PIR; JN0027; JN0027.  
 SQ SEQUENCE 9 AA; 924 MW; 93245729CDC5B8B5 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DS 2  
 DB 1 DS 2  
 RESULT 34  
 MOSH\_CLYJA STANDARD; PRT; 9 AA.  
 AC P19852;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Sperm-activating peptide SAP-b ([His6]-mosact).  
 OS Clypeaster japonicus (Sand dollar).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;  
 OC Clypeasteridae; Clypeaster.  
 OX NCBI\_TaxID=7644;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Egg jelly;  
 RA Suzuki N., Kurita M., Yoshino K.I., Kajiuira H., Nomura K.,  
 RA Yamaguchi M.;  
 RT "Purification and structure of mosact and its derivatives from the  
 RT egg jelly of the sea urchin Clypeaster japonicus.";  
 RL Zool. Sci. 4:649-656(1987).  
 CC [2]  
 RP BROMINATION OF HIS-6.

RX MEDLINE=91167743; PubMed=2076468;  
 RA Takao T., Yoshino K., Suzuki N., Shimonishi Y.;  
 RT "Analysis of post-translational modifications of proteins by accurate  
 RT mass measurement in fast atom bombardment mass spectrometry.";  
 RL Biomed. Environ. Mass Spectrom. 19:705-712(1990).  
 CC -!- FUNCTION: Stimulates sperm respiration and motility.  
 DR PIR; JN0026; JN0026.  
 KW Bromination.  
 FT MOD\_RES 6 6 BROMINATION (PARTIAL).  
 SQ SEQUENCE 9 AA; 914 MW; 93245721EDC5B8B5 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DS 2  
 DB 1 DS 2  
 RESULT 35  
 OXYA\_SCYCA STANDARD; PRT; 9 AA.  
 AC P42996;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Asvatocin.  
 OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyllorhinidae; Scyllorhinus.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Bituitary;  
 RX MEDLINE=95062247; PubMed=7972045;  
 RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;  
 RT "Special evolution of neurohypophyseal hormones in cartilaginous  
 RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides  
 RT isolated from the spotted dogfish (Scyllorhinus caniculus).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).  
 CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR InterPro: IPR000981; Neurhyp\_horm.  
 DR Pfam: PF00220; hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PV 6  
 DB 7 PV 8  
 RESULT 36  
 OXYF\_SCYCA STANDARD; PRT; 9 AA.  
 AC P42997;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Phasvatocin.  
 OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyllorhinidae; Scyllorhinus.

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OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE
RC TISSUE=Pituitary; PubMed=7972045;
RX MEDLINE=95062247; Chauvet M.-T., Acher R.;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: aspartocin and phaevatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -|- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurohyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1016 MW; 17EDD76EB4449DB CRC64;
SQ
Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 PV 6
Db 7 PV 8

RESULT 37
OXVY_SQUAC STANDARD; PRT; 9 AA.
AC PA3000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;
SQ
Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 PV 6
Db 7 PV 8

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RESULT 38
RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -|- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -|- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;
SQ
Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 QP 4
Db 5 QP 6

RESULT 39
THYF_PIG STANDARD; PRT; 9 AA.
AC P01255;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thymic factor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=78026571; PubMed=914862;
RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
RT "Structural study of circulating thymic factor: a peptide isolated
RT from pig serum. II. Amino acid sequence.";
RL J. Biol. Chem. 252:8045-8047(1977).
CC -|- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
DR PIR; A01523; YFPG.
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT SEQUENCE 9 AA; 876 MW; D500B87866C5B33D CRC64;
SQ
Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 SQ 3
Db 4 SQ 5

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KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

RESULT 42
BPP2 BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
enzyme inhibitor)
OS Bothrops insularis (Island jararaca) (Queimada jararaca)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]_TaxID=8723;
RP SEQUENCE=Venom;
RC MEDLINE=90351557; PubMed=2386615;
RX Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -I- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of the
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 9 PP 10

RESULT 43
BPP2 BOTJA STANDARD; PRT; 10 AA.
AC P01072;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
inhibitor V-6-II).
OS Bothrops jararaca (Jararaca)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]_TaxID=8724;
RP SEQUENCE=Venom;
RC MEDLINE=72118526; PubMed=4334402;
RX Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;

KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

RESULT 42
BPP2 BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
enzyme inhibitor)
OS Bothrops insularis (Island jararaca) (Queimada jararaca)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]_TaxID=8723;
RP SEQUENCE=Venom;
RC MEDLINE=90351557; PubMed=2386615;
RX Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -I- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of the
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

RESULT 41
AH3 PRUSE STANDARD; PRT; 10 AA.
AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]_TaxID=23207;
RP SEQUENCE=Seed;
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -I- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -I- SUBUNIT: Monomer.
CC -I- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -I- PTM: GLYCOSYLATED.

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RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis.";  
 RL Biochemistry 10:4033-4039(1971).  
 CC -1- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A01255; XAVI6B.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 Db 9 PP 10

RESULT 44  
 BPP8 BOTIN STANDARD; PRT; 10 AA.  
 ID BPP8 BOTIN STANDARD; PRT; 10 AA.  
 AC P30426;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S5.1 (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O.; Vieira C.A.; Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -1- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; H37196; H37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1173 MW; 2FFB35945761F6D8 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 Db 9 PP 10

RESULT 45  
 BPP VIPAS STANDARD; PRT; 10 AA.  
 ID BPP VIPAS STANDARD; PRT; 10 AA.  
 AC P31351;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Viperas aspis (Aspic viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Viperinae; Vipera.  
 OX NCBI\_TaxID=8706;  
 RN [1]  
 RP SEQUENCE.  
 RX TISSUE=Venom;  
 RX MEDLINE=90382616; PubMed=2169439;  
 RA Komori Y.; Sugihara H.;  
 RT "Characterization of a new inhibitor for angiotensin converting  
 RT enzyme from the venom of Vipera aspis aspis.";  
 RL Int. J. Biochem. 22:767-771(1990).  
 CC -1- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A60377; XASNPC.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 Db 9 PP 10

RESULT 46  
 BRK ONCMY STANDARD; PRT; 10 AA.  
 ID BRK ONCMY STANDARD; PRT; 10 AA.  
 AC QSPZ21;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lysyl-bradykinin-like.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94039817; PubMed=8224232;  
 RA Conlon J.M.; Olson K.R.;  
 RT "Purification of a vasoactive peptide related to lysyl-bradykinin from  
 RT trout plasma.";  
 RL FEBS Lett. 334:75-78(1993).  
 CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR  
 CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Plasma.  
 CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
 DR PIR; S39030; S39030.  
 KW Bradykinin; Vasodilator.  
 SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 Db 3 PP 4

RESULT 47  
 CATB SHEEP STANDARD; PRT; 10 AA.  
 ID CATB SHEEP STANDARD; PRT; 10 AA.  
 AC P83205;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).  
 GN CTSB.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RC SEQUENCE.  
 RX MEDLINE=22394055; PubMed=12506352;  
 RA El Amiri B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,  
 RA Mboko H.B., Beckers J.-F.M.P.;  
 RT "Isolation and partial characterization of three pregnancy-associated  
 RT glycoproteins from the ewe placenta.";  
 RL Mol. Reprod. Dev. 64:199-206(2003).  
 CC -1- FUNCTION: Thiol protease which is believed to participate in  
 CC intracellular degradation and turnover of proteins. Has also been  
 CC implicated in tumor invasion and metastasis.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
 CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in  
 CC small molecule substrates (thus differing from cathepsin L). In  
 CC addition to being an endopeptidase, shows peptidyl-dipeptidase  
 CC activity, liberating C-terminal dipeptides.  
 CC -1- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked  
 CC by a disulfide bond (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Lysosomal (By similarity).  
 CC InterPro: IPR000169; SHprot\_acsite.  
 DR PROSITE; PS00640; THIOL\_PROTEASE ASN; PARTIAL.  
 DR PROSITE; PS00139; THIOL\_PROTEASE CVS; PARTIAL.  
 DR PROSITE; PS00639; THIOL\_PROTEASE HIS; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 117 MW; 8795780DDAA9D5BA CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DS 2  
 ||  
 DB 3 DS 4

RESULT 48  
 FAR6\_PANRE STANDARD; PRT; 10 AA.  
 AC P82660;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE FMRamide-like neuropptide PF6 (NGAPQPFVRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]  
 RC SEQUENCE, FUNCTION, AND AMIDATION.  
 RA Moffatt C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
 RA Maule A.G.;  
 RT "Isolation, characterization and pharmacology of RMRamide-related  
 RT peptides (FARpe) from free-living nematode, Panagrellus redivivus.";  
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: MYOACTIVE.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC Neuropeptide; Amidation.  
 KW MOD RES 10 10 AMIDATION.  
 FT MOD RES 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;  
 SQ SEQUENCE 10 AA; 1132 MW; 8795780DDAA9D5BA CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QP 4  
 ||  
 DB 5 QP 6  
 ||  
 RESULT 49  
 GAJU\_HUMAN STANDARD; PRT; 10 AA.  
 ID GAJU\_HUMAN  
 AC P01358;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Gastric juice peptide.  
 DE Homo sapiens (Human)  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RC SEQUENCE.  
 RX MEDLINE=75150968; PubMed=5538385;  
 RA Heathcote J.G., Washington R.J.;  
 RT "Peptides of normal human gastric juice.";  
 RL Int. J. Protein Res. 2:117-126(1970).  
 DR PIR; A01628; GXHU1.  
 DR MIM; 137220;  
 DR CO; GO:0007586; P.digestion; NAS.  
 DR GO; GO:0007586; P.digestion; NAS.  
 FT PEPTIDE 1 10 GASTRIC JUICE PEPTIDE 1.  
 FT PEPTIDE 2 10 GASTRIC JUICE PEPTIDE 2.  
 SQ SEQUENCE 10 AA; 1004 MW; CFECCGAB02C3387D CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DS 2  
 ||  
 DB 8 DS 9

RESULT 50  
 GON1\_ALLMI STANDARD; PRT; 10 AA.  
 ID GON1\_ALLMI  
 AC P37041; P20407;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)  
 DE (Luliberin I).  
 OS Alligator mississippiensis (American alligator).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
 OX NCBI\_TaxID=8496;  
 RN [1]  
 RC SEQUENCE.  
 RP TISSUE=Brain;  
 RX MEDLINE=9152338; PubMed=1882082;  
 RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,  
 RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure of two forms of gonadotropin-releasing hormone  
 RT from brains of the American alligator (Alligator mississippiensis).";  
 RL Regul. Pept. 33:105-116(1991).  
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the GNRH family.  
 DR PIR; A60066; RHAQ1.  
 DR InterPro: IPR002012; GNRH.  
 DR Pfam: PF00446; GNRH; 1.  
 DR PROSITE; PS00473; GNRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.

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SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QP 4
DB 8 QP 9
RESULT 51
MOSQ_CLYJA STANDARD; PRT; 10 AA.
AC F19962; 1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Gln6]-mosact.
OS Clypeaster japonicus (Sand dollar).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;
OC Clypeasteridae; Clypeaster.
OX NCBI_TaxID=7644;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg jelly;
RA Suzuki N., Kurita M., Yoshino K., Kajiuura H., Nomura K., Yamaguchi M.;
RT "Purification and structure of mosact and its derivatives from the
RT egg jelly of the sea urchin Clypeaster japonicus.";
RL Zool. Sci. 4:649-656(1987).
CC -!- FUNCTION: Stimulates sperm respiration and motility.
DR PIR; JN0025; JN0025.
SQ SEQUENCE 10 AA; 1019 MW; 9AFB032456DDC5BA CRC64;
Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DS 2
DB 1 DS 2
RESULT 52
RRPL_PHODV STANDARD; PRT; 10 AA.
AC P35946;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein) (Fragment).
GN L.
OS Phocine distemper virus (PDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U1ster/88;
RX MEDLINE=92268877; PubMed=1588321;
RA Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
RT "Molecular characterization of phocine distemper virus: gene order
RT and sequence of the gene encoding the attachment (H) protein.";
RL J. Gen. Virol. 73:1189-1194(1992).
CC -!- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
CC FUNCTION IN RNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)
CC SYNTHESIS/OF NEWLY SYNTHESIZED VIRAL MRNAs, RNA EDITING OF THE P
CC GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
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EMBL; D10371; BAA01208.1;
KW Transferase; RNA-directed RNA polymerase.
FT NON TER 10
SQ SEQUENCE 10 AA; 1105 MW; 9C2B7PD452D5A2D5 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DS 2
DB 2 DS 3
RESULT 53
TKNB_CHICK STANDARD; PRT; 10 AA.
AC P19831;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurokinin A (Substance K) (Neuromedin L).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=88204283; PubMed=2452461;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL Regul. Pept. 20:171-180(1988).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; JN0024; JN0024.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 10
SQ SEQUENCE 10 AA; 1134 MW; 8A6B4062C9D5B8B1 CRC64;
Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DS 2
DB 4 DS 5
RESULT 54
TKNB_RANCA STANDARD; PRT; 10 AA.
AC P22689;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
```

DE Ranatachykinin B (RTK B).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]\_TaxID=8400;  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RX MEDLINE=91254337; PubMed=2043143;  
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
brain and intestine.";  
RL Regul. Pept. 46:81-88(1993).  
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
MUSCLES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR: B61033; B61033.  
DR InterPro: IPR002040; Tachykinin.  
DR PROSITE: PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA; 1210 MW; 917E556B59DSBAB5 CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DS 2  
DB 4 DS 5

RESULT 55  
TKNB\_RANRI STANDARD; PRT; 10 AA.  
AC P29135;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Neurokinin A.  
OS Rana ridibunda (Laughing frog) (Marsh frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8406;  
RN [1]\_TaxID=8406;  
RP SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=93075037; PubMed=1332683;  
RA Wang Y., Badgery-Parker T., Lovas S., Chartrel N., Vaudry H.,  
Burcher E., Conlon J.M.;  
RT "Primary structure and receptor-binding properties of a neurokinin A-  
related peptide from frog gut.";  
RL Biochem. J. 287:827-832(1992).  
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
MUSCLES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR: S27178; S27178.  
DR InterPro: IPR002040; Tachykinin.  
DR Pfam: PF02202; Tachykinin; 1.

DR PROSITE: PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA; 1160 MW; 526B407059DSBAA7 CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DS 2  
DB 4 DS 5

RESULT 56  
TKUL\_UREUN STANDARD; PRT; 10 AA.  
AC P40751;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Urechistachykinin I.  
OS Urechis uncinatus.  
OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.  
OX NCBI\_TaxID=6432;  
RN [1]\_TaxID=6432;  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Ventral nerve cord;  
RX MEDLINE=93236558; PubMed=8476410;  
RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;  
RT "Two novel tachykinin-related neuropeptides in the echiuroid worm,  
Urechis uncinatus.";  
RL Biochem. Biophys. Res. Commun. 192:1-6(1993).  
CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL  
MUSCLE OF THE ANIMAL.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA; 1177 MW; C6D1C462C9D6C5A6 CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 SQ 3  
DB 4 SQ 5

RESULT 57  
TWOF\_AEDAE STANDARD; PRT; 10 AA.  
AC P19425;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Trypsin-modulating oostatic factor (TWOF) (OOSH).  
OS Aedes aegypti (Yellowfever mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
OX NCBI\_TaxID=7159;  
RN [1]\_TaxID=7159;  
RP SEQUENCE.  
RC STRAIN=Vero beach; TISSUE=Ovary;  
RX MEDLINE=90367888; PubMed=2394318;  
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
RT "Mosquito oostatic factor: a novel decapeptide modulating  
trypsin-like enzyme biosynthesis in the midgut.";  
RL FASEB J. 4:3015-3020(1990).  
RN [2]  
RP SEQUENCE.  
RC STRAIN=Vero beach; TISSUE=Ovary;

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RX MEDLINE=93357794; PubMed=8353526;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
  modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -1- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
  IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
  CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
  DEVELOPMENT.
CC -1- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
  EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
  36 HRS AND STOPS AT 56 HRS.
DR PIR; A36454; A36454.
KW Hormone.
FT DOMAIN 3 10 POLY-PRO.
FT VARIANT 1 2 YD -> DY (IN TMFO(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 5 PP 6

RESULT 58
UPA2_HUMAN STANDARD; PRT; 10 AA.
AC P30088;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochrassner D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
  PROTEIN IS: 4.4, ITS MW IS: 49 kDa.
CC SWISS-2DPAGE; P30088; HUMAN.
DR NON TER 1 1
FT UNSURE 6 6
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 5 PP 6

RESULT 59
UPAS_HUMAN STANDARD; PRT; 10 AA.
AC P30091;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochrassner D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
  PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
CC -1- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
  ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
  PROTEIN.
CC SWISS-2DPAGE; P30091; HUMAN.
DR NON TER 1 1
FT VARIANT 9 9 G -> Y. /FTID=VAR_000002.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 3 QP 4

RESULT 60
URE3_MORMO STANDARD; PRT; 10 AA.
AC P17379;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
  amidohydrolase) (Fragment).
GN UREA
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
ON NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RC MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
  isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -1- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
DR PIR; C35389; C35389.
KW Hydrolase.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 5 PP 6

RESULT 61

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UXB1 YEAST
ID UXB1 YEAST STANDARD; PRT; 10 AA.
AC P99012;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unknown protein from 2D-page (Spot 2D-000JYC) (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RC STRAIN=X2180-1A;
RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,
RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
RL Submitted (AUG-1995) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC SWISS-2DPAGE; P99012; YEAST.
DR PROTEIN IS: 5.71, ITS MW IS: 12.4 kDa.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1074 MW; 9E7BEF7AEB0AF6C5 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3
DB 3 SQ 4

RESULT 62
BPP3 BOTIN
ID BPP3 BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Iland jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 4 PP 5

RESULT 63
BPP4 BOTIN
ID BPP4 BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Iland jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 4 PP 5

RESULT 64
BPPB AGKHA
ID BPPB AGKHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNEA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 4 PP 5

RESULT 65

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QY 4 PP 5
Db 4 PP 5

RESULT 65
BPP ACKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys
pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydus.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
angiotensin-converting enzyme and enhances the action of
bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JCO002; XAIBH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
Db 4 PP 5

RESULT 66
BRK MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
peptide ([Thr6]bradykinin)].
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Scolioidea;
OC Scoliidae; Megascolia.
OX NCBI_TaxID=7437;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088;
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT "Two kinins isolated from an extract of the venom reservoirs of the
solitary wasp Megascolia flavifrons.";
RL Toxicon 25:527-535(1987).
RN [2]
RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yasuhara T., Mantel P.;
RT "Two kinins isolated from the venom of Megascolia flavifrons.";

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RL Toxicon 26:34-34(1988).
CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
activities (e.g. smooth muscle contraction).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; B26744; B26744.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 338673930771A9C8 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
Db 2 PP 3

RESULT 67
CXSB CONAL STANDARD; PRT; 11 AA.
AC P58849;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conotoxin ausb.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Litazan M.B., Cruz L.J.,
Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
Bandyopadhyay P., Craig A.G., Olivera B.M.;
RA J. Biol. Chem. 274:36030-36030(1999).
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RT "The T-superfamily of conotoxins.";
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Litazan M.B., Cruz L.J.,
Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
Bandyopadhyay P., Craig A.G., Olivera B.M.;
RA J. Biol. Chem. 274:36030-36030(1999).
CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
observed when injected into mice (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1398.6; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE T-SUPERFAMILY OF CONOTOXINS.
DR PIR; B59146; B59146.
KW Toxin.
FT DISULFID 2 9 BY SIMILARITY.
FT DISULFID 3 10 BY SIMILARITY.
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PV 6
Db 4 PV 5

RESULT 68
LADD ONCMY STANDARD; PRT; 11 AA.
AC P81018;

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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ladderlectin (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RN SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293419; Pubmed=9149391;
RA Jensen L.E., Thiel S., Petersen T.E., Jensenius J.C.;
RT "A rainbow trout lectin with multimeric structure.";
RL Comp. Biochem. Physiol. 116B:385-390(1997).
CC -1- FUNCTION: LECTIN THAT BINDS SEPHAROSE.
CC -1- COPACTOR: CALCIUM IS ESSENTIAL FOR SEPHAROSE BINDING.
CC -1- SUBUNIT: MULTIMERIC.
KW Lectin; Calcium.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 9 PP 10

RESULT 69
PVK1 PERAM ID PVK1 PERAM STANDARD; PRT; 11 AA.
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pea-pvk-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RN SEQUENCE AND SYNTHESIS.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=95232021; Pubmed=7716075;
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (pea-pvk): a novel myotrophic neuropeptide from the
RT perisymphathetic organs of the American cockroach.";
RL Peptides 16:61-66(1995).
CC -1- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
CC HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PV 6
DB 7 PV 8

RESULT 70
RRPL CHAV ID RRPL CHAV STANDARD; PRT; 11 AA.
AC P13179;
DT 01-JAN-1990 (Rel. 13, Created)

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DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
(L protein) (Fragment).
GN L
OS Chandipura virus (strain I653514).
OC Varuees; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11273;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=89299473; Pubmed=2741347;
RX Masters P.S., Shella R.S., Butcher M., Patel B., Ghosh H.P.,
RA Banerjee A.K.;
RT "Structure and expression of the glycoprotein gene of Chandipura
RT virus.";
RL Virology 171:285-290(1989).
CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
CC NUCLEOCAPSID (N) PROTEIN.
CC -1- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
CC PARAMYXOVIRUSES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; J04350; AAA42917.1; -.
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PV 6
DB 5 PV 6

RESULT 71
TKN1 PSEGU ID TKN1 PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-I (PG-KI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RN SEQUENCE.
RP TISSUE=Skin secretion;
RX MEDLINE=90287814; Pubmed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Espamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

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CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC PIR; B60409; B60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyroglutamate carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CBIAB7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e-03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 72
TKN1 UPERU STANDARD; PRT; 11 AA.
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspamer V., Endean R.;
RT "Structure of uperolein, a physalaemin-like endcapeptide occurring
in the skin of Uperoleia rugosa and Uperoleia marmorata.";
RL Experientia 31:394-395(1975).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyroglutamate carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e-03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Skin.
SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
InterPro; IPR003580; Protachykinin.
InterPro; IPR002040; Tachykinin.
Pfam; PF02202; Tachykinin; 1.
SMART; SM00203; TK; 1.
PROSITE; PS00267; TACHYKININ; 1.
Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
Pyroglutamate carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
MOD_RES 1 1
MOD_RES 11 11 AMIDATION.
SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e-03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

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RESULT 73
TKN2 PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; C60409; C60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyroglutamate carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CBIAB7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e-03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Skin.
SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
InterPro; IPR003580; Protachykinin.
InterPro; IPR002040; Tachykinin.
Pfam; PF02202; Tachykinin; 1.
SMART; SM00203; TK; 1.
PROSITE; PS00267; TACHYKININ; 1.
Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
Pyroglutamate carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
MOD_RES 1 1
MOD_RES 11 11 AMIDATION.
SEQUENCE 11 AA; 1246 MW; 3A247C37C9CBIAB7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e-03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

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CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; D60409; D60409.  
 DR InterPro; IPR003580; Protachykinin.  
 DR InterPro; IPR002040; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 1 1 AMIDATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1268 MW; 3DA7C37C9CB1457 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QP 4  
 DB 1 QP 2

RESULT 75  
 TKM4\_PSEGU  
 ID\_TKN4\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42989;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Substance P-like peptide I (PG-SPI).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC MYOBATRACHINAE; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RL the Australian frog Pseudophryne guentheri."; Peptides 11:299-304(1990).  
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; E60409; E60409.  
 DR InterPro; IPR003580; Protachykinin.  
 DR InterPro; IPR002040; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 1 1 AMIDATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4  
 DB 1 QP 2

Search completed: November 25, 2003, 18:17:33  
 Job time : 3.90426 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 14.4574 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-13  
Perfect score: 6  
Sequence: 1 DSQPPV 6

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL\_23.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mhc.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	66.7	19	13	Q9PRT0
2	3	50.0	9	10	P82429
3	3	50.0	9	16	Q935G1
4	3	50.0	10	2	Q9R5T2
5	3	50.0	11	10	Q9S8Z9
6	3	50.0	11	13	Q8UUP1
7	3	50.0	12	2	Q932U8
8	3	50.0	12	2	Q52112
9	3	50.0	12	2	Q8GMV1
10	3	50.0	12	2	Q8GMF8
11	3	50.0	12	2	Q8CML2
12	3	50.0	12	4	Q8NTR7
13	3	50.0	13	12	Q67604
14	3	50.0	14	4	P78359
15	3	50.0	15	5	Q9TWE9
16	3	50.0	15	10	Q9S8N8
					Q9PRT0 gallus gall
					P82429 nicotiana t
					Q935G1 salmonella
					Q9R5T2 acetobacter
					Q9S8Z9 psophocarpu
					Q8UUP1 xenopus lae
					Q932U8 acinetobact
					Q52112 acinetobact
					Q8GMV1 acinetobact
					Q8GMF8 acinetobact
					Q8CML2 acinetobact
					Q8NTR7 homo sapien
					Q67604 squash leaf
					P78359 homo sapien
					Q9TWE9 gallaria me
					Q9S8N8 hordeum vul

Q9UC44 homo sapien  
Q9UC52 homo sapien  
Q81026 homo sapien  
Q9E8Y6 lupinus arb  
Q14001 homo sapien  
Q9UC19 homo sapien  
Q9QVC2 rattus norv  
Q9TWV6 alysiacal  
Q46592 capra hircu  
Q9CUP4 mus musculu  
Q9JIE9 mus musculu  
Q90790 gallus gall  
Q9UC13 homo sapien  
Q9BX20 homo sapien  
Q16184 homo sapien  
Q15610 homo sapien  
Q8MCI9 aulacoseira  
Q8LVH6 aulacoseira  
Q8MCJ2 aulacoseira  
Q9S8G9 psophocarpu  
P82941 hordeum vul  
Q9PRN4 petromyzon  
Q9EB47 homo sapien  
Q8TE41 homo sapien  
Q9TRH7 canis famli  
Q9S8H0 psophocarpu  
Q9QUX7 rattus sp.  
Q8RGV4 fusobacteri  
Q50556 actinobacil  
P82214 amblyopyrum  
P92393 hordeum vul  
P92403 lophopyrum  
P92427 peridictyon  
P92430 aegilops ta  
P92221 bromus iner  
P92387 henrardia p  
P92381 hordeum bra  
P92425 pseudoroegn  
P92387 henrardia p  
P92210 agropyron c  
P92440 thinopyrum  
P92218 australopyr  
P92390 heteranthel  
P92372 haynaldia v  
P92442 taeniattheru  
P92226 crithopsis  
P92385 hordeum mar  
P92421 psathyrosta  
Q9ZER3 buchnera ap  
Q93454 thibacillu  
Q96GF9 homo sapien  
Q15890 homo sapien  
Q15893 homo sapien  
Q9TRX8 bos taurus  
Q29801 homo sapien  
Q29812 homo sapien  
Q29797 homo sapien  
Q94VF3 varanus kei  
Q81802 zea mays (m  
P82598 rattus norv  
Q83977 influenzavi  
Q9J205 hepatitis c  
Q89498 murine hepa  
Q9P669 gallus gall  
Q53914 streptomyce  
Q99193 pseudomonas  
Q9R7H9 haemophilus  
Q45533 bacillus su  
P82568 streptococ  
Q9P8E5 kluyveromyc  
Q9UC88 homo sapien  
Q9UK44 homo sapien  
Q9UCN5 homo sapien

90 Q9TW0 anthopleura  
91 P82208 bombyx mori  
92 Q9WFT4 diadema ant  
93 Q9FXL0 lilium long  
94 Q8VZ23 pinus radia  
95 P82440 nicotiana t  
96 O08979 mus musculu  
97 Q9PRJ4 lepisosteus  
98 Q8AYL5 carassius a  
99 Q8AUM7 carassius a  
100 Q64972 avian rous-

## ALIGNMENTS

RESULT 1  
Q9PRT0 PRELIMINARY; PRT; 19 AA.  
ID Q9PRT0  
AC Q9PRT0  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE 23A7 antigen (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95332492; PubMed=7608337;  
RA Denburg J.L., Caldwell R.T., Warner J.M.;  
RT "Developmental changes in epitope accessibility as an indicator of  
RT multiple states of an immunoglobulin-like neural cell adhesion  
RT molecule".  
RL J. Comp. Neurol. 354:533-550(1995).  
SQ SEQUENCE 19 AA; 2051 MW; 83E67BEE484EBD03 CRC64;

Query Match 66.7%; Score 4; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQPP 5  
Db 14 SQPP 17

RESULT 2  
P82429 PRELIMINARY; PRT; 9 AA.  
ID P82429  
AC P82429  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE 44 kDa cell wall protein (Fragment).  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=cv. PETIT HAVANA;  
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
RA Wojtaszek P., Bolwell G.P.;  
RT "Proteomic study of secondary cell wall proteins from transformed  
RT tobacco culture".  
RL Planta 0:0-0(2000).  
CC -|- SUBCELLULAR LOCATION: CELL WALL.  
CC -|- TISSUE SPECIFICITY: XYLEM.  
KW Cell wall.  
FT NON\_TER 9 9

SQ SEQUENCE 9 AA; 986 MW; C22CCAADC6C7776 CRC64;  
Query Match 50.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
Db 2 QPP 4

RESULT 3  
Q935G1 PRELIMINARY; PRT; 9 AA.  
ID Q935G1  
AC Q935G1  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Putative membrane protein (Fragment).  
GN HCM1.01C;  
OS Salmonella typhi.  
OG Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI\_TaxID=601;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608;  
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,  
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,  
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jegels K.,  
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrall B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella  
RT enterica serovar typhi CT18".  
RL Nature 413:848-852(2001).  
DR EMBL; ALS13383; CAD09867.1;  
KW Plasmid; Complete proteome.  
FT NON\_TER 9 9

SQ SEQUENCE 9 AA; 904 MW; 5FCDC7776D86767 CRC64;  
Query Match 50.0%; Score 3; DB 16; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
Db 5 QPP 7

RESULT 4  
Q9RST2 PRELIMINARY; PRT; 10 AA.  
ID Q9RST2  
AC Q9RST2  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).  
OS Acetobacter hansenii.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
OC Acetobacteraceae; Gluconacetobacter.  
OX NCBI\_TaxID=436;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92027789; PubMed=1929428;  
RA Levy H.R., Cook C.;  
RT "Purification and properties of NADP-linked glucose-6-phosphate  
RT dehydrogenase from Acetobacter hansenii (Acetobacter xylinum)".  
RL Arch. Biochem. Biophys. 291:161-167(1991).

```

FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D77767 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6
Db 4 PPV 6

RESULT 5
Q9S8Z9 PRELIMINARY; PRT; 11 AA.
AC Q9S8Z9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE W1 peptide (Fragment).
OS Peophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Peophocarpus.
OC NCBI_TaxID=3891;
RN [1]
RP SEQUENCE
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytochemistry 31:731-735(1992).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1120 MW; 8391BABCDD77772D1 CRC64;

Query Match 50.0%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6
Db 6 PPV 8

RESULT 6
Q8UUP1 PRELIMINARY; PRT; 11 AA.
AC Q8UUP1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Beta-TrCP protein (Fragment).
GN BETA-TRCP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N.A.
RA Carnevali F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RL "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis.";
RL Thesis (2001), Department of Genetica e Biologia Molecolare,
RL University of Rome La Sapienza, Rome, Italy.
DR EMBL; AJ428930; CAD21927.1; -.
FT NON_TER 11 11
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; CEB938BE35BEA5B9 CRC64;

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Query Match 50.0%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
Db 9 QPP 11

RESULT 7
Q932U8 PRELIMINARY; PRT; 12 AA.
AC Q932U8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Urf-2X protein.
OS URF-2X.
OS Acinetobacter sp.
OS Plasmid pKLH205, and Plasmid pKLH204.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OC NCBI_TaxID=472;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ED45-25; PLASMID=pKLH205, and pKLH204;
RX MEDLINE=21272500; PubMed=11376944;
RA Kholodii G.;
RT "The shuffling function of resolvases.";
RL Gene 269:121-130(2001).
DR EMBL; AJ251707; CAC39413.1; -.
DR EMBL; AJ250851; CAC39402.1; -.
KW Plasmid
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4
Db 4 SQP 6

RESULT 8
Q52112 PRELIMINARY; PRT; 12 AA.
AC Q52112; O08093; O08097; O08128; O08132; Q56909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE URF2X protein (Fragment).
OS URF-2X OR URF2X.
OS Acinetobacter calcoaceticus,
OS Pantoea agglomerans,
OS Alcaligenes sp.,
OS Enterobacter cloacae,
OS Escherichia coli,
OS Yersinia enterocolitica, and
OS mercury resistant bacterium '96 SE13.
OS Plasmid pKLH2, Plasmid pKLH256, Plasmid pKLH210, Plasmid pCL17, and
OG Plasmid pKLH201.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OC NCBI_TaxID=471, 549, 512, 550, 562, 630, 93601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=A. calcoaceticus; PLASMID=pKLH2;
RX MEDLINE=94134837; PubMed=8302940;
RA Kholodii G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin S.Z.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Molecular characterization of an aberrant mercury resistance

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RT transposable element from an environmental Acinetobacter strain.";  
RL Plasmid 30:303-308(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX SPECIES=P.agglomerans, Alcaligenes sp., E.cloacae, and E.coli;  
RC MEDLINE=97303088; PubMed=9159519;  
RA Nikiforov V., Kholodii G., Minakhin L., Gorlenko Z., Kalyaeva E.,  
RA Mindlin S., Nikiforov V.;  
RT "Intercontinental spread of promiscuous mercury-resistance transposons  
RT in environmental bacteria.";  
RL Mol. Microbiol. 24:321-329(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX SPECIES=Y.enterocolitica; STRAIN=Various strains;  
RA MEDLINE=95273477; PubMed=7753910;  
RA Osbourn S.E.V., Turner A.K., Gristed J.;  
RT "Nucleotide sequence within Tn3926 confirms this as a Tn21-like  
RT transposable element and provides evidence for the origin of the mer  
RT operon carried by plasmid pKLH2.";  
RL Plasmid 33:65-69(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX SPECIES=mercury resistant bacterium '96 SE13;  
RA Holt R.J., Bruce K.D., Strike P.;  
RT "Conservation of transposon structures in soil bacteria.";  
RL FEMS Microbiol. Ecol. 0:0-0(1999).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX SPECIES=A.calcoaceticus; STRAIN=KHW14; PLASMID=pKLH201;  
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,  
RA Nikiforov V.G.;  
RT "pKLH2-like aberrant transposons and possible mechanisms of their  
RT dissemination.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF213017; AA19685.1; -  
DR EMBL; Y08992; CAA70180.1; -  
DR EMBL; Y08993; CAA70193.1; -  
DR EMBL; Y09025; CAA70234.1; -  
DR EMBL; Y10102; CAA71186.1; -  
DR EMBL; X78059; CAA54979.1; -  
DR EMBL; AF134211; AAD34400.1; -  
DR EMBL; AJ251307; CAC80877.1; -  
KW Plasmid.  
FT NON TER  
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;  
  
Query Match 50.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 SQ 4  
Db |||  
4 SQ 6  
  
RESULT 9  
Q8GMV1 Q8GMV1 PRELIMINARY; PRT; 12 AA.  
ID Q8GMV1  
AC Q8GMV1  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Urf-2X protein.  
GN URF-2X.  
OS Acinetobacter lwofii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=28090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TC108;  
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,  
RT "pKLH2-like aberrant transposons and possible mechanisms of their  
RT dissemination.";  
RT

RA Nikiforov V.G.;  
RT "pKLH2-like aberrant transposons and possible mechanisms of their  
RT dissemination.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ250245; CAC80792.1; -  
KW Plasmid.  
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;  
  
Query Match 50.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 SQ 4  
Db |||  
4 SQ 6  
  
RESULT 10  
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ID Q8GMT8  
AC Q8GMT8  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Urf-2X protein.  
GN URF-2X.  
OS Acinetobacter junii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=40215;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NC13-1;  
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,  
RA Nikiforov V.G.;  
RT "pKLH2-like aberrant transposons and possible mechanisms of their  
RT dissemination.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ250494; CAC80763.1; -  
KW Plasmid.  
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;  
  
Query Match 50.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 SQ 4  
Db |||  
4 SQ 6  
  
RESULT 11  
Q8GML2 Q8GML2 PRELIMINARY; PRT; 12 AA.  
ID Q8GML2  
AC Q8GML2  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Urf-2X protein.  
GN URF-2X.  
OS Acinetobacter sp. ED23-35.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=109250;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ED23-35;  
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,  
RA Nikiforov V.G.;  
RT "pKLH2-like aberrant transposons and possible mechanisms of their  
RT dissemination.";  
RT



RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ251272; CAC80895.1; -  
 KW Plasmid.  
 SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
 ||||  
 Db 4 SQP 6

## RESULT 12

Q9NTR7 ID Q9NTR7 PRELIMINARY; PRT; 12 AA.  
 AC Q9NTR7; 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE DJ78N10.1 (Eyes absent (Drosophila) homolog 4) (Fragment).  
 GN EYA4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Dunn M.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; ALI21959; CAB92069.1; -  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1394 MW; C15EA7952D472AB6 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3  
 ||||  
 Db 3 DSQ 5

## RESULT 13

Q67604 ID Q67604 PRELIMINARY; PRT; 13 AA.  
 AC Q67604;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Movement protein (fragment).  
 GN BCL.  
 OS Squash leaf curl virus.  
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 OX NCBI\_TaxID=10829;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Los Mochis 1;  
 RA Loniello A.O., Ford R.B., Salinas R.A., Morales F.J., Maxwell D.P.;  
 RT "Diversity among geminiviruses associated with vegetables from Valle  
 del Fuerte, Sinaloa, Mexico."  
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; L27273; AAA47820.1; -  
 FT NON TER 1 1  
 FT NON TER 13 13  
 SQ SEQUENCE 13 AA; 1376 MW; D471DE4D634E76C2 CRC64;

Query Match 50.0%; Score 3; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5

Db ||||  
 7 QPP 9

## RESULT 14

P78359 ID P78359 PRELIMINARY; PRT; 14 AA.  
 AC P78359;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE NF-kappa-B transcription factor p65 (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Umbilical vein;  
 RA Remacle J.E., Brys R., Pype S., Nelles L., Huylebroeck D.;  
 RT "5' cDNA sequence RelA isolated from Human umbilical vein endothelial  
 RT cells."  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U88316; AAB48487.1; -  
 FT NON TER 14 14  
 SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
 ||||  
 Db 12 SQP 14

## RESULT 15

Q9TWE9 ID Q9TWE9 PRELIMINARY; PRT; 15 AA.  
 AC Q9TWE9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE PROPHENOLOXIDASE (fragment).  
 OS Galleria mellonella (Wax moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;  
 OC Pyralidae; Galleriinae; Galleria.  
 OX NCBI\_TaxID=7137;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=96137142; PubMed=8580908;  
 RA Kopacek P., Weise C., Gotz P.;  
 RT "The phenoloxidase from the wax moth Galleria mellonella:  
 RT purification and characterization of the proenzyme."  
 RL Insect Biochem. Mol. Biol. 25:1081-1091(1995).  
 SQ SEQUENCE 15 AA; 1695 MW; C78B5BB2430AFD4A CRC64;

Query Match 50.0%; Score 3; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3  
 ||||  
 Db 6 DSQ 8

## RESULT 16

Q9S8N8 ID Q9S8N8 PRELIMINARY; PRT; 15 AA.  
 AC Q9S8N8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Protein E-22 (Fragment).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94170739; PubMed=8125056;  
RA Flengsrud R.;  
RT "Separation of acidic barley endosperm proteins by two-dimensional electrophoresis."  
RL Electrophoresis 14:1060-1066(1993).  
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;  
  
Query Match 50.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 QPP 5  
DB 4 QPP 6  
  
RESULT 17  
Q9UC44 PRELIMINARY; PRT; 16 AA.  
ID Q9UC44;  
AC Q9UC44;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Interferon-alpha-induced protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96132854; PubMed=8557639;  
RA Rich S.A., Bose M., Tempst P., Rudofsky U.H.;  
RT "Purification, microsequencing, and immunolocalization of p36, a new interferon-alpha-induced protein that is associated with human lupus inclusions."  
RL J. Biol. Chem. 271:1118-1126(1996).  
SQ SEQUENCE 16 AA; 1730 MW; 40E50CDF175390A CRC64;  
  
Query Match 50.0%; Score 3; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DSQ 3  
DB 10 DSQ 12  
  
RESULT 18  
Q9UC52 PRELIMINARY; PRT; 16 AA.  
ID Q9UC52;  
AC Q9UC52;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13; Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Carboxylesterase isozyme (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96170127; PubMed=8597091;  
RA Satoh T., Hosokawa M.;  
RT "Molecular aspects of carboxylesterase isoforms in comparison with

RT other esterases.";  
RL Toxicol. Lett. 82:439-445(1995).  
SQ SEQUENCE 16 AA; 1599 MW; 5DA6286D3C6BFFED CRC64;  
  
Query Match 50.0%; Score 3; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 PPV 6  
DB 5 PPV 7  
  
RESULT 19  
Q8J026 PRELIMINARY; PRT; 16 AA.  
ID Q8J026;  
AC Q8J026;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE MRGX (Fragment).  
GN MRGX.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Myokai F., Oyama M.;  
RT "Mortality Factor Related Gene X 102 5'.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB050778; BAC22659.1; -  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1733 MW; FF7D79CB38B88EF6 CRC64;  
  
Query Match 50.0%; Score 3; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 SQP 4  
DB 8 SQP 10  
  
RESULT 20  
Q9S8Y6 PRELIMINARY; PRT; 16 AA.  
ID Q9S8Y6;  
AC Q9S8Y6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).  
OS Lupinus arboreus (Tree lupine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genistae; Lupinus.  
OX NCBI\_TaxID=3872;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92344803; PubMed=1368361;  
RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,  
RA Farnden K.J.;  
RL Phytochemistry 31:1519-1527(1992).  
SQ SEQUENCE 16 AA; 1499 MW; 901363908527BF0B CRC64;  
  
Query Match 50.0%; Score 3; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DSQ 3  
DB 8 DSQ 10

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RESULT 21
Q14001 ID Q14001 PRELIMINARY; PRT; 17 AA.
AC Q14001;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclic nucleotide phosphodiesterase (Fragment).
GN CGIPDE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97079687; PubMed=8921398;
RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;
RT "Molecular cloning and chromosomal assignment of the human homologue
of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved
in fat metabolism located at 11p15.1.";
RL Genomics 37:211-218(1996).
DR ENBL, X95522; CAA64776.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5
Db 15 QPP 17

RESULT 22
Q9UCL9 ID Q9UCL9 PRELIMINARY; PRT; 17 AA.
AC Q9UCL9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Proteoglycan 80 kDa polypeptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93054750; PubMed=1429726;
RA Perides G., Rahemtulla F., Lane W.S., Asher R.A., Bignami A.;
RT "Isolation of a large aggregating proteoglycan from human brain.";
RL J. Biol. Chem. 267:23883-23887(1992).
SQ SEQUENCE 17 AA; 1771 MW; 1BD8A561B2F71614 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6
Db 10 PPV 12

RESULT 23
Q9QVC2 ID Q9QVC2 PRELIMINARY; PRT; 17 AA.
AC Q9QVC2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Kallikrein light chain N-terminus (Fragment).
OS Rattus sp.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92329502; PubMed=1320938;
RA Wang C., Tang C.Q., Zhou G.X., Chao L., Chao J.;
RT "Biochemical characterization and substrate specificity of rat
prostate kallikrein (S3): comparison with tissue kallikrein, tonin and
T-kininogenase.";
RL Biochim. Biophys. Acta 1121:309-316(1992).
DR HSPP; P36368; IAO5.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1852 MW; A403B510DF5C096D CRC64;

Query Match 50.0%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4
Db 11 SQP 13

RESULT 24
Q9TWV6 ID Q9TWV6 PRELIMINARY; PRT; 18 AA.
AC Q9TWV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE APLYSIA gonad lectin (Fragment).
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anasipidea;
OC Aplysioidea; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE.
RX MEDLINE=93057436; PubMed=1431843;
RA Wilson M.P., Carrow G.M., Levitan I.B.;
RT "Modulation of growth of Aplysia neurons by an endogenous lectin.";
RL J. Neurobiol. 23:739-750(1992).
SQ SEQUENCE 18 AA; 2105 MW; 5652840B573057D8 CRC64;

Query Match 50.0%; Score 3; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4
Db 1 SQP 3

RESULT 25
Q46592 ID Q46592 PRELIMINARY; PRT; 18 AA.
AC Q46592;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Prolactin receptor short form (Fragment).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98001468; PubMed=9343303;
RA Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning

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RT and genomic analysis reveal that the two forms arise by different  
 RT alternative splicing mechanisms in ruminants and in rodents.";

RL J. Mol. Endocrinol. 19:109-120(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Bignon C.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RE EMBL; AF042781; AAB97749.1; -

KW Receptor.

FT NON TER 1

SQ SEQUENCE 18 AA; 2086 MW; 8C29297FA8816328D CRC64;

Query Match 50.0%; Score 3; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4

Db 9 SQP 11

RESULT 26

Q9CUP4

ID Q9CUP4 PRELIMINARY; PRT; 18 AA.

AC Q9CUP4;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE 4930428B01Rik protein (Fragment).

GN 4930428B01Rik.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RE MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaado I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.,

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK015215; BAB29751.1; -

DR MGI; MGI:1921104; 4930428B01Rik.

FT NON TER 1

SQ SEQUENCE 18 AA; 1878 MW; 35F8F315D79C93D CRC64;

Query Match 50.0%; Score 3; DB 11; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4

Db 4 SQP 6

RESULT 27

Q9JIE9

ID Q9JIE9 PRELIMINARY; PRT; 18 AA.

AC Q9JIE9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Protein arginine N-methyltransferase 1 (Fragment).

GN MGMT1

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RE MEDLINE=20307889; PubMed=10848611;

RA Pawlak M.R., Scherer C.A., Chen J., Roshon M.J., Ruley H.E.;

RT "Arginine N-methyltransferase 1 is required for early postimplantation

RT mouse development, but cells deficient in the enzyme are viable.";

RL Mol. Cell. Biol. 20:4859-4869(2000).

DR EMBL; AF232718; AAF37294.1; -

KW Methyltransferase; Transferase.

FT NON TER 1

FT NON TER 18

SQ SEQUENCE 18 AA; 1931 MW; 392E2C312C4A8372 CRC64;

Query Match 50.0%; Score 3; DB 11; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5

Db 13 QPP 15

RESULT 28

Q90790

ID Q90790 PRELIMINARY; PRT; 18 AA.

AC Q90790;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Gene encoding alpha-1 type III collagen. This is exon 16.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RE MEDLINE=83135706; PubMed=6298201;

RA Yamada Y., Mudryj M., Sullivan M., de Crombrughe B.;

RT "Isolation and characterization of a genomic clone encoding chick

RT alpha-1 type III collagen.";

RL J. Biol. Chem. 258:2758-2761(1983).

DR EMBL; V00391; CAA23689.1; -

KW Collagen.

SQ SEQUENCE 18 AA; 1732 MW; 439C34D5A9329EBC CRC64;

Query Match 50.0%; Score 3; DB 13; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6

Db 14 PPV 16

RESULT 29

Q9UCL3

ID Q9UCL3 PRELIMINARY; PRT; 19 AA.

AC Q9UCL3;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Insulin-like growth factor binding protein 34 kDa form (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93091816; PubMed=1726837;  
 RA Roghani M., Segovia B., Whitechurch O., Binoux M.;  
 RT "Purification from human cerebrospinal fluid of insulin-like growth  
 factor binding proteins (IGFBPs). Isolation of IGFBP-2, an altered form  
 of IGFBP-3 and a new IGFBP species.";  
 RT Growth Regul. 1:125-130(1991).  
 SQ SEQUENCE 19 AA; 2032 MW; A7497C418219088 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 ||||  
 DB 17 PPV 19

## RESULT 30

Q9BX20 PRELIMINARY; PRT; 19 AA.  
 ID Q9BX20  
 AC Q9BX20  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE BA470C13.1 (Hypothetical protein KIAA1272) (Fragment).  
 GN BA470C13.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Peck A.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL161658; CAC36066.1; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 19 AA; 2211 MW; 2BB8DB0ABFF5A5C0 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 ||||  
 DB 17 PPV 19

## RESULT 31

Q16184 PRELIMINARY; PRT; 19 AA.  
 ID Q16184  
 AC Q16184  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Phosphofructokinase-M (EC 2.7.1.11) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94311311; PubMed=8037209;  
 RA Sherman J.B., Raben N., Nicastri C., Argov Z., Nakajima H.,  
 RA Adams E.M., Eng C.M., Cowan T.M., Plotz P.H.;

RT "Common mutations in the phosphofructokinase-M gene in Ashkenazi  
 RT Jewish patients with glycogenesis VII--and their population  
 RT frequency.";  
 RL Am. J. Hum. Genet. 55:305-313(1994).  
 DR EMBL; S72312; AAB31343.2; -.  
 KW Kinase; Transferase.  
 RN NON TER 1  
 SQ SEQUENCE 19 AA; 2081 MW; 20175220E0432A63 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
 ||||  
 DB 3 SQP 5

## RESULT 32

Q15610 PRELIMINARY; PRT; 19 AA.  
 ID Q15610  
 AC Q15610  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Topoisomerase I (Fragment).  
 GN TOP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9109302; PubMed=2176592;  
 RA Kunze N., Klein M., Richter A., Knippers R.;  
 RT "Structural characterisation of the human DNA topoisomerase I gene  
 RT promoter.";  
 RL Eur. J. Biochem. 194:323-330(1990).  
 DR EMBL; X52601; CAA36834.1; -.  
 KW Isomerase.  
 RN NON TER 19  
 SQ SEQUENCE 19 AA; 2236 MW; 47BDB36F44FFEEFB CRC64;

Query Match 50.0%; Score 3; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3  
 ||||  
 DB 9 DSQ 11

## RESULT 33

Q8MCI9 PRELIMINARY; PRT; 19 AA.  
 ID Q8MCI9  
 AC Q8MCI9  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit  
 DE (EC 4.1.1.39) (Fragment).  
 GN RBCS  
 OS Aulacoseira baicalensis.  
 OG Chloroplast.  
 OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
 OC Coscinodiscophycidae; Aulacoseiraceae; Aulacoseira.  
 OX NCBI\_TaxID=202469;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sherbakova T.A., Likhoshvay Y.V., Medlin L.K.;  
 RT "Correlation of hypothesis on the evolution of Aulacoseira species  
 RT from Lake Baikal based on morphological and genetic data.";  
 RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

GN RBCS.  
OS Aulacoseira skvortzowii.  
OG Chloroplast.  
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
OC Coscinodiscophycidae; Aulacoseiraceae; Aulacoseira.  
OX NCBI\_TaxID=202471;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sherbakova T.A., Likhoshway Y.V., Medlin L.K.;  
RT "Correlation of hypothesis on the evolution of Aulacoseira species  
from Lake Baikal based on morphological and genetic data.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DE EMBL; AF522279; AAN03947.1;  
DR InterPro; IPR000894; RuBisCO\_small.  
DR Pfam; PF00101; RuBisCO\_small; 1.  
KW Lyase; Chloroplast.  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2172 MW; 47AEBE620D7FF5A2 CRC64;  
  
Query Match 50.0%; Score 3; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DSQ 3  
Db 16 DSQ 18  
  
RESULT 34  
Q8LVH6 PRELIMINARY; PRT; 19 AA.  
AC Q8LVH6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit  
DE (EC 4.1.1.39) (Fragment).  
GN RBCS.  
OS Aulacoseira islandica.  
OG Chloroplast.  
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
OC Coscinodiscophycidae; Aulacoseiraceae; Aulacoseira.  
OX NCBI\_TaxID=202470;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sherbakova T.A., Likhoshway Y.V., Medlin L.K.;  
RT "Correlation of hypothesis on the evolution of Aulacoseira species  
from Lake Baikal based on morphological and genetic data.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DE EMBL; AF522280; AAN03949.1;  
DR InterPro; IPR000894; RuBisCO\_small.  
DR Pfam; PF00101; RuBisCO\_small; 1.  
KW Lyase; Chloroplast.  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2172 MW; 47AEBE620D7FF5A2 CRC64;  
  
Query Match 50.0%; Score 3; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DSQ 3  
Db 16 DSQ 18  
  
RESULT 35  
Q8MCJ2 PRELIMINARY; PRT; 19 AA.  
AC Q8MCJ2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit  
DE (EC 4.1.1.39) (Fragment).  
GN RBCS.  
OS Aulacoseira skvortzowii.  
OG Chloroplast.  
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
OC Coscinodiscophycidae; Aulacoseiraceae; Aulacoseira.  
OX NCBI\_TaxID=202471;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sherbakova T.A., Likhoshway Y.V., Medlin L.K.;  
RT "Correlation of hypothesis on the evolution of Aulacoseira species  
from Lake Baikal based on morphological and genetic data.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DE EMBL; AF522279; AAN03947.1;  
DR InterPro; IPR000894; RuBisCO\_small.  
DR Pfam; PF00101; RuBisCO\_small; 1.  
KW Lyase; Chloroplast.  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2172 MW; 47AEBE620D7FF5A2 CRC64;  
  
Query Match 50.0%; Score 3; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DSQ 3  
Db 16 DSQ 18  
  
RESULT 36  
Q9S8G9 PRELIMINARY; PRT; 19 AA.  
AC Q9S8G9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Proline-rich protein (fragment).  
DE Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurooids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
OC Psophocarpus.  
OX NCBI\_TaxID=3891;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=95277008; PubMed=7757337;  
RA Saaka M., Hayakawa H.;  
RT "Specific secretion of proline-rich proteins by salt-adapted winged  
bean cells";  
RL Plant Cell Physiol. 36:441-446(1995).  
SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0F8779A CRC64;  
  
Query Match 50.0%; Score 3; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 PPV 6  
Db 5 PPV 7  
  
RESULT 37  
P82941 PRELIMINARY; PRT; 19 AA.  
AC P82941;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Unknown endosperm protein V (fragment).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
OC Triticaceae; Hordeum.  
OX NCBI\_TaxID=4513;

DR EMBL; AF522281; AAN03951.1; --  
DR InterPro; IPR000894; RuBisCO\_small.  
DR Pfam; PF00101; RuBisCO\_small; 1.  
KW Lyase; Chloroplast.  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2172 MW; 47AEBE620D7FF5A2 CRC64;  
  
Query Match 50.0%; Score 3; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DSQ 3  
Db 16 DSQ 18  
  
RESULT 34  
Q8LVH6 PRELIMINARY; PRT; 19 AA.  
AC Q8LVH6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit  
DE (EC 4.1.1.39) (Fragment).  
GN RBCS.  
OS Aulacoseira islandica.  
OG Chloroplast.  
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
OC Coscinodiscophycidae; Aulacoseiraceae; Aulacoseira.  
OX NCBI\_TaxID=202470;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sherbakova T.A., Likhoshway Y.V., Medlin L.K.;  
RT "Correlation of hypothesis on the evolution of Aulacoseira species  
from Lake Baikal based on morphological and genetic data.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DE EMBL; AF522280; AAN03949.1;  
DR InterPro; IPR000894; RuBisCO\_small.  
DR Pfam; PF00101; RuBisCO\_small; 1.  
KW Lyase; Chloroplast.  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2172 MW; 47AEBE620D7FF5A2 CRC64;  
  
Query Match 50.0%; Score 3; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DSQ 3  
Db 16 DSQ 18  
  
RESULT 35  
Q8MCJ2 PRELIMINARY; PRT; 19 AA.  
AC Q8MCJ2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit  
DE (EC 4.1.1.39) (Fragment).  
GN RBCS.  
OS Aulacoseira skvortzowii.  
OG Chloroplast.  
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
OC Coscinodiscophycidae; Aulacoseiraceae; Aulacoseira.  
OX NCBI\_TaxID=202471;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sherbakova T.A., Likhoshway Y.V., Medlin L.K.;  
RT "Correlation of hypothesis on the evolution of Aulacoseira species  
from Lake Baikal based on morphological and genetic data.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DE EMBL; AF522279; AAN03947.1;  
DR InterPro; IPR000894; RuBisCO\_small.  
DR Pfam; PF00101; RuBisCO\_small; 1.  
KW Lyase; Chloroplast.  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2172 MW; 47AEBE620D7FF5A2 CRC64;  
  
Query Match 50.0%; Score 3; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DSQ 3  
Db 16 DSQ 18  
  
RESULT 36  
Q9S8G9 PRELIMINARY; PRT; 19 AA.  
AC Q9S8G9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Proline-rich protein (fragment).  
DE Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurooids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
OC Psophocarpus.  
OX NCBI\_TaxID=3891;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=95277008; PubMed=7757337;  
RA Saaka M., Hayakawa H.;  
RT "Specific secretion of proline-rich proteins by salt-adapted winged  
bean cells";  
RL Plant Cell Physiol. 36:441-446(1995).  
SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0F8779A CRC64;  
  
Query Match 50.0%; Score 3; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 PPV 6  
Db 5 PPV 7  
  
RESULT 37  
P82941 PRELIMINARY; PRT; 19 AA.  
AC P82941;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Unknown endosperm protein V (fragment).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
OC Triticaceae; Hordeum.  
OX NCBI\_TaxID=4513;

RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. BOMI; TISSUE=Starchy endosperm;  
 RX MEDLINE=21088911; PubMed=11271488;  
 RA Kristoffersen H.E., Flengrød R.;  
 RT "Separation and characterization of basic barley seed proteins.";   
 RL Electrophoresis 21:3693-3700(2000).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN  
 CC PROTEIN IS: 7.0, ITS MW IS: 19.9 KDA.  
 FT NON TER 19  
 SQ SEQUENCE 19 AA; 2026 MW; 05398748ADC602E0 CRC64;

Query Match 50.0%; Score 3; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
 DB 3 PPV 5

## RESULT 38

Q9PRN4 PRELIMINARY; PRT; 19 AA.  
 ID Q9PRN4  
 AC Q9PRN4; (Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Melanotropin MSH-A.  
 OS Petromyzon marinus (Sea lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
 OX NCBI\_TaxID=7757;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=96122167; PubMed=8537171;  
 RA Takahashi A., Anemiyi Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,  
 RA Kawachi H.;  
 RT "Isolation and characterization of melanotropins from lamprey  
 RT pituitary glands.";   
 RL Int. J. Pept. Protein Res. 46:197-204(1995).  
 SQ SEQUENCE 19 AA; 2400 MW; 0F4CD35F7E0BC340 CRC64;

Query Match 50.0%; Score 3; DB 13; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
 DB 14 QPP 16

## RESULT 39

Q96B47 PRELIMINARY; PRT; 20 AA.  
 ID Q96B47  
 AC Q96B47; (Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Hypothetical protein (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bladder;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC015979; AH15979.1; -  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 20 AA; 1941 MW; E5B4330FF5048371 CRC64;

Query Match 50.0%; Score 3; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
 DB 14 QPP 16

Query Match 50.0%; Score 3; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3  
 DB 18 DSQ 20

## RESULT 40

Q8TE41 PRELIMINARY; PRT; 20 AA.  
 ID Q8TE41  
 AC Q8TE41; (Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DE Truncated steroid 11beta-hydroxylase (fragment).  
 GN CYP11B1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Penachioni J.Y., de Castro M., Bachega T.A., Mendonca B.B.,  
 RA de Mello M.P.;  
 RT "CYP11B1 new mutations R404-C and G267S leading to 11beta-hydroxylase  
 RT deficiency in Brazilian patients.";   
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Penachioni J.Y.;  
 RT "Mutations and polymorphisms in CYP11B1 human gene in individuals with  
 RT 11-beta-Hydroxylase deficiency.";   
 RL Thesis (2001), Department of College of Medical Sciences,  
 RL Campinas State University, Campinas, SP, Brazil.  
 DR EMBL; AJ431375; CAD24087.1; -  
 FT NON TER 1  
 SQ SEQUENCE 20 AA; 2130 MW; 78B715D5A3CD45BF CRC64;

Query Match 50.0%; Score 3; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
 DB 12 SQP 14

## RESULT 41

Q9TRH7 PRELIMINARY; PRT; 20 AA.  
 ID Q9TRH7  
 AC Q9TRH7; (Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Haptoglobin 17 kDa subunit (fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93213965; PubMed=8461423;  
 RA Tosa N., Morimatsu M., Nakagawa M., Miyoshi F., Uchida E., Niiyama M.,  
 RA Syuto B., Saito M.;  
 RT "Purification and identification of a serum protein increased by  
 RT anthelmintic drugs for Dirofilaria immitis in dogs.";   
 RL J. Vet. Med. Sci. 55:27-31(1993).  
 SQ SEQUENCE 20 AA; 2081 MW; 1CA608DBF58365F5 CRC64;

Query Match 50.0%; Score 3; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
 DB 14 QPP 16

Best Local Similarity 100.0%; Pred. No. 2.9e+03; Mismatches 0; Indels 0; Gaps 0;	
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 4 PPV 6	
DB 18 PPV 20	
RESULT 42	
Q9S8H0	PRELIMINARY; PRT; 20 AA.
ID Q9S8H0	SEQUENCE FROM N.A.
AC Q9S8H0	STRAIN=ATCC 25586;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)	MEDLINE=21889109;
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)	Ra Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
DE Proline-rich protein (fragment).	Vasileva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
OS Paophocarpus tetragonolobus (Goa bean) (Asparagaceae)	Larsen N., D'Souza M., Malunas T., Pusch G., Haselkorn R.,
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Fonstein M., Kyripides N., Overbeek R.;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	RT "Genome sequence and analysis of the oral bacterium Fusobacterium
OC eucorids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;	nucleatum strain ATCC 25586.";
OC Paophocarpus.	RT J. Bacteriol. 184:2005-2018(2002).
OX NCBI_TaxID=3891;	DR EMBL; A010528; AAL94347.1; -
RN [1]	KW Hypothetical protein; Complete proteome.
RP SEQUENCE.	SQ SEQUENCE 20 AA; 2542 MW; 15BD7516B34C2A14 CRC64;
RX MEDLINE=95277008; PubMed=7757337;	
RA Esaka M., Hayakawa H.;	Query Match 50.0%; Score 3; DB 16; Length 20;
RT "Specific secretion of proline-rich proteins by salt-adapted winged	Best Local Similarity 100.0%; Pred. No. 2.9e+03;
RT bean cells.";	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RL Plant Cell Physiol. 36:441-446(1995).	
SQ SEQUENCE 20 AA; 2246 MW; AEE9ED45C4F0F877 CRC64;	
QY 4 PPV 6	
DB 5 PPV 7	
RESULT 43	
Q9QUX7	PRELIMINARY; PRT; 20 AA.
ID Q9QUX7	SEQUENCE FROM N.A.
AC Q9QUX7	STRAIN=ATCC 33384;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)	MEDLINE=96355846; PubMed=8751884;
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	Kraig E.;
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)	RT "cis elements and trans factors are both important in strain-specific
DE Carboxylesterase isozyme (fragment).	regulation of the leukotoxin gene in Actinobacillus
OS Rattus sp.	actinomycetemcomitans.";
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RL Infect. Immun. 64:3451-3460(1996).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	DR EMBL; U51862; AAB88721.1; -
OX NCBI_TaxID=10118;	FT NON TER 1
RN [1]	SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
RP SEQUENCE.	
RX MEDLINE=96170127; PubMed=8597091;	Query Match 33.3%; Score 2; DB 2; Length 7;
RA Satoh T., Hosokawa M.;	Best Local Similarity 100.0%; Pred. No. 8.3e+05;
RT "Molecular aspects of carboxylesterase isoforms in comparison with	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RT other esterases.";	
RL Toxicol. Lett. 82:439-445(1995).	
SQ SEQUENCE 20 AA; 2133 MW; 435160FFA80E086D CRC64;	
QY 4 PPV 6	
DB 5 PPV 7	
RESULT 44	
Q8RGY4	PRELIMINARY; PRT; 20 AA.
ID Q8RGY4	SEQUENCE FROM N.A.
AC Q8RGY4	STRAIN=ATCC 33384;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)	MEDLINE=96355846; PubMed=8751884;
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)	Kraig E.;
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	RT "cis elements and trans factors are both important in strain-specific
DE Hypothetical protein FN0141.	regulation of the leukotoxin gene in Actinobacillus
OS Fusobacterium nucleatum (subsp. nucleatum).	actinomycetemcomitans.";
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;	RL Infect. Immun. 64:3451-3460(1996).
OC Fusobacterium.	DR EMBL; U51862; AAB88721.1; -
OX NCBI_TaxID=76856;	FT NON TER 1
RN [1]	SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
RP SEQUENCE FROM N.A.	
RC STRAIN=ATCC 25586;	Query Match 33.3%; Score 2; DB 2; Length 7;
RX MEDLINE=21889109;	Best Local Similarity 100.0%; Pred. No. 2.9e+03;
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,	
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,	
RA Larsen N., D'Souza M., Malunas T., Pusch G., Haselkorn R.,	
RA Fonstein M., Kyripides N., Overbeek R.;	
RT "Genome sequence and analysis of the oral bacterium Fusobacterium	
nucleatum strain ATCC 25586.";	
RT J. Bacteriol. 184:2005-2018(2002).	
DR EMBL; A010528; AAL94347.1; -	
KW Hypothetical protein; Complete proteome.	
SQ SEQUENCE 20 AA; 2542 MW; 15BD7516B34C2A14 CRC64;	
QY 3 QPP 5	
DB 12 QPP 14	
RESULT 45	
OS0556	PRELIMINARY; PRT; 7 AA.
ID OS0556	SEQUENCE FROM N.A.
AC OS0556	STRAIN=ATCC 33384;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)	MEDLINE=96355846; PubMed=8751884;
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)	Kraig E.;
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	RT "cis elements and trans factors are both important in strain-specific
DE GlyA (fragment).	regulation of the leukotoxin gene in Actinobacillus
GN GLYA.	actinomycetemcomitans.";
OS Actinobacillus actinomycetemcomitans (Haemophilus	RL Infect. Immun. 64:3451-3460(1996).
OC actinomycetemcomitans).	DR EMBL; U51862; AAB88721.1; -
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;	FT NON TER 1
OC Pasteurellaceae; Actinobacillus.	SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
OX NCBI_TaxID=714;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=ATCC 33384;	
RX MEDLINE=96355846; PubMed=8751884;	
RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,	
RA Kraig E.;	
RT "cis elements and trans factors are both important in strain-specific	
regulation of the leukotoxin gene in Actinobacillus	
actinomycetemcomitans.";	
RL Infect. Immun. 64:3451-3460(1996).	
DR EMBL; U51862; AAB88721.1; -	
FT NON TER 1	
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;	
QY 5 PV 6	
DB 4 PV 5	
RESULT 46	



P92214  
 ID P92214 PRELIMINARY; PRT; 7 AA.  
 AC P92214  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Amblyopyrum muticum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Amblyopyrum.  
 OX NCBI\_TaxID=4595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5572; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77756; CAB01346.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 33.3%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 DB 1 PP 2  
 RESULT 47  
 P92393  
 ID P92393 PRELIMINARY; PRT; 7 AA.  
 AC P92393  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Hordeum vulgare (Barley).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H3139; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77764; CAB01370.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 33.3%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 DB 1 PP 2  
 P92403  
 ID P92403 PRELIMINARY; PRT; 7 AA.  
 AC P92403  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Lophopyrum.  
 OX NCBI\_TaxID=4588;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6692; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77743; CAB01307.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 33.3%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 DB 1 PP 2  
 P92427  
 ID P92427 PRELIMINARY; PRT; 7 AA.  
 AC P92427  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Peridictyon sanctum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Peridictyon.  
 OX NCBI\_TaxID=37683;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5575; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77749; CAB01325.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 33.3%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 DB 1 PP 2

RESULT 48  
 P92403  
 ID P92403 PRELIMINARY; PRT; 7 AA.  
 AC P92403  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Lophopyrum.  
 OX NCBI\_TaxID=4588;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6692; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77743; CAB01307.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 33.3%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 DB 1 PP 2  
 RESULT 49  
 P92427  
 ID P92427 PRELIMINARY; PRT; 7 AA.  
 AC P92427  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Peridictyon sanctum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Peridictyon.  
 OX NCBI\_TaxID=37683;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5575; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77749; CAB01325.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 Query Match 33.3%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 DB 1 PP 2

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RESULT 50
P92430 PRELIMINARY; PRT; 7 AA.
ID P92430;
AC P92430;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Aegilops tauschii (Aegilops squarrosa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6668; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77758; CAB01352.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
Db 1 PP 2

RESULT 51
P92221 PRELIMINARY; PRT; 7 AA.
ID P92221;
AC P92221;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Bromus inermis (Smooth brome grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Bromaeae; Bromus.
OX NCBI_TaxID=15371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OSA414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01355.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
Db 1 PP 2

RESULT 52
P92425 PRELIMINARY; PRT; 7 AA.
ID P92425;
AC P92425;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Pseudoroegneria.
OX NCBI_TaxID=4604;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H9082; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77744; CAB01310.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
Db 1 PP 2

RESULT 53
P92381 PRELIMINARY; PRT; 7 AA.
ID P92381;
AC P92381;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum brachyantherum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=52712;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77761; CAB01361.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
Db 1 PP 2

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Db 1 PP 2

## RESULT 54

P92387 ID P92387 PRELIMINARY; PRT; 7 AA.  
 AC P92387; 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Henrardia persica.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Henrardia.  
 OX NCBI\_TaxID=37678;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5556; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77748; CAB01322.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5

Db 1 PP 2

## RESULT 55

P92210 ID P92210 PRELIMINARY; PRT; 7 AA.  
 AC P92210; 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Agropyron cristatum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Agropyron.  
 OX NCBI\_TaxID=4593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H4349; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77771; CAB01391.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5

Db 1 PP 2

## RESULT 56

P92440 ID P92440 PRELIMINARY; PRT; 7 AA.  
 AC P92440; 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Thinopyrum bessarabicum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Thinopyrum.  
 OX NCBI\_TaxID=4601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6725; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77769; CAB01385.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5

Db 1 PP 2

## RESULT 57

P92218 ID P92218 PRELIMINARY; PRT; 7 AA.  
 AC P92218; 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Australopyrum retrofractum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Australopyrum.  
 OX NCBI\_TaxID=4597;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6723; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77767; CAB01379.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5

QY 4 PP 5  
||  
Db 1 PP 2

RESULT 60

P92442 ID P92442 PRELIMINARY; PRT; 7 AA.  
AC P92442;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Taeniatherum caput-medusae (Medusahead).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Taeniatherum.  
OX NCBI\_TaxID=37687;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H10254; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77760; CAB01358.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
||  
Db 1 PP 2

RESULT 61

P92226 ID P92226 PRELIMINARY; PRT; 7 AA.  
AC P92226;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Crithopsis delileana.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Crithopsis.  
OX NCBI\_TaxID=37674;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5558; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77751; CAB01331.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
||  
Db 1 PP 2

RESULT 58

P92390 ID P92390 PRELIMINARY; PRT; 7 AA.  
AC P92390;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Heteranthellium piliferum.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Heteranthellium.  
OX NCBI\_TaxID=37679;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5557; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77750; CAB01328.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
||  
Db 1 PP 2

RESULT 59

P92372 ID P92372 PRELIMINARY; PRT; 7 AA.  
AC P92372;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Haynaldia villosa.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACAD clade; Panicoideae; Andropogoneae; Haynaldia.  
OX NCBI\_TaxID=40247;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5561; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77741; CAB01301.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
||  
Db 1 PP 2

## RESULT 62

P92385 PRELIMINARY; PRT; 7 AA.  
ID P92385; P92383;  
AC P92385; P92383; (T-EMBLrel. 03, Created)  
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)  
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)  
DE 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Hordeum marinum (Seaside barley).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OC NCBI\_TaxID=4519;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H299, and H801; TISSUE=Leaf;  
RA Petersen G., Seberg O.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z77763; CAB01367.1; --  
DR EMBL; Z77762; CAB01364.1; --  
KW Chloroplast; Ribosomal protein.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5  
||  
Db 1 PP 2

## RESULT 63

P92421 PRELIMINARY; PRT; 7 AA.  
ID P92421; P92419;  
AC P92421; P92419; (T-EMBLrel. 03, Created)  
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)  
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)  
DE 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Paathyoestachys fragilis.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Paathyoestachys.  
OC NCBI\_TaxID=37729;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H4372, and H917; TISSUE=Leaf;  
RA Petersen G., Seberg O.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z77753; CAB01337.1; --  
DR EMBL; Z77752; CAB01334.1; --  
KW Chloroplast; Ribosomal protein.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 33.3%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5

Db 1 PP 2  
||

## RESULT 64

Q9ZEZ9 PRELIMINARY; PRT; 8 AA.  
ID Q9ZEZ9;  
AC Q9ZEZ9; (T-EMBLrel. 10, Created)  
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)  
DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).  
GN LEUA.  
OS Buchnera aphidicola.  
OC Plasmid pBRC1.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Buchnera.  
OC NCBI\_TaxID=9;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99028904; PubMed=9812361;  
RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;  
RT "Structure and evolution of the leucine plasmids carried by the  
RT endosymbiont (Buchnera aphidicola) from aphids of the family  
RT Aphididae."  
RL FEMS Microbiol. Lett. 168:43-49(1998).  
DR EMBL; AJ006874; CAA07290.1; --  
KW Lyase; Plasmid.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3  
||  
Db 3 SQ 4

## RESULT 65

Q8RSR3 PRELIMINARY; PRT; 8 AA.  
ID Q8RSR3;  
AC Q8RSR3; (T-EMBLrel. 21, Created)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
DE PduG protein (Fragment).  
GN PDUG.  
OS Lactobacillus collinoides.  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OC NCBI\_TaxID=33960;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LUG 18850;  
RA Sauvageot N., Gouffi K., Laplace J.M., Auffray Y.;  
RT "Characterisation of the diol dehydratase pdu operon of Lactobacillus  
RT collinoides."  
RL FEMS Microbiol. Lett. 0:0-0(0).  
DR EMBL; AJ297723; CAD01093.1; --  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 882 MW; ECA40B05BAB5BDD6 CRC64;

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DS 2  
||  
Db 4 DS 5

Q15890	PRELIMINARY;	8 AA.	
ID	Q15890		
AC	Q15890;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	(Clone XP19G12A) (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Placenta;		
RA	Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,		
RA	Coolbaugh M.I., Chnault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,		
RA	Caskey C.T.H.;		
RT	"Isolation of chromosome-specific genes by reciprocal probing of		
RT	arrayed cDNAs and cosmid libraries.";		
RL	Hum. Mol. Genet. 0:0-0(1995).		
DR	EMBL; L32083; AAA73880.1; --		
FT	NON_TER 1 1		
FT	NON_TER 8 8		
SQ	SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;		
	Query Match 33.3%; Score 2; DB 4; Length 8;		
	Best Local Similarity 100.0%; Pred. No. 8.3e+05;		
	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	2 SQ 3		
Db	5 SQ 6		
RESULT 69			
Q15893	PRELIMINARY;	8 AA.	
ID	Q15893		
AC	Q15893;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	(Clone XP587A) (Fragment).		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Placenta;		
RA	Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,		
RA	Coolbaugh M.I., Chnault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,		
RA	Caskey C.T.H.;		
RT	"Isolation of chromosome-specific genes by reciprocal probing of		
RT	arrayed cDNAs and cosmid libraries.";		
RL	Hum. Mol. Genet. 0:0-0(1995).		
DR	EMBL; L32073; AAA73883.1; --		
FT	NON_TER 1 1		
FT	NON_TER 8 8		
SQ	SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;		
	Query Match 33.3%; Score 2; DB 4; Length 8;		
	Best Local Similarity 100.0%; Pred. No. 8.3e+05;		
	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	2 SQ 3		
Db	1 SQ 2		
RESULT 70			
Q9TRX8	PRELIMINARY;	8 AA.	
ID	Q9TRX8		
AC	Q9TRX8;		

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Osteopontin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RX MEDLINE=91282766; PubMed=1676261;
RA Prince C.W., Dickie D., Krundieck C.L.;
RT "Osteopontin, a substrate for transglutaminase and factor XIII
RT activity.";
RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;

Query Match 33.3%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PV 6
DB 2 PV 3

RESULT 71
ID Q29801 PRELIMINARY; PRT; 8 AA.
AC Q29801;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HLA class II DR-beta chain (Fragment).
GN HLA-DRB1*15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175156; PubMed=9110934;
RA Svensson A.C., Setterblad N., Pihlgren U., Rask L., Andersson G.;
RT "Evolutionary relationship between different human major
RT histocompatibility complex HLA-DR haplotypes.";
RL Immunogenetics 43:304-314(1996).
DR EMBL; X88791; CAA61270.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 953 MW; C2C6C5B9CAA731AA CRC64;

Query Match 33.3%; Score 2; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3
DB 6 SQ 7

RESULT 72
ID Q29812 PRELIMINARY; PRT; 8 AA.
AC Q29812;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HLA class II DR-beta chain (Fragment).
GN HLA-DRB6*01.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175156; PubMed=9110934;
RA Svensson A.C., Setterblad N., Pihlgren U., Rask L., Andersson G.;
RT "Evolutionary relationship between different human major
RT histocompatibility complex HLA-DR haplotypes.";
RL Immunogenetics 43:304-314(1996).
DR EMBL; X88794; CAA61273.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 953 MW; C2C6C5B9CAA731AA CRC64;

Query Match 33.3%; Score 2; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3
DB 6 SQ 7

RESULT 73
ID Q29797 PRELIMINARY; PRT; 8 AA.
AC Q29797;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HLA class II DR-beta chain (Fragment).
GN HLA-DRB1*01.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175156; PubMed=9110934;
RA Svensson A.C., Setterblad N., Pihlgren U., Rask L., Andersson G.;
RT "Evolutionary relationship between different human major
RT histocompatibility complex HLA-DR haplotypes.";
RL Immunogenetics 43:304-314(1996).
DR EMBL; X88793; CAA61272.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 953 MW; C2C6C5B9CAA731AA CRC64;

Query Match 33.3%; Score 2; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3
DB 6 SQ 7

RESULT 74
ID Q94VF3 PRELIMINARY; PRT; 8 AA.
AC Q94VF3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus keithhornei.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169844;
RN [1]

```

RP SEQUENCE FROM N.A.  
RA Ast J.C.;  
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";  
RL Cladistics 17:0-0(2001).  
DR EMBL; AF407508; AAL10078.1; -.  
KW Mitochondrion.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 950 MW; F171E9D5BAB411A6 CRC64;  
  
Query Match 33.3%; Score 2; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DS 2  
DB 4 DS 5  
  
RESULT 75  
QBL802 PRELIMINARY; PRT; 8 AA.  
AC QBL802;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Pat (Fragment).  
GN PAT.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ronning S.B., Berdal K.G., Vaitilingom M.M., Holst-Jensen A.;  
RT "Transformation event-specific quantitative real-time PCR for  
RT genetically modified Bt11 maize (Zea mays) and estimation of the  
RT impact of exogenous DNA on the limit of quantification.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY123624; AAM89275.1; -.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 909 MW; 6046C1B2D77412D7 CRC64;  
  
Query Match 33.3%; Score 2; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 PV 6  
DB 1 PV 2  
  
Search completed: November 25, 2003, 18:25:36  
Job time : 15.5074 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 19.4362 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-13

Perfect score: 6  
Sequence: 1 DSQPPV 6

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	22	Colostrinin derive
2	6	100.0	6	22	Colostrinin peptid
3	6	100.0	6	22	Colostrinin peptid
4	6	100.0	6	22	Ewe colostrinin pe
5	6	100.0	6	23	Colostrinin consti
6	6	100.0	6	23	Colostrinin consti
7	6	100.0	6	23	Neural cell regula
8	6	100.0	10	22	Ewe colostrinin pe
9	4	66.7	7	10	Sequence of part o

10	4	66.7	7	19	AAW70877	ICAM-1 peptide fra
11	4	66.7	7	23	AB876160	ICAM-1 sequence re
12	4	66.7	8	20	AAV40611	Al derivative #2,
13	4	66.7	8	20	AAW67834	Human secreted pro
14	4	66.7	8	21	AAW29950	Scaffold proteind S
15	4	66.7	8	22	ABB51285	Human secreted pro
16	4	66.7	9	18	AAW29260	Soybean hydrolasat
17	4	66.7	9	21	AAW07745	Repeat sequence fr
18	4	66.7	9	23	AAU82116	Human papillomavir
19	4	66.7	9	23	AAU82223	Human papillomavir
20	4	66.7	9	23	AAU82239	Human papillomavir
21	4	66.7	9	23	AAU82291	Human papillomavir
22	4	66.7	9	23	AAU82302	Human papillomavir
23	4	66.7	9	23	AAU82350	Human papillomavir
24	4	66.7	9	23	AAU82392	Human papillomavir
25	4	66.7	10	23	AAU82159	Human papillomavir
26	4	66.7	10	23	AAU82316	Human papillomavir
27	4	66.7	10	23	AAU82430	Human papillomavir
28	4	66.7	12	18	AAW38068	PPPPY motif contai
29	4	66.7	13	17	AAW07312	Botryosphacteria rib
30	4	66.7	13	21	AAW11570	SEN virus epitope
31	4	66.7	13	21	AAW86583	Human gene 93-enco
32	4	66.7	14	18	AAW15699	Internal fragment
33	4	66.7	14	21	AAW39103	Human secreted pro
34	4	66.7	14	22	ABB56724	Human SNP related
35	4	66.7	14	22	AAU18753	Human heart and tu
36	4	66.7	14	22	AAW65330	Human interleukin-
37	4	66.7	14	22	AAW65331	Human interleukin-
38	4	66.7	14	24	ABP99640	Human secreted pro
39	4	66.7	15	22	AAE02774	Human NKp30 recept
40	4	66.7	15	23	ABP98954	Ring finger protei
41	4	66.7	15	23	ABP54412	Human proteasome p
42	4	66.7	18	19	AAW74977	Human secreted pro
43	4	66.7	18	21	AAW27645	Human secreted pro
44	4	66.7	18	22	AAW75574	Human secreted pro
45	4	66.7	18	23	ABG95437	Human colon cancer
46	4	66.7	18	23	ABG40649	Human novel secret
47	4	66.7	18	24	ABP83106	Human peptide enco
48	4	66.7	19	22	ABG50962	G protein-coupled
49	4	66.7	19	22	ABG36114	Human liver peptid
50	4	66.7	19	22	ABB21502	Peptide #3620 enco
51	4	66.7	19	22	AAW56897	Protein #3501 enco
52	4	66.7	19	22	AAW69285	Human brain expres
53	4	66.7	19	22	AAW17114	Human bone marrow
54	4	66.7	19	22	AAW29605	Peptide #3548 enco
55	4	66.7	19	23	ABG71082	Peptide #3642 enco
56	4	66.7	19	23	ABG38899	Mouse scotin pepti
57	4	66.7	20	16	AAW72264	Human scotin enco
58	4	66.7	20	21	AAW59549	Glutamic acid deca
59	4	66.7	20	23	ABG71083	GAD65 fragment, pe
60	3	50.0	3	23	ABG77821	Human scotin pepti
61	3	50.0	4	15	AAW45397	Targetting peptide
62	3	50.0	4	15	AAW45399	Prolyl endopeptida
63	3	50.0	4	15	AAW45401	Prolyl endopeptida
64	3	50.0	4	15	AAW50249	Platelet GpIb alph
65	3	50.0	4	15	AAW66123	Peptide derived fr
66	3	50.0	4	16	AAW76701	N-terminal sequenc
67	3	50.0	4	21	ABJ18192	Growth hormone rel
68	3	50.0	4	22	AAU05448	Synthetic tetrapep
69	3	50.0	4	23	ABG69226	Protein SBRP2 rep
70	3	50.0	4	23	ABW77684	Linker peptide seq
71	3	50.0	5	15	AAW45396	Prolyl endopeptida
72	3	50.0	5	15	AAW60599	Proline rich seque
73	3	50.0	5	16	AAW83783	Monocyte cytotoxic
74	3	50.0	5	18	AAW29522	Platelet aggregati
75	3	50.0	5	19	AAW81247	Human iNOS peptide
76	3	50.0	5	19	AAW81307	Human iNOS peptide
77	3	50.0	5	19	AAW87382	Peptide determined
78	3	50.0	5	19	AAW65843	Peptide #68 from p
79	3	50.0	5	20	AAW67905	Human JAGGED1 wild
80	3	50.0	5	22	AAW63123	Amino acid sequenc
81	3	50.0	5	22	AAU00355	Binding motif #9 u
82	3	50.0	5	22	AAU00359	Binding motif #13

83 3 50.0 5 22 AAU00371 Binding motif #25  
 84 3 50.0 5 23 ABG69217 Hydroxyproline ric  
 85 3 50.0 5 23 ABG69227 Protein SRAPR2 rep  
 86 3 50.0 5 23 ABG60396 Selective targetin  
 87 3 50.0 5 23 ABG60397 Selective targetin  
 88 3 50.0 5 23 ABB78404 Hydroxyproline-ric  
 89 3 50.0 5 23 ABB78406 Hydroxyproline-ric  
 90 3 50.0 5 23 ABG35148 Ovarian cancer tar  
 91 3 50.0 5 23 ABG35149 Ovarian cancer tar  
 92 3 50.0 5 24 ABU64703 Motif-specific and  
 93 3 50.0 5 24 ABU64704 Motif-specific and  
 94 3 50.0 5 24 ABP60583 Peptide #16 relati  
 95 3 50.0 6 12 AAR11738 Peptide epitope de  
 96 3 50.0 6 15 AAR45393 Prolyl endopeptida  
 97 3 50.0 6 15 AAR45394 Prolyl endopeptida  
 98 3 50.0 6 15 AAR62181 UI snRNP 70K prote  
 99 3 50.0 6 16 AAW93998 Antineoplastic pep  
 100 3 50.0 6 16 AAW93997 Antineoplastic pep

## ALIGNMENTS

RESULT 1  
 AAB72258  
 ID AAB72258 standard; peptide; 6 AA.

XX AAB72258;

XX 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 13.

XX Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQPPV 6  
 |||||  
 Db 1 DSQPPV 6

## RESULT 2

AAB72511  
 ID AAB72511 standard; Peptide; 6 AA.

XX AAB72511;

XX 09-MAY-2001 (first entry)

XX Colostrinin peptide #12.

XX Dermatological; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US222665.

XX 17-AUG-1999; 99US-0149310.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -

XX Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQPPV 6  
 |||||  
 Db 1 DSQPPV 6

## RESULT 3

AAB72543  
 ID AAB72543 standard; Peptide; 6 AA.

XX AAB72543;

XX 09-MAY-2001 (first entry)

XX

```

DE Colostrinin peptide #12.
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX Unidentified.
OS
XX WO200112651-A2.
XX 22-FEB-2001.
XX 17-AUG-2000; 2000WO-US22774.
XX 17-AUG-1999; 99US-0149633.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Boldogh I;
XX WPI; 2001-226545/23.
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX
XX Claim 6; Page 21; 35pp; English.
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 6; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSQPPV 6
Db 1 DSQPPV 6

RESULT 5
AAE20240
ID AAE20240 standard; peptide; 6 AA.
XX AC AAE20240;
XX DT 18-JUN-2002 (first entry)
XX DE Colostrinin constituent peptide #12.
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulneryary.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT Modified-site 6
FT /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
XX 21-FEB-2002.
XX PF 17-AUG-2000; 2000WO-US22776.
XX 17-AUG-2000; 2000WO-US22776.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2002-269151/31.
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 25; 51pp; English.
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/

DE Colostrinin peptide #12.
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX Unidentified.
OS
XX WO200112651-A2.
XX 22-FEB-2001.
XX 17-AUG-2000; 2000WO-US22774.
XX 17-AUG-1999; 99US-0149633.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Boldogh I;
XX WPI; 2001-226545/23.
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX
XX Claim 6; Page 21; 35pp; English.
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 6; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSQPPV 6
Db 1 DSQPPV 6

RESULT 4
AAB59319
ID AAB59319 standard; Peptide; 6 AA.
XX AC AAB59319;
XX DT 21-MAR-2001 (first entry)
XX DE Ewe colostrinin peptide fragment B-4.
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX Ovis sp.
XX WO200075173-A2.
XX 14-DEC-2000.
XX 02-JUN-2000; 2000WO-GB02128.
XX 02-JUN-1999; 99GB-0012852.
XX (REGE-) REGEN THERAPEUTICS PLC.
XX Georgiades JA;
XX WPI; 2001-071058/08.
XX Peptides having an N-terminal amino acid sequence isolated from
PT

```

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidizing species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 6 AA;

Query Match 100.0%; Score 6; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQPPV 6  
 |||||  
 Db 1 DSQPPV 6

# RESULT 6

AAW51047  
 ID AAW51047 standard; Peptide; 6 AA.

XX AAW51047;

AC AAW51047;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide.

CC Colostrinin; colostrum; immunomodulator; cardiovascular;  
 CC blood cell regulator; cytokine inducer; beta-casein; human.  
 CC Homo sapiens.

XX Key Location/Qualifiers  
 FH Modified-site 6 /note= "optional C-terminal amidation"  
 FT  
 XX

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 XX blood cell regulator selected from colostrinin, its constituent peptide  
 XX and/or analogue

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. The peptide is  
 CC classified as having a beta-casein homologue precursor. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific; an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide.

XX Sequence 6 AA;

Query Match 100.0%; Score 6; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQPPV 6  
 |||||  
 Db 1 DSQPPV 6

# RESULT 7

AAO14589  
 ID AAO14589 standard; peptide; 6 AA.

XX AAO14589;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 12.

CC Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 CC neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 CC neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers  
 FH Modified-site 6 /note= "Optional C-terminal amide"  
 FT  
 XX

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 XX regulator selected from colostrinin, its constituent peptide and/or  
 XX analog

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 6; DB 23; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQPPV 6

DB 1 DSQPPV 6

RESULT 8

AAB59349

ID AAB59349 standard; Peptide; 10 AA.

XX AC AAB59349;

XX DT 21-MAR-2001 (first entry)

XX Ewe colostrinin peptide fragment derived sequence #9.

XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;

KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REG- ) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system

PT and immune system, viral and bacterial infections, and diseases

PT characterized by amyloid plaques -

XX Claim 8; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.

XX Sequence 10 AA;

Query Match 100.0%; Score 6; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQPPV 6

DB 5 DSQPPV 10

RESULT 9

AAP80454

ID AAP80454 standard; protein; 7 AA.

XX

AC AAP80454;

XX DT 28-DEC-1990 (first entry)

XX Sequence of part of human intercellular adhesion molecule-1 (ICAM-1).

DE Lymphocyte recognition; antiinflammatory agent;

XX Lymphocyte function associated antigen 1 (LFA-1).

KW Homo sapiens.

XX AU8815518-A.

XX PN 10-NOV-1988.

XX PD 29-APR-1988; 88AU-0106901.

XX PF 04-MAY-1987; 87US-0045963.

XX PR 01-NOV-1987; 87US-0115798.

XX PR 16-FEB-1988; 88US-0155954.

XX (DANA-) DANA FARBER CANCER.

XX PA Springer TA, Rothlein R, Marlin SD, Dustin ML;

XX WPI; 1989-033081/05.

XX New inter-cellular adhesion molecule-7; derived antibodies etc. -

PT are used for diagnosis and treatment of inflammation and

PT tumours, and for new DNA coding sequences

XX Claim 3(n); Page 52; 74pp; English.

XX ICAM-1 and its functional derivs. are new. Also new are recombinant DNA

CC able to express ICAM-1 or derivs. ICAM-1 is able to bind to a molecule

CC present on the surface of lymphocytes and contains at least one of 17

CC specified polypeptide sequences (see AAP80441-57). ICAM-1 is a 76-97kD

CC glycoprotein which is a binding partner for LFA-1, and is involved in

CC lymphocyte recognition and adhering to cell surfaces. ICAM-1 contains

CC 5 Ig-like domains.

XX SQ Sequence 7 AA;

Query Match 66.7%; Score 4; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4

DB 3 DSQP 6

RESULT 10

AAW70877

ID AAW70877 standard; Peptide; 7 AA.

XX AC AAW70877;

XX DT 02-MAR-1999 (first entry)

XX ICAM-1 peptide fragment possibly recognised by LFA-1.

DE Intracellular adhesion molecule; ICAM-1; LFA-1; immune response;

XX inflammation; lymphocyte function-associated antigen; tumour cell;

KW metastasis; binding ligand; detection; assay; peptide; polypeptide;

KW immune response; inflammation; immunosuppression.

XX Mus musculus.

XX US5831036-A.

XX 03-NOV-1998.

PF 25-OCT-1993; 93US-0140354.  
 XX  
 PR 27-APR-1990; 90US-0515478.  
 PR 04-MAY-1987; 87US-0045963.  
 PR 02-NOV-1987; 87US-0115798.  
 PR 16-FEB-1988; 88US-0155943.  
 PR 03-MAY-1988; 88US-0189815.  
 PR 28-SEP-1988; 88US-0250446.  
 PR 16-MAR-1989; 89US-0324481.  
 PR 30-JUN-1989; 89US-0373882.  
 PR 25-OCT-1993; 93US-0140554.  
 XX

(DAND ) DANA FARBER CANCER INST INC.

PI Dustin ML, Marlin SD, Rothlein R, Springer TA;  
 XX WPI; 1998-609323/51.  
 XX

PT Soluble fragments of human intercellular adhesion molecule 1 -  
 PT useful for inhibition of binding of leukocytes in immune responses  
 PT e.g. organ transplantation

XX Example 18; Column 47; 70pp; English.

XX ICAM-1 fragments obtained from recombinant expression of truncated  
 CC ICAM-1 coding sequences can be used in the control of adhesion  
 CC events in inflammatory conditions and immune responses. This is  
 CC achieved by the ICAM-1 fragments binding to and inhibiting the  
 CC action of Leukocyte surface molecules e.g. LFA-1 which mediate  
 CC cell-cell adhesion events during immune responses. This inhibition  
 CC is useful for suppressing immune responses after organ  
 CC transplantation or skin grafting. Ligands derived from ICAM-1  
 CC which are possibly recognised by LFA-1 are described in GENESEQ  
 CC records AAW70872-W70880.  
 XX

SQ Sequence 7 AA;

Query Match 66.7%; Score 4; DB 19; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSQP 4  
 ||||  
 Db 3 DSQP 6

RESULT 11

ABB76160  
 ID ABB76160 standard; Peptide; 7 AA.  
 XX  
 AC ABB76160;  
 XX

DT 22-JUL-2002 (first entry)

DE ICAM-1 sequence recognised by LFA-1.

XX Intercellular adhesion molecule-1; ICAM-1; human; LFA-1;  
 KW lymphocyte function-associated antigen-1; inflammation;  
 KW antiinflammatory; tumour; metastasis; antitumour.  
 XX

OS Homo sapiens.

XX US6358510-B1.

PN 19-MAR-2002.

XX 07-JUN-1995; 95US-0479763.

PR 27-APR-1990; 90US-0515478.

PR 25-JAN-1994; 94US-0186456.

PR 04-MAY-1987; 87US-0045963.

PR 02-NOV-1987; 87US-0115798.

PR 16-FEB-1988; 88US-0155943.  
 PR 03-MAY-1988; 88US-0189815.  
 PR 28-SEP-1988; 88US-0250446.  
 PR 16-MAR-1989; 89US-0324481.  
 PR 30-JUN-1989; 89US-0373882.  
 PR 22-DEC-1989; 89US-0456647.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 XX  
 PI Springer TA, Dustin ML, Rothlein R, Marlin SD;  
 XX WPI; 2002-302950/34.  
 XX

PT Novel derivatives of intercellular adhesion molecule-1 (ICAM-1) with  
 PT altered ability to bind lymphocyte function-associated antigen-1  
 PT (LFA-1) -  
 XX

XX Example 18; Column 47; 72pp; English.

XX The present sequence is that of a peptide within the human  
 CC intercellular adhesion molecule-1 (ICAM-1) sequence that is  
 CC possibly recognised by lymphocyte function-associated antigen-1  
 CC (LFA-1). The peptide corresponds to amino acid residues 85-91  
 CC of the ICAM-1 sequence given in ABB76147. ICAM-1 functions as a  
 CC ligand for LFA-1 in lymphocyte interactions with a number of  
 CC different cell types. The invention provides functional derivatives  
 CC of ICAM-1 comprising a soluble fragment of ICAM-1 containing a  
 CC specific amino acid substitution. These have an altered ability to  
 CC bind LFA-1. The invention provides methods for using ICAM-1, its  
 CC functional derivatives, and antibodies, for the treatment and  
 CC diagnosis of inflammation, haematopoietic tumour cell metastasis,  
 CC and ICAM-1-expressing tumours.  
 XX

SQ Sequence 7 AA;

Query Match 66.7%; Score 4; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSQP 4  
 ||||  
 Db 3 DSQP 6

RESULT 12

AAY40611  
 ID AAY40611 standard; peptide; 8 AA.

XX  
 AC AAY40611;

XX 01-DEC-1999 (first entry)

DE A1 derivative #2, beta strand of scaffold protein structure.

XX Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;  
 KW tumour; chemotherapeutic agent.  
 XX

OS Synthetic.

XX EP947582-A1.

XX 06-OCT-1999.

XX 31-MAR-1998; 98EP-0870065.

XX 31-MAR-1998; 98EP-0870065.

XX (INNO-) INNOGENETICS NV.

XX Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 1999-542958/46.

XX

PT New scaffold protein, useful for stabilizing antigens used as vaccines  
 PT  
 XX  
 PS  
 XX  
 XX  
 XX  
 CC Sequences AAY40610-Y40619 are functionally equivalent derivatives of the  
 CC A1 peptide (AAY40601) which forms part of a scaffold protein. A1 is a  
 CC beta strand peptide which forms part of a beta sheet. Peptides  
 CC (AAY40601-Y40609) together form a single-chain scaffold protein which  
 CC contains at least 1 disulfide bond, contains less than 10% alpha helix  
 CC and contains at least 6 beta-strands. The scaffold protein is constructed  
 CC of beta strands S1-S6, and may also include beta strands A1-A3, or any  
 CC functionally equivalent derivative of these sequences. The beta strands  
 CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to  
 CC the next by hydrogen bonds, which generate a beta sandwich architecture.  
 CC If the additional beta strands A1-A3 are included in the structure the  
 CC scaffold is constructed of two beta sheets, with the structures  
 CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each  
 CC other via amino acid loops, where at least one of the loops binds to a  
 CC receptor or antigen. The scaffold protein is used to stabilize antigens  
 CC or whole proteins such as receptors, or their fragments. It may be used  
 CC to bind two separate molecules. For example, one surface of the scaffold  
 CC may be bound to a protein which binds to a tumour antigen. This will  
 CC target the complex to tumour cells. Another surface may be bound to a  
 CC cytotoxic molecule or an autoimmune antibody which may then kill the  
 CC tumour cells. Therefore the scaffold protein may be used to target  
 CC chemotherapeutic agents to specific cells. It may also be used to  
 CC stabilize individual peptides in a peptide library and may be used in  
 CC diagnostic techniques, and to stabilize antigens used as vaccines.  
 XX  
 SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 20; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPVP 6  
 DB 2 QPVP 5  
 ||||  
 ||||

RESULT 13  
 AAW67834  
 ID AAW67834 standard; Protein; 8 AA.  
 AC  
 AC AAW67834;  
 XX  
 XX  
 DT 25-MAR-1999 (first entry)  
 XX

DE Human secreted protein encoded by gene 28 clone HLHSH36.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.  
 XX  
 XX WO9842738-A1.  
 XX  
 XX 01-OCT-1998.  
 PD  
 XX  
 XX 19-MAR-1998; 98WO-US05311.  
 XX  
 XX 30-MAY-1997; 97US-0050937.  
 PR 21-MAR-1997; 97US-0041276.  
 PR 21-MAR-1997; 97US-0041277.  
 PR 21-MAR-1997; 97US-0041281.  
 PR 21-MAR-1997; 97US-0042344.

PR 30-MAY-1997; 97US-0048069.  
 PR 30-MAY-1997; 97US-0048094.  
 PR 30-MAY-1997; 97US-0048095.  
 PR 30-MAY-1997; 97US-0048096.  
 PR 30-MAY-1997; 97US-0048099.  
 PR 30-MAY-1997; 97US-0048131.  
 PR 30-MAY-1997; 97US-0048135.  
 PR 30-MAY-1997; 97US-0048154.  
 PR 30-MAY-1997; 97US-0048160.  
 PR 30-MAY-1997; 97US-0048186.  
 PR 30-MAY-1997; 97US-0048187.  
 PR 30-MAY-1997; 97US-0048188.  
 PR 30-MAY-1997; 97US-0048350.  
 PR 30-MAY-1997; 97US-0048351.  
 PR 30-MAY-1997; 97US-0048352.  
 PR 30-MAY-1997; 97US-0048355.  
 PR 05-AUG-1997; 97US-0054804.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.

XX  
 PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA,  
 PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;  
 PI Rosen CA, Ruben SM, Shi Y, Young P;  
 XX

DR WPI; 1999-070066/06.  
 DR N-PSDB; AAX00638.

XX New isolated human genes and the secreted polypeptides they encode -  
 PT useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders

XX Claim 11; Page 287; 385pp; English.

XX This sequence represents a secreted human protein encoded by the gene  
 CC clone detailed in the descriptor line. The gene can be used to generate  
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
 CC portion (e.g. AAX00602) for increasing the stability of the fused  
 CC protein as compared to the human protein only.

CC The invention relates to 87 novel genes and their fragments (nucleic  
 CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC conditions can be diagnosed by determining the amount of the new  
 CC polypeptides in a sample or by determining the presence of mutations in  
 CC the new polynucleotides. Specific uses are described for each of the 87  
 CC polynucleotides, based on which tissues they are most highly expressed in  
 CC (see AAX00611 for described uses).

XX Sequence 8 AA;

Query Match 66.7%; Score 4; DB 20; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
 DB 5 DSQP 8  
 ||||  
 ||||

RESULT 14  
 AAB29950  
 ID AAB29950 standard; Peptide; 8 AA.  
 XX  
 XX AAB29950;  
 XX

DT 09-FEB-2001 (first entry)

XX Scaffold protein SCA A1 peptide SEQ ID NO: 11.

XX Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;  
 KW SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;  
 KW diabetic retinopathy; atherosclerosis.  
 XX





PR 11-DEC-1995; 95JP-0349939.  
 PA (SUET/) SUETSUNA Y.  
 XX  
 DR WPI; 1997-369469/34.  
 XX  
 XX New hexa:peptide and nona:peptide from soybean hydrolysate - useful  
 PT as active oxygen inhibitors, for treating arthritis, rheumatism,  
 PT cardiac infarction and Behcet's disease  
 XX  
 PS Claim 3; Page 2; 8pp; Japanese.  
 CC  
 CC AAW29259-60 were isolated from soybean (Glycine max) hydrolysate after  
 CC pepsin digestion. The hexa- and nonapeptide are useful in active oxygen  
 CC inhibitors. The oxygen inhibitors are useful for treating arthritis,  
 CC rheumatism, Behcet's disease and cardiac infarction.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 66.7%; Score 4; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QPPV 6  
 DB 5 QPPV 8  
 RESULT 17  
 AAB07745  
 ID AAB07745 standard; Peptide; 9 AA.  
 XX  
 AC AAB07745;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Repeat sequence from snake venom protease (SVPH-1) variant SVPH-1c.  
 XX  
 KW Snake venom protease; SVPH; SVPH-1; metalloproteinase-disintegrin;  
 KW chromosome 1; chromosome 4; immune system; splice variant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200043525-A2.  
 XX  
 PD 27-JUL-2000.  
 XX  
 PF 21-JAN-2000; 2000WO-US01338.  
 XX  
 PR 21-JAN-1999; 99US-0116670.  
 PR 14-JUN-1999; 99US-0138682.  
 PR 27-SEP-1999; 99US-0155798.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 PA  
 PI Cerretti DP;  
 XX  
 XX WPI; 2000-482914/42.  
 DR  
 XX Snake venom protease (SVPH) nucleic acids, and polypeptides, used to  
 PT identify proteins having metalloproteinase-disintegrin activity, and  
 PT inhibitors of the proteins for use in therapeutics -  
 XX  
 XX Example 2; Page 64; 105pp; English.  
 XX  
 CC The present sequence represents a repeat sequence from an alternatively  
 CC spliced snake venom protease-1 (SVPH-1) polypeptide, designated SVPH-1c.  
 CC The SVPH polypeptides are metalloproteinase-disintegrin protein family  
 CC members. The SVPH polynucleotides can be used as probes to identify  
 CC nucleic acids encoding proteins having metalloproteinase-disintegrin  
 CC activity, to identify human chromosome 1 or 4, to map genes on those  
 CC chromosomes, to identify genes associated with diseases, syndromes and  
 CC conditions associated with the chromosomes, and to study proteinases and

CC their activities on cell/cell interactions and the immune system. Sense  
 CC or antisense oligonucleotides of SVPH can be used to inhibit gene  
 CC expression of SVPH 1, 3, or 4. The SVPH polypeptides can be used to  
 CC study cell/cell and cell/matrix interactions involved in cellular  
 CC processes and in the immune system. The polypeptides may also be used to  
 CC screen for inhibitors of the polypeptide's activity, which are used in  
 CC therapeutics. The antibodies can be used in assays to detect the  
 CC presence of the polypeptides in vitro or in vivo, and to purify the  
 CC polypeptides by affinity chromatography.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 66.7%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SQPP 5  
 DB 3 SQPP 6  
 RESULT 18  
 AAU82116  
 ID AAU82116 standard; Peptide; 9 AA.  
 XX  
 AC AAU82116;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human papillomavirus (HPV) E7 antigenic peptide #2.  
 XX  
 KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;  
 KW cytostatic; heat shock protein; hap; anogenital wart; planar wart;  
 KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;  
 KW recurrent respiratory papillomatosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200242-A2.  
 XX  
 XX 03-JAN-2002.  
 PD  
 XX 26-JUN-2001; 2001WO-US20240.  
 PF  
 XX 26-JUN-2000; 2000US-214202P.  
 PR  
 XX (STES-) STESSEN BIOTECHNOLOGIES CORP.  
 PA  
 PI Neefe J, Goldstone S, Winnett M, Siegel M;  
 XX  
 DR WPI; 2002-130834/17.  
 XX  
 XX Treating human papillomavirus infection, in a subject, involves  
 PT administering a fusion protein comprising a protein of HPV which is  
 PT different from the type of HPV that causes the disease or condition -  
 XX  
 XX Example; Page 25; 34pp; English.  
 XX  
 CC The invention relates to treating a disease or condition associated with  
 CC a human papillomavirus (HPV) infection, comprising administering a fusion  
 CC protein of a protein of HPV, or its antigenic fragment, which is  
 CC different from the type of HPV that causes the disease or condition, and  
 CC a heat shock protein (hap), or its immunostimulatory fragment. The fusion  
 CC proteins are useful for treating diseases or conditions associated with  
 CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical  
 CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory  
 CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic  
 CC peptides of the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 66.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSOP 4  
 Db 1 DSOP 4

RESULT 19  
 AAU82223  
 ID AAU82223 standard; Peptide; 9 AA.  
 XX AC AAU82223;  
 XX DT 09-APR-2002 (first entry)  
 XX DE Human papillomavirus (HPV) E7 antigenic peptide #109.  
 XX KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;  
 KW cytotostatic; heat shock protein; hsp; anogenital wart; plantar wart;  
 KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;  
 KW recurrent respiratory papillomatosis.  
 XX OS Homo sapiens.  
 XX PN WO200200242-A2.  
 XX PD 03-JAN-2002.  
 XX PF 26-JUN-2001; 2001WO-US20240.  
 XX PR 26-JUN-2000; 2000US-214202P.  
 XX PA (STES-) STESSGEN BIOTECHNOLOGIES CORP.  
 XX PI Neefe J, Goldstone S, Winnett M, Siegel M;  
 XX DR WPI; 2002-130834/17.  
 XX PT Treating human papillomavirus infection, in a subject, involves  
 PT administering a fusion protein comprising a protein of HPV which is  
 PT different from the type of HPV that causes the disease or condition -  
 XX Example; Page 26; 34pp; English.  
 XX PS The invention relates to treating a disease or condition associated with  
 CC a human papillomavirus (HPV) infection, comprising administering a fusion  
 CC protein of a protein of HPV, or its antigenic fragment, which is  
 CC different from the type of HPV that causes the disease or condition, and  
 CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion  
 CC proteins are useful for treating diseases or conditions associated with  
 CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical  
 CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory  
 CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic  
 CC peptides of the invention.  
 XX SQ Sequence 9 AA;

Query Match 66.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSOP 4  
 Db 5 DSOP 8

RESULT 20  
 AAU82239  
 ID AAU82239 standard; Peptide; 9 AA.  
 XX AC AAU82239;  
 XX DT 09-APR-2002 (first entry)

Query Match 66.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSOP 4  
 Db 5 DSOP 8

RESULT 21  
 AAU82291  
 ID AAU82291 standard; Peptide; 9 AA.  
 XX AC AAU82291;  
 XX DT 09-APR-2002 (first entry)  
 XX DE Human papillomavirus (HPV) E7 antigenic peptide #177.  
 XX KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;  
 KW cytotostatic; heat shock protein; hsp; anogenital wart; plantar wart;  
 KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;  
 KW recurrent respiratory papillomatosis.  
 XX OS Homo sapiens.  
 XX PN WO200200242-A2.  
 XX PD 03-JAN-2002.  
 XX PF 26-JUN-2001; 2001WO-US20240.  
 XX PR 26-JUN-2000; 2000US-214202P.  
 XX PA (STES-) STESSGEN BIOTECHNOLOGIES CORP.  
 XX PI Neefe J, Goldstone S, Winnett M, Siegel M;  
 XX DR WPI; 2002-130834/17.  
 XX PT Treating human papillomavirus infection, in a subject, involves  
 PT administering a fusion protein comprising a protein of HPV which is  
 PT different from the type of HPV that causes the disease or condition -  
 XX Example; Page 26; 34pp; English.  
 XX PS The invention relates to treating a disease or condition associated with  
 CC a human papillomavirus (HPV) infection, comprising administering a fusion  
 CC protein of a protein of HPV, or its antigenic fragment, which is  
 CC different from the type of HPV that causes the disease or condition, and  
 CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion  
 CC proteins are useful for treating diseases or conditions associated with  
 CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical  
 CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory  
 CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic  
 CC peptides of the invention.

XX DE Human papillomavirus (HPV) E7 antigenic peptide #125.  
 XX KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;  
 KW cytotostatic; heat shock protein; hsp; anogenital wart; plantar wart;  
 KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;  
 KW recurrent respiratory papillomatosis.  
 XX OS Homo sapiens.  
 XX PN WO200200242-A2.  
 XX PD 03-JAN-2002.  
 XX PF 26-JUN-2001; 2001WO-US20240.  
 XX PR 26-JUN-2000; 2000US-214202P.  
 XX PA (STES-) STESSGEN BIOTECHNOLOGIES CORP.  
 XX PI Neefe J, Goldstone S, Winnett M, Siegel M;  
 XX DR WPI; 2002-130834/17.  
 XX PT Treating human papillomavirus infection, in a subject, involves  
 PT administering a fusion protein comprising a protein of HPV which is  
 PT different from the type of HPV that causes the disease or condition -  
 XX Example; Page 26; 34pp; English.  
 XX PS The invention relates to treating a disease or condition associated with  
 CC a human papillomavirus (HPV) infection, comprising administering a fusion  
 CC protein of a protein of HPV, or its antigenic fragment, which is  
 CC different from the type of HPV that causes the disease or condition, and  
 CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion  
 CC proteins are useful for treating diseases or conditions associated with  
 CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical  
 CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory  
 CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic  
 CC peptides of the invention.  
 XX SQ Sequence 9 AA;

Query Match 66.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSOP 4  
 Db 1 DSOP 4

RESULT 21  
 AAU82291  
 ID AAU82291 standard; Peptide; 9 AA.  
 XX AC AAU82291;  
 XX DT 09-APR-2002 (first entry)  
 XX DE Human papillomavirus (HPV) E7 antigenic peptide #177.  
 XX KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;  
 KW cytotostatic; heat shock protein; hsp; anogenital wart; plantar wart;  
 KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;  
 KW recurrent respiratory papillomatosis.  
 XX OS Homo sapiens.  
 XX PN WO200200242-A2.  
 XX PD 03-JAN-2002.  
 XX PF 26-JUN-2001; 2001WO-US20240.  
 XX PR 26-JUN-2000; 2000US-214202P.  
 XX PA (STES-) STESSGEN BIOTECHNOLOGIES CORP.  
 XX PI Neefe J, Goldstone S, Winnett M, Siegel M;  
 XX DR WPI; 2002-130834/17.  
 XX PT Treating human papillomavirus infection, in a subject, involves  
 PT administering a fusion protein comprising a protein of HPV which is  
 PT different from the type of HPV that causes the disease or condition -  
 XX Example; Page 26; 34pp; English.  
 XX PS The invention relates to treating a disease or condition associated with  
 CC a human papillomavirus (HPV) infection, comprising administering a fusion  
 CC protein of a protein of HPV, or its antigenic fragment, which is  
 CC different from the type of HPV that causes the disease or condition, and  
 CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion  
 CC proteins are useful for treating diseases or conditions associated with  
 CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical  
 CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory  
 CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic  
 CC peptides of the invention.

PF 26-JUN-2001; 2001WO-US20240.  
 PR  
 XX  
 CC  
 CC  
 PA (STES-) STESSGEN BIOTECHNOLOGIES CORP.  
 XX  
 PI Neefe J, Goldstone S, Winnett M, Siegel M;  
 XX WPI; 2002-130834/17.  
 DR  
 XX  
 XX Treating human papillomavirus infection, in a subject, involves  
 PT administering a fusion protein comprising a protein of HPV which is  
 PT different from the type of HPV that causes the disease or condition -  
 XX  
 XX Example; Page 26; 34pp; English.  
 PS  
 CC The invention relates to treating a disease or condition associated with  
 CC a human papillomavirus (HPV) infection, comprising administering a fusion  
 CC protein of a protein of HPV, or its antigenic fragment, which is  
 CC different from the type of HPV that causes the disease or condition, and  
 CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion  
 CC proteins are useful for treating diseases or conditions associated with  
 CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical  
 CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory  
 CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic  
 CC peptides of the invention.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 66.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSQP 4  
 ||||  
 Db 1 DSQP 4

RESULT 22  
 AAU82302  
 ID AAU82302 standard; Peptide; 9 AA.  
 XX  
 AC AAU82302;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human papillomavirus (HPV) E7 antigenic peptide #188.  
 XX  
 KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;  
 KW cytostatic; heat shock protein; hsp; anogenital wart; plantar wart;  
 KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;  
 KW recurrent respiratory papillomatosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200242-A2.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 26-JUN-2001; 2001WO-US20240.  
 XX  
 PR 26-JUN-2000; 2000US-214202P.  
 XX  
 PA (STES-) STESSGEN BIOTECHNOLOGIES CORP.  
 XX  
 PI Neefe J, Goldstone S, Winnett M, Siegel M;  
 XX WPI; 2002-130834/17.  
 DR  
 XX  
 XX Treating human papillomavirus infection, in a subject, involves  
 PT administering a fusion protein comprising a protein of HPV which is  
 PT different from the type of HPV that causes the disease or condition -  
 XX

PS Example; Page 26; 34pp; English.  
 XX  
 CC The invention relates to treating a disease or condition associated with  
 CC a human papillomavirus (HPV) infection, comprising administering a fusion  
 CC protein of a protein of HPV, or its antigenic fragment, which is  
 CC different from the type of HPV that causes the disease or condition, and  
 CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion  
 CC proteins are useful for treating diseases or conditions associated with  
 CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical  
 CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory  
 CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic  
 CC peptides of the invention.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 66.7%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSQP 4  
 ||||  
 Db 5 DSQP 8

RESULT 23  
 AAU82350  
 ID AAU82350 standard; Peptide; 9 AA.  
 XX  
 AC AAU82350;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human papillomavirus (HPV) E7 antigenic peptide #236.  
 XX  
 KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;  
 KW cytostatic; heat shock protein; hsp; anogenital wart; plantar wart;  
 KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;  
 KW recurrent respiratory papillomatosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200242-A2.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 26-JUN-2001; 2001WO-US20240.  
 XX  
 PR 26-JUN-2000; 2000US-214202P.  
 XX  
 PA (STES-) STESSGEN BIOTECHNOLOGIES CORP.  
 XX  
 PI Neefe J, Goldstone S, Winnett M, Siegel M;  
 XX WPI; 2002-130834/17.  
 DR  
 XX  
 XX Treating human papillomavirus infection, in a subject, involves  
 PT administering a fusion protein comprising a protein of HPV which is  
 PT different from the type of HPV that causes the disease or condition -  
 XX  
 XX Example; Page 27; 34pp; English.  
 PS  
 CC The invention relates to treating a disease or condition associated with  
 CC a human papillomavirus (HPV) infection, comprising administering a fusion  
 CC protein of a protein of HPV, or its antigenic fragment, which is  
 CC different from the type of HPV that causes the disease or condition, and  
 CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion  
 CC proteins are useful for treating diseases or conditions associated with  
 CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical  
 CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory  
 CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic  
 CC peptides of the invention.  
 XX  
 XX Sequence 9 AA;  
 SQ

```

Query Match      66.7%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DSQP 4
      ||||
Db      1 DSQP 4

RESULT 24
AAU82392
ID AAU82392 standard; Peptide; 9 AA.
XX
AC AAU82392;
XX
DT 09-APR-2002 (first entry)
XX
DE Human papillomavirus (HPV) E7 antigenic peptide #278.
XX
KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;
KW cytostatic; heat shock protein; hsp; anogenital wart; plantar wart;
KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;
KW recurrent respiratory papillomatosis.
XX
OS Homo sapiens.
XX
PN WO200200242-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US20240.
XX
PR 26-JUN-2000; 2000US-214202P.
XX
PA (STES-) STESSGEN BIOTECHNOLOGIES CORP.
XX
PI Neefe J, Goldstone S, Winnett M, Siegel M;
XX WPI; 2002-130834/17.
XX
DR Treating human papillomavirus infection, in a subject, involves
XX administering a fusion protein comprising a protein of HPV which is
XX different from the type of HPV that causes the disease or condition -
XX Example; Page 27; 34pp; English.
XX
CC The invention relates to treating a disease or condition associated with
CC a human papillomavirus (HPV) infection, comprising administering a fusion
CC protein of a protein of HPV, or its antigenic fragment, which is
CC different from the type of HPV that causes the disease or condition, and
CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion
CC proteins are useful for treating diseases or conditions associated with
CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical
CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory
CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic
CC peptides of the invention.
XX
SQ Sequence 9 AA;

Query Match      66.7%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DSQP 4
      ||||
Db      1 DSQP 4

RESULT 25
AAU82159
ID AAU82159 standard; Peptide; 10 AA.
XX

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AC AAU82159;
XX
DT 09-APR-2002 (first entry)
XX
DE Human papillomavirus (HPV) E7 antigenic peptide #45.
XX
KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;
KW cytostatic; heat shock protein; hsp; anogenital wart; plantar wart;
KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;
KW recurrent respiratory papillomatosis.
XX
OS Homo sapiens.
XX
PN WO200200242-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US20240.
XX
PR 26-JUN-2000; 2000US-214202P.
XX
PA (STES-) STESSGEN BIOTECHNOLOGIES CORP.
XX
PI Neefe J, Goldstone S, Winnett M, Siegel M;
XX WPI; 2002-130834/17.
XX
DR Treating human papillomavirus infection, in a subject, involves
XX administering a fusion protein comprising a protein of HPV which is
XX different from the type of HPV that causes the disease or condition -
XX Example; Page 25; 34pp; English.
XX
CC The invention relates to treating a disease or condition associated with
CC a human papillomavirus (HPV) infection, comprising administering a fusion
CC protein of a protein of HPV, or its antigenic fragment, which is
CC different from the type of HPV that causes the disease or condition, and
CC a heat shock protein (hsp), or its immunostimulatory fragment. The fusion
CC proteins are useful for treating diseases or conditions associated with
CC HPV, such as anogenital warts, plantar warts, cervical cancer, cervical
CC dysplasia, anal cancer, anal dysplasia, or recurrent respiratory
CC papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic
CC peptides of the invention.
XX
SQ Sequence 10 AA;

Query Match      66.7%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DSQP 4
      ||||
Db      6 DSQP 9

RESULT 26
AAU82316
ID AAU82316 standard; Peptide; 10 AA.
XX
AC AAU82316;
XX
DT 09-APR-2002 (first entry)
XX
DE Human papillomavirus (HPV) E7 antigenic peptide #202.
XX
KW Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;
KW cytostatic; heat shock protein; hsp; anogenital wart; plantar wart;
KW cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;
KW recurrent respiratory papillomatosis.
XX
OS Homo sapiens.
XX
PN WO200200242-A2.

```

	XX	03-JAN-2002.
	XX	26-JUN-2001; 2001WO-US20240.
	XX	26-JUN-2000; 2000US-214202P.
	XX	(STES-) STESSGEN BIOTECHNOLOGIES CORP.
	PA	Neefe J, Goldstone S, Winnett M, Siegel M;
	PI	WPI; 2002-130834/17.
	DR	Treating human papillomavirus infection, in a subject, involves
	XX	administering a fusion protein comprising a protein of HPV which is
	PT	different from the type of HPV that causes the disease or condition -
	PT	Example; Page 27; 34pp; English.
	XX	The invention relates to treating a disease or condition associated with
	CC	a human papillomavirus (HPV) infection, comprising administering a fusion
	CC	protein of a protein of HPV, or its antigenic fragment, which is
	CC	different from the type of HPV that causes the disease or condition, and
	CC	a heat shock protein (hsp), or its immunostimulatory fragment. The fusion
	CC	proteins are useful for treating diseases or conditions associated with
	CC	HPV, such as anogenital warts, plantar warts, cervical cancer, cervical
	CC	dysplasia, anal cancer, anal dysplasia, or recurrent respiratory
	CC	papillomatosis. Sequences AAU82115-AAU82434 represent HPV E7 antigenic
	CC	peptides of the invention.
	XX	Sequence 10 AA;
	SQ	
		Query Match      66.7%; Score 4; DB 23; Length 10;
		Best Local Similarity 100.0%; Pred.No. 2.3e+02;
	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0
	Qy	1 DSQP 4 
	Db	6 DSQP 9
	RESULT 27	
	AAU82430	ID AAU82430 standard; Peptide; 10 AA.
	AC	AAU82430;
	XX	09-APR-2002 (first entry)
	DT	Human papillomavirus (HPV) E7 antigenic peptide #316.
	DE	Human; human papillomavirus; HPV; E7 antigen; dermatological; virucide;
	XX	cycostatic; heat shock protein; hsp; angenital wart; plantar wart;
	KW	cervical cancer; cervical dysplasia; anal cancer; anal dysplasia;
	KW	recurrent respiratory papillomatosis.
	XX	Homo sapiens.
	OS	WO200200242-A2.
	XX	03-JAN-2002.
	XX	26-JUN-2001; 2001WO-US20240.
	PD	26-JUN-2000; 2000US-214202P.
	PF	(STES-) STESSGEN BIOTECHNOLOGIES CORP.
	XX	Neefe J, Goldstone S, Winnett M, Siegel M;
	PA	WPI; 2002-130834/17.
	PB	Treating human papillomavirus infection, in a subject, involves
	XX	

CC novel protein. The WW domain is a small functional domain. Its name  
 CC is derived from the observation that two tryptophan residues, one in the  
 CC amino terminal portion of the WW domain and one in the carboxyl terminal  
 CC portion, are conserved. Most proteins containing WW domains have a  
 CC function involving cell signalling and growth regulation or the  
 CC organisation of the cytoskeleton. Polypeptides containing a WW domain  
 CC are identified by treating a multivalent recognition unit complex that  
 CC has selective binding affinity for a WW domain, with many polypeptides  
 CC and identifying those with selective affinity for the complex. Proteins  
 CC containing WW domains are used for targeted drug screening, i.e. to  
 CC identify potential modulators of specific WW domain interactions.

XX Sequence 12 AA;

Query Match 66.7%; Score 4; DB 18; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SQPP 5

DB 2 SQPP 5

RESULT 29

AAW07312

ID AAW07312 standard; peptide; 13 AA.

XX

AC AAW07312;

XX

DT 06-JUN-1997 (first entry)

XX

DE Botryosphaeria ribis alkaline lipase fragment.

XX

XX Fungal alkaline lipase; detergent; pH 10; Botryosphaeria; Guignardia;

KW

XX lipolysis; aa; amino acid.

XX

OS Botryosphaeria ribis CBS 504.94.

XX

PN W09630502-A1.

XX

XX 03-OCT-1996.

XX

PF 27-MAR-1996; 96WO-DK00123.

XX

PR 14-JUL-1995; 95DK-0000830.

XX

PR 30-MAR-1995; 95DK-0000344.

XX

PA (NOVO) NOVO-NORDISK AS.

XX

PI Halkier T, Hirayama S;

XX

XX WPI; 1996-455350/45.

XX

XX Alkaline lipase derived from Botryosphaeria or Guignardia strains -

PT

PT for use as a detergent additive

XX

PS Example 7; Page 28; 43pp; English.

XX

XX AAW07312-16 are peptide fragments of a new alkaline lipase derived  
 CC from the fungus B. ribis. The peptides were aligned to the known  
 CC sequence of lipase LIP 1 from Candida cylindracea CBS 6330 and found to  
 CC correspond to residues 35-47, 148-187, 255-276, 296-331 and 365-403  
 CC respectively. The new lipase has optimum activity at pH 10 in the  
 CC presence of 50 mM Ca<sup>2+</sup>. The enzyme can be used as a detergent additive.

XX Sequence 13 AA;

Query Match 66.7%; Score 4; DB 17; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 QPPV 6

DB 3 QPPV 6

Db 6 QPPV 9

RESULT 30

AAB11570

ID AAB11570 standard; Peptide; 13 AA.

XX

AC AAB11570;

XX

DT 12-OCT-2000 (first entry)

XX

DE SEN virus epitope mapping peptide SEQ ID NO: 160.

XX

XX SEN virus; SENV; gastrointestinal tract disorder; inflammatory disease;  
 KW proliferative disorder; hepatopathy; hepatitis; viral infection;  
 KW vaccination; gene therapy.

XX

OS Hepatitis virus.

XX

PN W0200028039-A2.

XX

PD 18-MAY-2000.

XX

PF 09-NOV-1999; 99WO-EP08566.

XX

PR 10-NOV-1998; 98IT-MI02437.

XX

PR 30-APR-1999; 99IT-MI0923.

XX

PR 14-MAY-1999; 99EP-0830298.

XX

PR 16-JUL-1999; 99EP-0113932.

XX

PA (DIAS-) DIASORIN SRL.

XX

PI Primi D, Fiordalisi G, Mantero GL, Mattioli S, Sottini A;

XX

PI Bonelli F, Vaglini L, Olivero P, Dal Corso A, Bonelli M;

XX

XX WPI; 2000-376551/32.

XX

XX Nucleic acids representing the genome of the SEN virus (SENV) and

PT

PT encoded proteins, useful for treatment of hepatopathies, inflammatory

PT

PT diseases and proliferative disorders such as cancer -

XX

PS Example 28; Page 104; 392pp; English.

XX

XX The present invention is concerned with the sequence of the genome of  
 CC the SEN virus (SENV), and the proteins encoded by it. SENV is thought to  
 CC be the cause of hepatopathies which are not linked to the presence of  
 CC the hepatitis A, B and E viruses in man. The genome and proteins of this  
 CC virus can be used in gene therapy and vaccination against the virus,  
 CC which also causes disorders of the gastrointestinal tract, including  
 CC Crohn's disease and lupus erythematosus, inflammatory diseases, and  
 CC proliferative disorders such as cancer. The peptides AAB11549-B11581  
 CC were used in epitope mapping assays to identify the immunologically  
 CC reactive areas of the SENV proteins.

XX Sequence 13 AA;

Query Match 66.7%; Score 4; DB 21; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SQPP 5

DB 1 SQPP 4

RESULT 31

AAY86583

ID AAY86583 standard; peptide; 13 AA.

XX

AC AAY86583;

XX

DT 19-APR-2000 (first entry)

XX



KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;  
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.  
 OS WO200058513-A1.  
 PN  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 22-MAR-2000; 2000WO-US07506.  
 XX  
 PR 26-MAR-1999; 99US-0126505.  
 PR 17-DEC-1999; 99US-0172412.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 XX

PI Rosen CA, Ruben SM, Komatsoulis G;  
 XX WPI; 2000-594649/56.  
 DR N-PSDB; AAC73875.  
 XX  
 XX Forty-nine polynucleotide sequences, and their encoded secreted  
 PT polypeptides, used in the treatment and diagnosis of cancers,  
 PT autoimmune disorders, and skin disorders -  
 XX  
 PS Claim 11; Page 373; 413pp; English.

XX Sequences AAB39093-B39141 represent the amino acid sequences of 49  
 CC human secreted proteins encoded by the genes AAC73865-C73913. The genes  
 CC and proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
 CC a range of human tissues disclosed in the specification. The nucleic  
 CC acids, proteins, antibodies and (ant)agonists are useful in the  
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.

XX Sequence 14 AA;  
 SQ  
 Query Match 66.7%; Score 4; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
 ||||  
 Db 3 SQPP 6

RESULT 34  
 ABB56724  
 ID ABB56724 standard; Peptide; 14 AA.

XX AC ABB56724;  
 XX  
 XX 05-MAR-2002 (first entry)  
 DT  
 DE Human SNP related amino acid sequence SEQ ID NO:1289.  
 XX  
 KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;  
 KW immunosuppressive; anti-inflammatory; neuroprotective; antimicrobial;  
 KW autoimmune disease; inflammation; cancer; nervous system disease;  
 KW infection; polymorphic protein.

XX Homo sapiens.  
 OS WO200139586-A2.  
 PN  
 XX 31-MAY-2001.  
 PD  
 XX 22-NOV-2000; 2000WO-US32311.  
 PF  
 PR 24-NOV-1999; 99US-0167383.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 XX Shinkets RA, Leach M;  
 XX WPI; 2001-355949/37.  
 DR  
 XX Isolated human nucleic acids comprising one or more single nucleotide  
 PT polymorphisms, useful for treating a subject suffering from a  
 PT pathology, e.g. autoimmune diseases, ascribed to the presence of a  
 PT sequence polymorphism -

XX Claim 1; Page 631; 674pp; English.  
 XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides  
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
 CC to ABB56903 represent human peptides encoded by some of the SNP  
 CC oligonucleotides. The sequences from the present invention can have  
 CC immunosuppressive, cytostatic, anti-inflammatory, neuroprotective and  
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides  
 CC and antibodies from the present invention can be used for treating a  
 CC subject suffering from, at risk for, or suspected of, suffering from a  
 CC pathology ascribed to the presence of a sequence polymorphism. The  
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of  
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs  
 CC are also useful for determining which forms of a characterised  
 CC polymorphism are present in individuals. The antibodies may be used in  
 CC the detection, quantitation and/or cellular or tissue localisation of a  
 CC polymorphic protein (e.g., for use in measuring levels of the  
 CC polymorphic protein within appropriate physiological samples).

XX Sequence 14 AA;  
 SQ  
 Query Match 66.7%; Score 4; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
 ||||  
 Db 5 SQPP 8

RESULT 35  
 AAU18753  
 ID AAU18753 standard; peptide; 14 AA.

XX AC AAU18753;  
 XX  
 XX 21-NOV-2001 (first entry)  
 DT  
 DE Human heart and tumour cell targeting peptide #38.  
 XX  
 KW Human; tumour; carcinoma; gene therapy; coronary heart disease;  
 KW heart failure; infarction; myocarditis; ischaemia; restenosis;  
 KW atherosclerosis; hyperproliferative disorder; cancer; cardiac;  
 KW vasotropic; cytostatic.

XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 1 /note= "X= any amino acid sequence of n amino acids,  
 FT where n varies from 0-50"  
 FT



FT Misc-difference 14  
 FT /note= "X= any amino acid sequence of n amino acids,  
 FT where n varies from 0-50"  
 XX  
 XX WO200157069-A2.  
 XX  
 XX 09-AUG-2001.  
 XX  
 XX 26-JAN-2001; 2001WO-EP00894.  
 XX  
 XX 02-FEB-2000; 2000EP-0440030.  
 PR 03-MAR-2000; 2000US-0186760.  
 PR 21-AUG-2000; 2000EP-0440229.  
 PR 07-NOV-2000; 2000US-0246091.  
 XX  
 XX (TRGE ) TRANSGENE SA.  
 PA  
 XX Schugart K, Rassmusen U, Schreiber V;  
 PI  
 XX WPI; 2001-536478/59.  
 DR  
 XX New targeting peptides useful for targeting heart and various tumours  
 XX PT and for treating coronary heart diseases, heart failure, infarction,  
 PT myocarditis, ischaemia, restenosis, atherosclerosis, cancer and  
 PT tumour -  
 XX  
 XX Disclosure; Page 6; 53pp; English.  
 PS  
 XX The present invention relates to novel peptides that target heart  
 CC or tumour cells, particularly in humans. The peptides of the invention  
 CC are useful for targeting a target cell, e.g. a heart cell, a tumour  
 CC cell, a metastasis, a tumour vasculature, a colorectal tumour cell or  
 CC a carcinoma tumour cell. The peptides are useful for the study,  
 CC isolation and purification of the cell surface markers to which the  
 CC peptide specifically binds, in diagnostic purposes, and as a therapeutic  
 CC for the treatment of animal or human body. A composition comprising at  
 CC least one therapeutic agent and at least one peptide of the invention,  
 CC or a nucleic acid molecule encoding such a peptide can be used for the  
 CC preparation of a drug for gene transfer. Such compositions are useful for  
 CC the treatment and prevention of any diseases affecting the heart or its  
 CC vasculature (e.g. coronary heart disease, heart failure, hypertrophy,  
 CC infarction, myocarditis, ischaemia, restenosis, atherosclerosis), and  
 CC hyperproliferative disorders (e.g. cancer). The systemic delivery of  
 CC vectors targeted with the peptides of the invention avoid regional  
 CC delivery to the coronary artery that requires an invasive and  
 CC cumbersome operation, and limits the spread of vectors after local  
 CC administration. Systemic administration of peptides of the invention  
 CC allows the targeting of tumours that are difficult to reach surgically.  
 CC AAU18716-AAU18792 represent the human heart and tumour cell targeting  
 CC peptides of the present invention.  
 XX  
 XX Sequence 14 AA;  
 SQ  
 Query Match 66.7%; Score 4; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SQPP 5  
 Db |||||  
 4 SQPP 7  
 RESULT 36  
 AAG65330  
 ID AAG65330 standard; peptide; 14 AA.  
 XX  
 AC AAG65330;  
 XX  
 DT 30-NOV-2001 (first entry)  
 XX  
 DE Human interleukin-18 (IL-18) peptide epitope.  
 XX  
 XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;

KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;  
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; epitope.  
 XX Homo sapiens.  
 XX WO200158956-A2.  
 XX  
 XX 16-AUG-2001.  
 XX  
 XX 09-FEB-2001; 2001WO-US04170.  
 XX  
 XX 10-FEB-2000; 2000US-0181608.  
 PR  
 XX (BADI ) BASF AG.  
 PA  
 XX Chayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;  
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;  
 PI Lennard SN;  
 XX  
 XX WPI; 2001-550020/61.  
 DR  
 XX Novel antibodies and compounds capable of binding to human  
 XX PT interleukin-18 useful for treating, e.g., inflammatory disorders,  
 PT neurological disorders, heart failure, myocardial infarction, and  
 PT autoimmune diseases -  
 XX  
 XX Example 1; Page 13; 91pp; English.  
 PS  
 XX The invention provides isolated antibodies, or antigen-binding portions,  
 CC that are capable of binding to human interleukin-18 (IL-18). The  
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a  
 CC disorder where IL-18 is detrimental in, a human subject suffering from,  
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,  
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders  
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and  
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such  
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders  
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18  
 CC antibody may occur before, concurrent, or after administration of a  
 CC second agent selected from an antibody, or fragment, capable of binding  
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,  
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory  
 CC agents. The present sequence represents a human IL-18 peptide epitope.  
 XX  
 XX Sequence 14 AA;  
 SQ  
 Query Match 66.7%; Score 4; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSQP 4  
 Db |||||  
 9 DSQP 12  
 RESULT 37  
 AAG65331  
 ID AAG65331 standard; peptide; 14 AA.  
 XX  
 AC AAG65331;  
 XX  
 DT 30-NOV-2001 (first entry)  
 XX  
 DE Human interleukin-18 (IL-18) peptide epitope.  
 XX  
 XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;  
 KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;  
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; epitope.  
 XX Homo sapiens.  
 OS  
 XX WO200158956-A2.  
 PN  
 XX

PD 16-AUG-2001.  
 XX 09-FEB-2001; 2001WO-US04170.  
 PF 10-FEB-2000; 2000US-0181608.  
 XX (BADI ) BASF AG.  
 XX Chayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;  
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;  
 PI Lennard SN;  
 XX WPI; 2001-550020/61.  
 DR Novel antibodies and compounds capable of binding to human  
 XX interleukin-18 useful for treating, e.g., inflammatory disorders,  
 PT neurological disorders, heart failure, myocardial infarction, and  
 PT autoimmune diseases -  
 XX  
 PS Example 1; Page 13; 91pp; English.  
 XX The invention provides isolated antibodies, or antigen-binding portions,  
 CC that are capable of binding to human interleukin-18 (IL-18). The  
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a  
 CC disorder where IL-18 is detrimental in, a human subject suffering from,  
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,  
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders  
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and  
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such  
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders  
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18  
 CC antibody may occur before, concurrent, or after administration of a  
 CC second agent selected from an antibody, or fragment, capable of binding  
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,  
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory  
 CC agents. The present sequence represents a human IL-18 peptide epitope.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 66.7%; Score 4; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSQP 4  
 DB |||||  
 4 DSQP 7  
 RESULT 38  
 ABP99640  
 ID ABP99640 standard; Protein; 14 AA.  
 XX  
 AC ABP99640;  
 XX  
 DT 26-MAR-2003 (first entry)  
 XX  
 DE Human secreted protein SEQ ID NO 584.  
 XX  
 KW Human; secreted protein; neurotropic; neuroprotective; cytostatic;  
 KW virucide; dermatological; immunosuppressive; anti-inflammatory; anti-HIV;  
 KW vulvarity; antibacterial; antiparkinsonian; antischlicking; antianaemic;  
 KW antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective;  
 KW antiinflammatory; antiallergic; antidiabetic; antitumor; anticonvulsant;  
 KW antifungal; antiparasitic; cardiant; immune disorder; infection; vaccine;  
 KW cardiovascular disorder; neurological disease; nephrotropic;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200277186-A2.  
 XX  
 PD 03-OCT-2002.  
 XX

PF 26-MAR-2002; 2002WO-US09188.  
 XX  
 PR 27-MAR-2001; 2001US-278650P.  
 PR 12-SEP-2001; 2001US-0950082.  
 PR 12-SEP-2001; 2001US-0950083.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ruben SM;  
 XX WPI; 2003-040583/03.  
 DR N-PSDB; ABZ67061.  
 XX  
 XX New human secreted proteins encoded by genes contained in cDNA clones  
 PT (e.g. HGCA19), useful for preventing, treating or diagnosing e.g.  
 PT AIDS, multiple sclerosis, herpes virus, leukemia, tick-borne  
 PT encephalitis or West Nile fever -  
 XX  
 PS Claim 1; Page 1440; 2423pp; English.  
 XX  
 CC The invention relates to novel human genes (ABZ66891-ABZ68209) and the  
 CC encoded secreted proteins (ABP99470-ABP99872) useful for preventing,  
 CC treating or ameliorating medical conditions e.g. by protein or gene  
 CC therapy. The genes are isolated from a range of human tissues disclosed  
 CC in the specification. The nucleic acids, proteins, antibodies and  
 CC (ant)agonists are useful in the diagnosis, treatment and prevention of:  
 CC (a) cancer, e.g. breast and ovarian cancer and other cancers of the  
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,  
 CC lung or urogenital; (b) immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as  
 CC myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.  
 CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,  
 CC bacterial, fungal and parasitic infections.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 66.7%; Score 4; DB 24; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SQPP 5  
 DB |||||  
 3 SQPP 6  
 RESULT 39  
 AAE02774  
 ID AAE02774 standard; peptide; 15 AA.  
 XX  
 AC AAE02774;  
 XX  
 DT 06-AUG-2001 (first entry)  
 XX  
 DE Human NKp30 receptor immunogenic peptide for antiserum production.  
 XX  
 KW Human; NKp30 receptor; natural killer cell; cytostatic; antimicrobial;  
 KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
 KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
 KW therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200136630-A2.  
 XX  
 PD 25-MAY-2001.  
 XX  
 XX 15-NOV-2000; 2000WO-EP11697.  
 PF  
 XX 15-NOV-1999; 99CA-2288307.  
 PR  
 XX 15-NOV-1999; 99US-0440514.  
 PD  
 XX

PA (INNA-) INNATE PHARMA SAS.  
XX (UYGE-) UNIV GENOVA.  
PI Moretta A, Bottino C, Biassoni R;  
XX WPI; 2001-329221/34.  
XX Novel compound, useful for detection and/or quantifying the presence of  
PT NK cells, comprises the amino acid sequences of the Nkp30 molecule -  
XX Claim 1; Page 33; 83pp; English.  
XX The invention relates to human Nkp30 receptor and its corresponding cDNA  
CC molecule which is involved in natural cytotoxicity mediated by natural  
CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor  
CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively  
CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are  
CC useful for detecting and/or quantifying the presence of NK cells in a  
CC biological sample. The invention also provides kits for detecting and/or  
CC quantifying the presence of NK cells, for the selective removal of NK  
CC cells from a biological sample, for the positive and selective  
CC purification of NK cells from a biological sample and for the in vitro  
CC stimulation of NK cell cytotoxicity. The invention further provides a  
CC pharmaceutical composition which is used as a drug for grafting  
CC enhancement, graft versus host (GvH) inhibition, stimulation of graft  
CC versus tumour (Gvt) and especially graft versus leukaemia (GvL), and for  
CC the prevention, palliation and/or therapy of solid or liquid tumours,  
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
CC microorganism, notably viral infection. Nkp30 antibodies are useful for  
CC identifying Nkp30 natural ligands and allow assessment of the level of  
CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the  
CC comparison of this level to the standard physiological one. Hence Nkp30  
CC antibodies are useful in the diagnosis of tumours or of infection.  
CC The present sequence is human Nkp30 receptor immunogenic peptide fragment  
CC which is used for Nkp30 polyclonal antiserum production.  
XX  
SQ Sequence 15 AA;  
  
Query Match 66.7%; Score 4; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 SQPP 5  
DB 3 SQPP 6  
|||||  
  
RESULT 40  
ABB98954  
ID ABB98954 standard; Peptide; 15 AA.  
XX ABB98954;  
AC ABB98954;  
DT 14-APR-2003 (first entry)  
XX  
DE Ring finger protein 27.17 peptide fragment.  
XX  
KW Ring finger protein 27.17; tumour; cytostatic; inflammation;  
KW immunological disease; haemopathy; HIV infection; anti-HIV.  
XX Unidentified.  
OS  
XX CN1361114-A.  
PN  
XX 31-JUL-2002.  
PD  
XX 26-DEC-2000; 2000CN-0135911.  
PF  
XX 26-DEC-2000; 2000CN-0135911.  
PR  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
PA  
XX Mao Y, Xie Y;  
PI

XX WPI; 2002-751533/82.  
XX New polypeptide ring finger protein 27.17 and polynucleotides encoding  
PT this polypeptide -  
XX  
PS Example 6; Page 28 (Disclosure); 32pp; Chinese.  
XX The present invention relates to ring finger protein 27.17 (see  
CC ABB98953). The protein can be used for treating various diseases, such as  
CC malignant tumours, inflammations, immunological diseases, haemopathy and  
CC HIV infection. The present sequence is an N-terminal peptide fragment of  
CC the protein, which was used in an example in the invention.  
CC Note: The present sequence is SEQ ID 7 shown in the sequence listing.  
CC This sequence differs from the SEQ ID 7 shown in the disclosure (see  
CC ABB95111).  
XX  
SQ Sequence 15 AA;  
  
Query Match 66.7%; Score 4; DB 23; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 SQPP 5  
DB 3 SQPP 6  
|||||  
  
RESULT 41  
ABP54412  
ID ABP54412 standard; Peptide; 15 AA.  
XX ABP54412;  
AC ABP54412;  
XX  
DT 21-JAN-2003 (first entry)  
XX  
DE Human proteasome p40.5 subunit 20.24 N-terminal peptide SEQ ID NO:7.  
XX  
KW Human; proteasome p40.5 subunit 20.24; malignant tumour; haemopathy;  
KW human immunodeficiency virus infection; HIV infection; inflammation;  
KW immunological disease.  
XX  
OS Homo sapiens.  
XX  
XX CN1345974-A.  
PN  
XX 24-APR-2002.  
PD  
XX 22-SEP-2000; 2000CN-0125327.  
PF  
XX 22-SEP-2000; 2000CN-0125327.  
PR  
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
PA  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-539372/58.  
DR  
XX New polypeptide-proteasome p40.5 subunit 20.24 for treating malignant  
PT tumor, hemopathy, human immunodeficiency virus infection, immunological  
PT disease and various inflammations -  
XX  
PS Example 5; Page 18 (Disclosure); 32pp; Chinese.  
XX  
CC The present invention describes human proteasome p40.5 subunit 20.24 (I).  
CC Also described is a process used for producing (I) using DNA  
CC recombination technology. (I) can be used in the treatment of several  
CC diseases, such as malignant tumour, haemopathy, human immunodeficiency  
CC virus (HIV) infection, immunological disease and various inflammations.  
CC The present sequence represents the N-terminal peptide of (I), which is  
CC used in an example from the present invention.  
XX  
SQ Sequence 15 AA;



PS Claim 1; Page 685; 721pp; English.

XX This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 104 from the human cDNA clone HCUBC79 (deposited as clone ATCC 97901 and ATCC 209047).

CC The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

CC The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW4731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).

XX

SQ Sequence 18 AA;

Query Match 66.7%; Score 4; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
|||||

Db 14 SQPP 17

## RESULT 43

AAAB27645

ID AAB27645 standard; Peptide; 18 AA.

XX

AC AAB27645;

XX 02-FEB-2001 (first entry)

XX Human secreted protein BLAST search protein SEQ ID NO: 146.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer; vulnary; anticonvulsant; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX WO200055175-A1.

XX 21-SEP-2000.

XX 09-MAR-2000; 2000WO-US06049.

XX 12-MAR-1999; 99US-0124144.

XX 11-JUN-1999; 99US-0138574.

XX 03-DEC-1999; 99US-0168667.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-638175/61.

XX Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition -

XX Disclosure; Page 420; 428pp; English.

XX The invention relates to the isolation of genes AAC58990-C59039 encoding the human secreted proteins AAB27560-B27609. This sequence represents a fragment of the protein encoded by the gene given in the descriptor line. The sequence is used as a query sequence for doing BLASTX searches to determine homologous sequence to the protein. The genes and proteins

CC are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

SQ Sequence 18 AA;

Query Match 66.7%; Score 4; DB 21; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
|||||

Db 8 SQPP 11

## RESULT 44

AAAG75974

ID AAG75974 standard; Protein; 18 AA.

XX

AC AAG75974;

XX 03-SEP-2001 (first entry)

XX Human colon cancer antigen protein SEQ ID NO:6738.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma.

XX Homo sapiens.

XX WO200122920-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-US26524.

XX 29-SEP-1999; 99US-0157137.

XX 03-NOV-1999; 99US-0163280.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Birse CE, Rosen CA;

XX WPI; 2001-235357/24.

XX N-PSDB; AAH35379.

XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -

XX Claim 11; Page 8201; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Pa,



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PR 02-OCT-1997; 97US-061060P.
XX 06-MAR-1998; 98WO-US04493.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Latleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI: 2002-634796/68.
DR N-PSDB; ABS73755.
XX
XX New isolated human secreted protein for diagnosing, preventing,
PT treating or ameliorating medical conditions and used as a food additive
PT or preservative -
XX
XX Example 1; SEQ ID No 577; 129pp; English.
PS
XX
XX The invention relates to an isolated protein that is one of 186 human
CC secreted proteins, given in the specification, encoded by one of
CC 309 cDNA sequences also given in the specification. The protein is used
CC in a pharmaceutical composition used to prevent, treat or ameliorate a
CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. The present sequence represents one of the novel human
CC secreted proteins of the invention.
CC Note: This sequence did not form part of the printed specification,
CC but was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=642052651.
XX
XX Sequence 18 AA;
SQ
Query Match 66.7%; Score 4; DB 23; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 SQPP 5
Db 14 SQPP 17
RESULT 46
ABG40649
ID ABG40649 standard; Peptide; 18 AA.
XX
XX ABG40649;
AC
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Human peptide encoded by genome-derived single exon probe SEQ ID 30314.
DE
XX
XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
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XX OS Homo sapiens.
XX PN WC200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US00665.
XX
XX 04-FEB-2000; 2000US-180312P.
XX 26-MAY-2000; 2000US-207456P.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-234687P.
XX 27-SEP-2000; 2000US-236359P.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
XX Claim 27; SEQ ID No 30314; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a peptide/protein
CC encoded by a single exon probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 18 AA;
SQ
Query Match 66.7%; Score 4; DB 23; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
|  
|  
|  
|  
8 SQPP 11

Db

RESULT 47  
ABP83106  
ID ABP83106 standard; Peptide; 18 AA.

XX  
AC ABP83106;

XX  
DT 04-MAR-2003 (first entry)

XX  
DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1779.

XX  
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.

XX  
OS Homo sapiens.

XX  
PN WO200261087-A2.

XX  
PD 08-AUG-2002.

XX  
PF 19-DEC-2001; 2001WO-US50107.

XX  
PR 19-DEC-2000; 2000US-257144P.

XX  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX  
PI Burmer GC, Roush CL, Brown JP;

XX  
DR WPI; 2003-046718/04.

XX  
PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating  
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
PT cancer or autoimmune diseases -

XX  
PS Claim 1; Fig 2; 523pp; English.

XX  
CC The present invention describes antigenic peptides (I) comprising:  
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular  
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity  
CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and  
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting  
CC an antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related disease, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or

CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention.

XX  
SQ Sequence 18 AA;

Query Match 66.7%; Score 4; DB 24; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.8e-02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 1 DSQP 4  
|  
|  
|  
3 DSQP 6

Db

RESULT 48  
ABG50962  
ID ABG50962 standard; Peptide; 19 AA.

XX  
AC ABG50962;

XX  
DT 25-FEB-2003 (first entry)

XX  
DE Human liver peptide, SEQ ID No 29610.

XX  
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KW hypercholesterolaemia; coronary heart disease.

XX  
OS Homo sapiens.

XX  
PN WO200157273-A2.

XX  
PD 09-AUG-2001.

XX  
PF 30-JAN-2001; 2001WO-US00664.

XX  
PR 04-FEB-2000; 2000US-0180312.

XX  
PR 26-MAY-2000; 2000US-0207456.

XX  
PR 30-JUN-2000; 2000US-0608408.

XX  
PR 03-AUG-2000; 2000US-0632366.

XX  
PR 21-SEP-2000; 2000US-0234687.

XX  
PR 27-SEP-2000; 2000US-0236359.

XX  
PR 04-OCT-2000; 2000GB-0024263.

XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.

XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX  
DR WPI; 2001-488898/53.

XX  
PT Human genome-derived single exon nucleic acid probes useful for  
PT analysing gene expression in human adult liver -

XX  
PS Claim 27; SEQ ID No 29610; 658pp; English.

XX  
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult  
CC liver. (I) may be used for predicting, measuring and displaying gene  
CC expression in samples derived from human adult liver. The genes  
CC identified may be involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which  
CC is associated with coronary heart disease. ABG47348-ABG59930 represent  
CC human liver single exon encoded peptides of the invention.

XX  
CC Note: The sequence information for this patent does not appear in the  
CC printed specification but was obtained in electronic format directly  
CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

XX  
SQ Sequence 19 AA;



Query Match 66.7%; Score 4; DB 22; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||  
Db 16 DSQP 19

RESULT 49  
ABB36114  
ID ABB36114 standard; Peptide; 19 AA.  
XX  
AC ABB36114;  
XX  
DT 04-FEB-2002 (first entry)  
XX  
DE Peptide #3620 encoded by human foetal liver single exon probe.  
XX  
KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX  
OS Homo sapiens.  
XX  
PN WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00669.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483447/52.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human fetal liver -  
XX  
PS Claim 27; SEQ ID NO 28749; 639pp + sequence listing; English.  
XX  
CC The invention relates to a single exon nucleic acid probe for  
CC measuring human gene expression in a sample derived from human foetal  
CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC foetal liver. The present sequence is a peptide encoded by a single exon  
CC nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 19 AA;

Query Match 66.7%; Score 4; DB 22; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||  
Db 16 DSQP 19

RESULT 50  
ABB21502  
ID ABB21502 standard; Protein; 19 AA.  
XX

AC ABB21502;  
XX  
DT 23-JAN-2002 (first entry)  
XX  
DE Protein #3501 encoded by probe for measuring heart cell gene expression.  
XX  
KW Human; gene expression; heart; microarray; vascular system;  
KW cardiovascular disease; hypertension; cardiac arrhythmia;  
KW congenital heart disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200157274-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00666.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488899/53.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts -  
XX  
PS Claim 15; SEQ ID No 23272; 530pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting,  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 19 AA;

Query Match 66.7%; Score 4; DB 22; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||  
Db 16 DSQP 19

RESULT 51  
AAM56897  
ID AAM56897 standard; Protein; 19 AA.  
XX  
AC AAM56897;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29002.  
XX  
KW Human; brain expressed exon; gene expression analysis; probe;  
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer.  
 XX Homo sapiens.  
 OS WO200157275-A2.  
 PN 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US000667.  
 PP 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-483446/52.  
 DR Single exon nucleic acid probes for analyzing gene expression in human brains -  
 XX Example 4; SEQ ID NO: 29002; 650pp + Sequence Listing; English.  
 PS The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, CC which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, CC epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.  
 CC  
 XX  
 SQ Sequence 19 AA;  
 Query Match 66.7%; Score 4; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DSQP 4  
 Db |||||  
 16 DSQP 19  
 RESULT 52  
 AAM69285  
 ID AAM69285 standard; Protein; 19 AA.  
 XX  
 AC AAM69285;  
 XX  
 DT 06-NOV-2001 (first entry)  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29591.  
 XX  
 KW Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200157276-A2.  
 PN 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US000668.  
 PP 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-488900/53.  
 DR Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -  
 XX Example 4; SEQ ID NO: 29591; 658pp + Sequence Listing; English.  
 PS The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers CC such as lymphoma, leukaemia and myeloma. The present sequence is a CC protein encoded by one of the probes of the invention.  
 CC  
 XX  
 SQ Sequence 19 AA;  
 Query Match 66.7%; Score 4; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DSQP 4  
 Db |||||  
 16 DSQP 19  
 RESULT 53  
 AAM17114  
 ID AAM17114 standard; Protein; 19 AA.  
 XX  
 AC AAM17114;  
 XX  
 DT 12-OCT-2001 (first entry)  
 DE Peptide #3548 encoded by probe for measuring cervical gene expression.  
 XX  
 KW Probe; human; microarray; gene expression; cervical epithelial cell;  
 KW cervical cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200157278-A2.  
 PN 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US000670.  
 PP 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-488901/53.  
 DR Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -  
 XX Claim 27; SEQ ID No 21940; 487pp; English.  
 PS  
 XX

CC The present invention relates to human single exon nucleic acid probes  
 CC (SENP; see AAI10068-AA128459). The present sequence is a peptide encoded  
 CC by one such probe. The SENPs are derived from human Hela cells. The SENPs  
 CC can be used to produce a single exon microarray, which can be used for  
 CC measuring human gene expression in a sample derived from human cervical  
 CC epithelial cells. By measuring gene expression, the probes are therefore  
 CC useful in grading and/or staging of diseases of the cervix, notably  
 CC cervical cancer.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 19 AA;

Query Match 66.7%; Score 4; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSQP 4  
 Db 16 DSQP 19

#### RESULT 54

AAAM29605  
 ID AAM29605 standard; Protein; 19 AA.

AC AAM29605; 4

XX 17-OCT-2001 (first entry)

DE Peptide #3642 encoded by probe for measuring placental gene expression.

KW Probe; microarray; human; placenta; antenatal diagnosis;  
 KW Genetic disorder.

OS Homo sapiens.

PN W0200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00663.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human placenta -

XX Claim 27; SEQ ID No 29874; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP;  
 CC see AAI13115-AA157546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for  
 CC predicting, measuring and displaying gene expression in samples derived  
 CC from human placenta. The probes are useful for antenatal diagnosis of  
 CC human genetic disorders.

XX Sequence 19 AA;

Query Match 66.7%; Score 4; DB 22; Length 19;

Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSQP 4  
 Db 16 DSQP 19

#### RESULT 55

ABG71082  
 ID ABG71082 standard; Peptide; 19 AA.

XX AC ABG71082;

XX 19-DEC-2002 (first entry)

DE Mouse scotin peptide.

XX p53-inducible polypeptide; cancer; drug therapy; apoptosis;  
 KW cell proliferation disorder; eczema; mouse; scotin.

OS Mus sp.

XX W0200268465-A2.

XX 06-SEP-2002.

XX 25-FEB-2002; 2002WO-GB008004.

XX 24-FEB-2001; 2001GB-0004588.

XX (UYDU-) UNIV DUNDEE.

XX Lane DP, Bourdon J, Renzing J;

XX WPI; 2002-706968/76.

XX New pro-apoptotic p53-inducible protein, useful for treating diseases  
 PT associated with abnormal cell proliferation, e.g. cancer or eczema, or  
 PT for determining p53 activity and/or p53 responsiveness to cancer drug  
 PT therapy -

XX Claim 17; Page 63; 89pp; English.

XX The invention describes a p53-inducible polypeptide, or its functionally  
 CC active fragments, derivatives or homologues. The nucleotide sequence  
 CC encoding the p53-inducible protein is useful in microarrays, DNA arrays  
 CC or DNA chips, or for determining p53 activity and/or p53 responsiveness  
 CC to cancer drug therapy from a biopsy. The nucleotide sequence is also  
 CC useful for determining a loss of expression of the p53-inducible gene  
 CC (particularly by RT-PCR), for isolating and identifying a promoter  
 CC and/or regulatory sequence (7634s) associated with any of the sequences,  
 CC for identifying and isolating agents (e.g. chemical compounds) that  
 CC promote apoptosis, or in the manufacture of a medicament for treating  
 CC diseases associated with abnormal proliferation of cells. These diseases  
 CC include cancer or eczema. The p53-inducible protein is useful for  
 CC treating diseases associated with abnormal cell proliferation, or in the  
 CC manufacture of a medicament for treating cancer. The treatment also  
 CC includes the application of an adenovirus containing the nucleotide  
 CC sequence encoding the p53-inducible protein. This is the amino acid  
 CC sequence of a mouse scotin peptide used in the production of anti-scotin  
 CC antibodies.

XX Sequence 19 AA;

Query Match 66.7%; Score 4; DB 23; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQPP 5  
 Db 10 SQPP 13

RESULT 56  
 ID ABG38899 standard; Peptide; 19 AA.  
 AC ABG38899;  
 XX  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 28564.  
 XX  
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00665.  
 XX  
 PR 04-FEB-2000; 2000US-180312P.  
 PR 26-MAY-2000; 2000US-207456P.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-234687P.  
 PR 27-SEP-2000; 2000US-236359P.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples -  
 XX  
 PS Claim 27; SEQ ID No 28564; 634pp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of  
 CC probes; the novel set of probes which hybridise at high stringency to a  
 CC nucleic acid expressed in the human lung; measuring gene expression in a  
 CC sample derived from human lung, comprising (a) contacting the array with  
 CC a collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of  
 CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open readings (ORF). The probes are used for gene

CC expression analysis, and for identifying exons in a gene, particularly  
 CC using human lung derived mRNA and for the study of lung diseases  
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
 CC haemorrhoidosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
 CC and hyaline membrane disease. The present sequence is a peptide/protein  
 CC encoded by a single exon probe of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 19 AA;  
 SQ  
 Query Match 66.7%; Score 4; DB 23; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSQP 4  
 Db 16 DSQP 19  
 |||||  
 RESULT 57  
 AAR72264  
 ID AAR72264 standard; Peptide; 20 AA.  
 XX  
 AC AAR72264;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 13-NOV-1995 (first entry)  
 XX  
 DE Glutamic acid decarboxylase (GAD65) fragment.  
 XX  
 KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;  
 KW insulin-dependent diabetes mellitus; stiff man disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9507992-A2.  
 XX  
 PD 23-MAR-1995.  
 XX  
 PF 24-AUG-1994; 94WO-US09478.  
 XX  
 PR 17-SEP-1993; 93US-0123859.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Tobin AV, Erlander MG, Kaufman DL, Claesalzier MJ;  
 XX  
 DR WPI; 1995-131360/17.  
 XX  
 XX New polypeptide fragments of glutamic acid decarboxylase - for  
 XX diagnosis and treatment of autoimmune disease, esp. insulin  
 XX dependent diabetes, also related nucleic acid, vectors,  
 XX antibodies, hybridoma (s) etc.  
 XX  
 PS Example 11; Page 76; 100pp; English.  
 XX  
 CC AAQ86481 and AAQ86482 encode AAR71733 and AAR79105, rat and human  
 CC glutamic acid decarboxylase (GAD65) respectively, from which the GAD65  
 CC fragments described in AAR72261-R72298 were derived. These fragments  
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose  
 CC and treat GAD-related autoimmune disorders, such as insulin  
 CC dependent diabetes mellitus or stiff man disease.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 CC

```

SQ Sequence 20 AA;
Query Match 66.7%; Score 4; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5
Db 15 SQPP 18

RESULT 58
AAY59549
ID AAY59549 standard; peptide; 20 AA.
XX AC AAY59549;
XX AC AAY59549;
DT 03-APR-2000 (first entry)
XX DE GAD65 fragment, peptide #4.
XX KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
KW insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
KW therapy.
XX OS Homo sapiens.
XX XX US5998366-A.
XX PN 07-DEC-1999.
XX PD 09-APR-1997; 97US-0827618.
XX PR 07-JUN-1995; 95US-0485725.
XX PR 21-SEP-1990; 90US-0586536.
XX PR 18-JUN-1991; 91US-0716909.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Tobin AJ, Kaufman DL, Erlander MG;
XX DR WPI; 2000-095930/08.
XX XX
XX Ameliorating glutamic acid decarboxylase associated autoimmune
PT disorders such as insulin dependent diabetes mellitus and Stiff man
PT disease -
XX Claim 1; Column 42; 61pp; English.
XX
CC This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and Stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.
XX
SQ Sequence 20 AA;
Query Match 66.7%; Score 4; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5
Db 15 SQPP 18

RESULT 59
ABG71083
ID ABG71083 standard; Peptide; 20 AA.
XX AC ABG71083;
XX DT 19-DEC-2002 (first entry)
XX DE Human scotin peptide.
XX KW p53-inducible polypeptide; cancer; drug therapy; apoptosis;
KW cell proliferation disorder; eczema; human; scotin.
XX OS Homo sapiens.
XX PN WO200268465-A2.
XX PD 06-SEP-2002.
XX PF 25-FEB-2002; 2002WO-GB00804.
XX PR 24-FEB-2001; 2001GB-0004588.
XX PA (UYDU-) UNIV DUNDEE.
XX PI Lane DP, Bourdon J, Renzing J;
XX DR WPI; 2002-706968/76.
XX XX
XX New pro-apoptotic p53-inducible protein, useful for treating diseases
PT associated with abnormal cell proliferation, e.g. cancer or eczema, or
PT for determining p53 activity and/or p53 responsiveness to cancer drug
PT therapy -
XX Claim 17; Page 63; 89pp; English.
XX
CC The invention describes a p53-inducible polypeptide, or its functionally
CC active fragments, derivatives or homologues. The nucleotide sequence
CC encoding the p53-inducible protein is useful in microarrays, DNA arrays
CC or DNA chips, or for determining p53 activity and/or p53 responsiveness
CC to cancer drug therapy from a biopsy. The nucleotide sequence is also
CC useful for determining a loss of expression of the p53-inducible gene
CC (particularly by RT-PCR), for isolating and identifying a promoter
CC and/or regulatory sequence(7634s) associated with any of the sequences,
CC for identifying and isolating agents (e.g. chemical compounds) that
CC promote apoptosis or in the manufacture of a medicament for treating
CC diseases associated with abnormal proliferation of cells. These diseases
CC include cancer or eczema. The p53-inducible protein is useful for
CC treating diseases associated with abnormal cell proliferation, or in the
CC manufacture of a medicament for treating cancer. The treatment also
CC includes the application of an adenovirus containing the nucleotide
CC sequences encoding the p53-inducible protein. This is the amino acid
CC sequence of a human scotin peptide used in the production of anti-scotin
CC antibodies.
XX
SQ Sequence 20 AA;
Query Match 66.7%; Score 4; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5
Db 16 SQPP 19

RESULT 60
ABG77821
ID ABG77821 standard; Peptide; 3 AA.
XX AC ABG77821;
XX DT 05-NOV-2002 (first entry)
XX

```

Targetting peptide selective for human organ, tissue or cell type #354.

Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;  
immunomodulator; antibacterial; antiviral; gene therapy; cancer;  
arthritis; diabetes; inflammatory disease; atherosclerosis;  
autoimmune disease; bacterial infection; viral infection;  
cardiovascular disease; degenerative disease.

Homo sapiens.

WO200220723-A2.

14-MAR-2002.

07-SEP-2001; 2001WO-US28044.

08-SEP-2000; 2000US-231266P.

17-JAN-2001; 2001US-0765101.

(TEXA ) UNIV TEXAS SYSTEM.

Arap W, Pasqualini R;

WPI; 2002-599247/64.

New targeting peptides identified by phage display, useful for treating  
a disease state, e.g. cancer, diabetes, inflammatory disease, or  
atherosclerosis, autoimmune disease, bacterial or viral infection or  
cardiovascular disease

Example 3; Page 82; 269pp; English.

The invention describes an isolated peptide of 100 amino acids or less  
in size. The peptide is useful for treating a disease state, e.g. cancer,  
arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune  
disease, bacterial infection, viral infection, cardiovascular disease  
or degenerative disease. This sequence represents a human targeting  
peptide selective for human organs, tissues or cell types.

Sequence 3 AA;

Query Match 50.0%; Score 3; DB 23; Length 3;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 1 PPV 3

RESULT 61

AAR45397  
ID AAR45397 standard; peptide; 4 AA.

AC AAR45397;

DT 11-JUL-1994 (first entry)

DE Prolyl endopeptidase inhibitor peptide-6.

Corn; maize; prolyl endopeptidase; dementia; gamma-zein;  
protease inhibitor; Alzheimer's Disease.

OS Zea mays.

PN JP053331072-A.

PD 14-DEC-1993.

XX 27-MAY-1992; 92JP-0160354.

XX 27-MAY-1992; 92JP-0160354.

PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.

PA (SHOS ) SHOWA SANGYO CO.

XX WPI; 1994-022830/03.

XX Prolyl endopeptidase inhibitor for treating dementia - are  
PT prepared by hydrolysis of corn protein

XX Claim 1; Page 2; 8pp; Japanese.

XX This peptide is one of 10 claimed peptides having prolyl  
CC endopeptidase inhibitory activity; the peptide is expected to be of  
CC use for the prophylaxis and treatment of dementia. The peptide can  
CC be prepared by hydrolysis of gamma-zein from corn or by standard  
CC peptide synthesis.

XX Sequence 4 AA;

Query Match 50.0%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 2 PPV 4

RESULT 62

AAR45399  
ID AAR45399 standard; peptide; 4 AA.

AC AAR45399;

XX DT 11-JUL-1994 (first entry)

XX Prolyl endopeptidase inhibitor peptide-8.

XX Corn; maize; prolyl endopeptidase; dementia; gamma-zein;  
KW protease inhibitor; Alzheimer's Disease.

XX Synthetic.

XX JP053331072-A.

XX 14-DEC-1993.

XX 27-MAY-1992; 92JP-0160354.

XX 27-MAY-1992; 92JP-0160354.

PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.

PA (SHOS ) SHOWA SANGYO CO.

XX WPI; 1994-022830/03.

XX Prolyl endopeptidase inhibitor for treating dementia - are  
PT prepared by hydrolysis of corn protein

XX Claim 1; Page 2; 8pp; Japanese.

XX This peptide is one of 10 claimed peptides having prolyl  
CC endopeptidase inhibitory activity; the peptide is expected to be of  
CC use for the prophylaxis and treatment of dementia. The peptide is  
CC synthesised by standard methods.

XX Sequence 4 AA;

Query Match 50.0%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 1 PPV 3

```

Db          2 PPV 4

RESULT 63
AAR45401
ID AAR45401 standard; peptide; 4 AA.
XX
AC AAR45401;
XX
DT 11-JUL-1994 (first entry)
XX
DE Prolyl endopeptidase inhibitor peptide-10.
XX
CC Corn; maize; prolyl endopeptidase; dementia; gamma-zetin;
KW protease inhibitor; Alzheimer's Disease.
XX
OS Synthetic.
XX
PN JP05331072-A.
XX
PD 14-DEC-1993.
XX
PF 27-MAY-1992; 92JP-0160354.
XX
PR 27-MAY-1992; 92JP-0160354.
XX
PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA (SHOS ) SHOWA SANGYO CO.
XX
DR WPI; 1994-022830/03.
XX
PT Prolyl endopeptidase inhibitor for treating dementia - are
PT prepared by hydrolysis of corn protein
XX
PS Claim 1; Page 2; 8pp; Japanese.
XX
CC This peptide is one of 10 claimed peptides having prolyl
CC endopeptidase inhibitory activity; the peptide is expected to be of
CC use for the prophylaxis and treatment of dementia. The peptide is
CC synthesised by standard methods.
XX
SQ Sequence 4 AA;
Query Match 50.0%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6
DB 2 PPV 4

RESULT 64
AAR50249
ID AAR50249 standard; peptide; 4 AA.
XX
AC AAR50249;
XX
DT 10-MAR-2003 (updated)
DT 02-NOV-1994 (first entry)
XX
DE Platelet GPIb alpha chain residues 319-322.
XX
KW platelet; thrombocyte; ITP; idiopathic thrombocytopenic purpura;
KW haemocatharsis; coagulation; GPIb alpha chain; vWF;
KW von Willebrand Factor.
XX
OS Synthetic.
XX
PN JP06065298-A.
XX
PD 08-MAR-1994.
XX

PF 18-AUG-1992; 92JP-0219311.
XX
PR 18-AUG-1992; 92JP-0219311.
XX
PA (TOYM ) TOYOBO KK.
XX
DR WPI; 1994-115197/14.
XX
PT Platelet-derived polypeptide and antiplatelet antibody adsorbing
PT material - for treatment of severe ITP and a hemocatharsis
XX
PS Claim 1; Page 2; 11pp; Japanese.
XX
CC New polypeptides contain at least one of the nine peptide fragments
CC AAR50246-R50250 and AAR51219-R51223 in an amino acid chain of at least
CC 70 residues. The fragments are derived from GPIb protein alpha
CC chain and can be immobilised, e.g. on cellulose, to provide an
CC anti-platelet antibody adsorbing material useful for treating
CC severe ITP or haemocatharsis.
CC (Updated on 10-MAR-2003 to add missing OS field.)
XX
SQ Sequence 4 AA;
Query Match 50.0%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3
DB 1 DSQ 3

RESULT 65
AAR66123
ID AAR66123 standard; peptide; 4 AA.
XX
AC AAR66123;
XX
DT 07-JUL-1995 (first entry)
XX
DE Peptide derived from platelet GPIb receptor alpha chain a.a. 319-22.
XX
KW Platelet; GPI; GP2b; GP3a; receptor; blood; factor; fibrinogen; plasma;
KW von Willebrand factor; immobilisation; adsorbent; autoimmune disease;
KW antibody; idiopathic thrombocytopenic purpura; ITP; circulation; ligand.
XX
OS Synthetic.
XX
PN JP06269498-A.
XX
PD 27-SEP-1994.
XX
PF 17-MAR-1993; 93JP-0057207.
XX
PR 17-MAR-1993; 93JP-0057207.
XX
PA (TOYM ) TOYOBO KK.
XX
DR WPI; 1994-346230/43.
XX
PT Anti-platelet-antibody adsorbent useful for external circulation
PT therapy - consisting of opt. modified peptide(s) having
PT binding-affinity and immobilised to nonwoven fabric
XX
PS Disclosure; Page 3; 11pp; Japanese.
XX
CC A series of peptides (AAR66112-35), optionally modified, derived from
CC GPI alpha-chain, GP2b or GP3a receptors on platelets, which bind blood
CC factors such as fibrinogen and von Willebrand factor. The modified
CC peptides can be immobilised on a non-woven fabric adsorbent. The
CC adsorbent can be used to remove anti-platelet-antibodies useful in
CC treating patients with autoimmune diseases such as severe idiopathic
CC thrombocytopenic purpura (ITP). The use of the non-woven fabric

```

CC eliminates the need for the separation of the blood plasma and permits  
 CC external circulation for treatment of the entire blood. The functional  
 CC groups facilitate the introduction of peptides as ligands.

XX SQ Sequence 4 AA;  
 Query Match 50.0%; Score 3; DB 15; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSQ 3  
 Db 1 DSQ 3

RESULT 66  
 AAR76701  
 ID AAR76701 standard; peptide; 4 AA.

XX AC AAR76701;  
 XX DT 25-MAR-2003 (updated)  
 DT 02-DEC-1995 (first entry)  
 XX DE N-terminal sequence of Shigella enterotoxin 1 (ShET1).  
 XX KW Shigella flexneri 2a; enterotoxin.  
 XX OS Shigella flexneri 2a.

XX FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "duplicate signal detected for Asp"  
 FT Misc-difference 2 /note= "duplicate signal detected for Thr"  
 FT Misc-difference 4 /note= "duplicate signal detected for Leu"  
 XX WO9515396-A1.

XX PD 08-JUN-1995.  
 XX PF 01-DEC-1994; 94WO-US13289.  
 XX PR 30-NOV-1994; 94US-0351147.  
 PR 02-DEC-1993; 93US-0160317.  
 XX (UYMA-) UNIV MARYLAND BALTIMORE.

XX PI Fasano A, Levine MM, Nataro JP, Noriega F;  
 XX WPI; 1995-215275/28.

XX PT Enterotoxin(s) of Shigella flexneri and DNA encoding them - used to  
 PT isolate antibodies and to develop non-reactogenic vaccine.

XX PS Example; Table 2, page 32; 88pp; English.

XX CC Large-scale prepn. of Shigella flexneri 2a enterotoxin was  
 CC undertaken in order to obtain sufficient material for further  
 CC characterization and analyses. Three bands were selected on the  
 CC basis of enterotoxin activity. These bands had approx. MW of 63 kDa,  
 CC 52 kDa and 41 kDa. The N-terminal sequences of these bands were  
 CC analysed. AAR76701 shows the N-terminal sequence of both the 63 kDa  
 CC and the 53 kDa bands in which the proposed A:B subunit ratios are  
 CC 1:3 and 1:2 respectively. The N-terminal sequence of the 41kDa band  
 CC is given in AAR76702. The proposed A:B subunit ratio of this band is  
 CC 1:1. A definitive extended sequence could not be determined from the  
 CC material available for any of the three bands. However, the  
 CC identical putative AA sequence was found for the first four  
 CC residues of all three bands. Moreover, the data derived suggested  
 CC that two distinct N-termini were being identified.  
 CC (Updated oh 25-MAR-2003 to correct PN field.)

XX SQ Sequence 4 AA;  
 Query Match 50.0%; Score 3; DB 16; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PPV 6  
 Db 2 PPV 4  
 RESULT 67  
 ABJ18192  
 ID ABJ18192 standard; Peptide; 4 AA.  
 XX AC ABJ18192;  
 XX DT 30-JAN-2003 (first entry)  
 XX DE Growth hormone releasing peptide #40.  
 XX KW Growth hormone releasing peptide; GH; blood growth hormone level;  
 KW hypothalamic pituitary dwarfism; osteoporosis; burn; wound healing;  
 KW surgery recovery; debilitating illness recovery; cachexia; sleep;  
 KW atherosclerosis; congestive heart failure; fur production;  
 KW body growth enhancement; milk production enhancement; wool production.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 1 /label= Aib  
 FT /note= "Alpha-2-aminoisobutyric acid"  
 FT Misc-difference 2 /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Misc-difference 4 /note= "D-form residue; C-terminal amide"  
 XX WO200009537-A2.  
 XX PD 24-FEB-2000.  
 XX PF 06-AUG-1999; 99WO-US17867.  
 XX PR 14-AUG-1998; 98US-0096795.  
 PR 16-APR-1999; 99US-0129806.  
 XX (TULA) TULANE EDUCATIONAL FUND.  
 XX PI Bowers CY, Momany F, Liang Y;  
 XX WPI; 2000-205974/18.  
 XX PT New growth hormone releasing peptides, useful for treating e.g.  
 PT dwarfism, osteoporosis, burns, wounds, cachexia, atherosclerosis or  
 PT cardiac disorders or for increasing muscle, milk, wool or fur  
 PT production in animals -  
 XX Claim 29; Page 20; 63pp; English.  
 XX CC The invention comprises peptides that promote the release of growth  
 CC hormone. The growth hormone releasing peptides of the invention are  
 CC useful for promoting the release and elevation of blood growth hormone  
 CC (GH) levels. The peptides of the invention can be used to treat  
 CC hypothalamic pituitary dwarfism, osteoporosis and burns. The peptides of  
 CC the invention can also be used for: promoting wound healing; promoting  
 CC recovery from surgery or from acute/chronic debilitating illnesses;  
 CC prevention/reduction of cachexia in cancer patients; decreasing  
 CC atherosclerosis, improving cardiac performance in congestive heart  
 CC failure, or to improve sleep. The peptides of the invention can further



CC be used to enhance body growth in animals, enhance milk production in  
 CC cows and enhance wool/fur production in mammals. The peptides of the  
 CC invention can also be used diagnostically (e.g. to discover the loss of  
 CC GH receptor functioning). The present amino acid sequence represents a  
 CC growth hormone releasing peptide of the invention.

XX Sequence 4 AA;

Query Match 50.0%; Score 3; DB 21; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6

DB 2 PPV 4

RESULT 68

AAU05448

ID AAU05448 standard; Peptide; 4 AA.

XX

AC AAU05448;

XX

DT 24-OCT-2001 (first entry)

DE Synthetic tetrapeptide ligand 30.

XX

KW Tetrapeptide ligand; drug design; high throughput screening; HTS; MQSAR;  
 KW Multivariate Quantitative Structure Activity relationships.

XX

OS Synthetic.

XX

PN WO200136980-A2.

XX

PD 25-MAY-2001.

XX

PF 20-NOV-2000; 2000WO-GB04420.

XX

PR 18-NOV-1999; 99GB-0027346.

XX

PA (MELA-) MELACURE THERAPEUTICS AB.

PA (PETT/) PETT C P.

XX

PI Lundstedt T, Andersson P, Wikberg J, Muceniece R, Prusis P;

XX

XX WPI; 2001-432565/46.

DR

XX

PT A novel method for identifying the interaction site, binding site or  
 PT active site in a macromolecule, using of informative combinatorial  
 PT chemistry, informative peptide libraries and Multivariate Quantitative  
 PT Structure Activity Relationships -

XX

PS Example 5; Fig 27; 131pp; English.

XX

CC The sequence represents a tetrapeptide ligand selected according to  
 CC 2 (12-7) fractional factorial design +3 cp (or 1 cp 2 random), which  
 CC were used to model the interaction of a ligand with its target. The  
 CC invention relates to characterizing the interaction between a Ligand Y  
 CC and a Target X by obtaining information (e.g. Multivariate Quantitative  
 CC Structural Activity Relationships, MQSAR) representing one or more  
 CC physical and/or chemical properties of targets of type X and type Y  
 CC to produce a model of interaction. The methods of the invention are  
 CC useful for identifying outliers of type X or outliers  
 CC of type Y, drug design, design or identification of lead compounds (e.g.  
 CC by high throughput screening, HTS), design of ligands of type Y with  
 CC improved affinity and/or selectivity for targets of type X, protein  
 CC engineering, design of DNA or RNA molecules, design of artificial targets  
 CC of type X/or artificial ligands of type Y, analysis and/or in the  
 CC engineering of regions and/or parts of targets of type X and/or ligands  
 CC of type Y, design of organic compound, catalyst, pharmaceutical, drug,  
 CC macromolecule being capable of binding a molecule, peptidomimetic,  
 CC protein, enzyme, antibody, molecule, macromolecule, DNA, RNA or a  
 CC carbohydrate. The methods are also useful for designing new ligands for

CC known targets and/or for new targets.

XX

SQ Sequence 4 AA;

Query Match 50.0%; Score 3; DB 22; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4

DB 1 SQP 3

RESULT 69

ABG69226

ID ABG69226 standard; Peptide; 4 AA.

XX

AC ABG69226;

XX

DT 21-OCT-2002 (first entry)

XX

DE Protein SBRPR2 repeat unit #1.

XX

KW Amino acid repetitive unit; structural protein; prosthetic device;  
 KW synthetic fibre; silk fibroin; elastin; collagen; fibronectin; FCB.

XX

OS Unidentified.

XX

PN US6355776-B1.

XX

PD 12-MAR-2002.

XX

PF 22-NOV-1999; 99US-0444791.

XX

PR 29-OCT-1987; 87US-0114618.

PR

07-JUN-1995; 95US-0482085.

PR

04-NOV-1986; 86US-0927258.

PR

22-APR-1993; 93US-0053049.

PR

29-DEC-1993; 93US-0175155.

XX

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX

PI Ferrari FA, Richardson C, Chambers J, Causey S, Pollock TJ;

XX

PI Cappello J, Crissman JW;

XX

XX WPI; 2002-572759/61.

DR

XX

PS Claim 3; Column 178; 101pp; English.

XX

CC The invention relates to a recombinantly produced protein of 30-250 kD  
 CC comprising at least 50% (by number of amino acids (aa)) of a naturally  
 CC occurring repeat unit, of 3-20 aa, from a naturally occurring  
 CC structural protein (especially silk fibroin and elastin, also  
 CC collagen and fibronectin (FCB)). The recombinant proteins are useful,  
 CC e.g. as structural components of prosthetic devices or synthetic fibres.  
 CC The physical properties of the protein can be adjusted by varying  
 CC the combination of repeat units, and the protein may retain the  
 CC properties of natural proteins while also having additional properties.  
 CC The present sequence is a structural protein repeat unit suitable  
 CC for incorporation into the protein of the invention.

XX Sequence 4 AA;

Query Match 50.0%; Score 3; DB 23; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6

DB 1

Db 1 PPV 3

RESULT 70  
ABB77684  
ID ABB77684 standard; peptide; 4 AA.

AC ABB77684;  
XX  
XX 01-JUL-2002 (first entry)

DE Linker peptide sequence.

KW Intracellular delivery; transfection agent; cancer; infectious disease;  
KW peptide vector.

OS Synthetic.

PN WO200210201-A2.

PD 07-FEB-2002.

PF 26-JUL-2001; 2001WO-US23406.

PR 31-JUL-2000; 2000US-221932P.

XX (ACTI-) ACTIVE MOTIF.

PA (CNRS) CENT NAT RECH SCI.

XX Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;  
PI Horndorp K;

XX WPI; 2002-329441/36.

XX Transfection agent that comprises a peptide comprising hydrophobic and  
PT hydrophilic domain and having amino acid residues of specified length  
PT is useful for a non-covalent association with and transport of a  
PT heterologous compound into a cell -

PS Example 2; Page 61; 156pp; English.

XX The invention relates to a transfection agent comprising a peptide of  
CC about 16 - 30 amino acids in length. Peptides of the invention comprise  
CC a hydrophobic domain, a hydrophilic domain, optionally a spacer sequence  
CC between the domains and a functional group conjugated to at least one  
CC terminal of the peptide. Peptides of the invention are useful for a  
CC non-covalent association with and transport of a heterologous compound  
CC into a cell. They are also useful for promoting the cellular  
CC internalisation of at least one member e.g. peptide, proteins,  
CC antibodies, their derivatives and/or conjugates. They may form part of a  
CC pharmaceutical composition to deliver the compound selected from a  
CC diagnostic or therapeutic compound, to treat at least one condition such  
CC as cancer or an infectious disease, or which targets a cancerous cell or  
CC pathogen-infected cell and to deliver a peptide or inhibitor that  
CC disrupts the activity of the enzyme. The agent of the invention has a  
CC transfection efficiency of at least 5% for at least two of the members of  
CC the group of the compounds. The agent has a good delivery efficiency for  
CC a broad spectrum of compounds and cell types, has a low toxicity, are  
CC easy to handle and easy to formulate in conjunction with the many  
CC different compound types that it can deliver. The peptides are serum  
CC sensitive, thus they bode particularly well for systemic and/or localised  
CC in patients. The current sequence represents a linker peptide that is  
CC used in the synthesis of new peptide vectors.

XX Sequence 4 AA;

Query Match 50.0%; Score 3; DB 23; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
|||  
Db 2 SQP 4

RESULT 71

AAR45396  
ID AAR45396 standard; peptide; 5 AA.

XX AAR45396;

XX 11-JUL-1994 (first entry)

XX Prolyl endopeptidase inhibitor peptide-5.

KW Corn; maize; prolyl endopeptidase; dementia; gamma-zein;  
KW protease inhibitor; Alzheimer's Disease.

XX Zea mays.

XX JP05331072-A.

XX 14-DEC-1993.

XX 27-MAY-1992; 92JP-0160354.

XX 27-MAY-1992; 92JP-0160354.

XX (AGEN) AGENCY OF IND SCI & TECHNOLOGY.

XX (SHOS) SHOWA SANGYO CO.

XX WPI; 1994-022830/03.

XX Prolyl endopeptidase inhibitor for treating dementia - are  
PT prepared by hydrolysis of corn protein

XX Claim 1; Page 2; 8pp; Japanese.

XX This peptide is one of 10 claimed peptides having prolyl  
CC endopeptidase inhibitory activity; the peptide is expected to be of  
CC use for the prophylaxis and treatment of dementia. The peptide can  
CC be prepared by hydrolysis of gamma-zein from corn or by standard  
CC peptide synthesis.

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 3 PPV 5

RESULT 72

AAR60999  
ID AAR60999 standard; peptide; 5 AA.

XX AAR60999;

XX 25-MAR-2003 (updated)

XX 14-APR-1995 (first entry)

XX Proline rich sequence in the Ras GAP protein.

KW CD4; T cell; surface antigen; receptor; MHC class II antigen;  
KW protein-tyrosine kinase; p56lck; tcr/CD3 complex; PI 3-kinase;  
KW PI 4-kinase; lipid kinase; T cell receptor complex; Ras GAP.

XX Synthetic.

XX WO9418832-A1.

XX 01-SEP-1994.

XX

PF 25-FEB-1994; 94WO-US01840.  
 XX  
 PR  
 XX 26-FEB-1993; 93US-0023915.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 XX  
 PI Cantley L, Kanteti P, Rudd CE;  
 XX WPI; 1994-293868/36.  
 DR  
 XX Method for inhibiting or reducing signal transduction - utilises  
 PT peptide or corresp. nucleic acid which decreases association of  
 PT PI 3- or 4- kinase with CD4/p56lck  
 XX  
 PS Example; Page 32; 46pp; English.  
 XX  
 CC In order for certain T cells to make an optimal response to antigen,  
 CC it is necessary for the T cell surface antigen CD4 to couple to the  
 CC protein-tyrosine kinase p56lck. (CD4-p56lck is known to associate  
 CC with and functionally synergise with the Tcr/CD3 complex.) CD4-p56lck  
 CC complex in T cells associates with two lipid kinases: PI 3-kinase  
 CC and PI 4-kinase, which suggests that these lipid kinases are also  
 CC involved in intracellular signalling via the T cell receptor complex.  
 CC The interaction of a lipid kinase, such as PI 3-kinase or PI 4-  
 CC kinase, with CD4-p56lck, may be blocked by administering a peptide.  
 CC This peptide may be a fragment of the cytoplasmic domain of CD4  
 CC (eg AAR60987-R60991), a fragment of p56lck (eg AAR60992, AAR60993),  
 CC a fragment of PI 3-kinase (eg AAR60994, AAR60995), or a fragment of  
 CC PI 4-kinase. Other proline-rich peptides that bind to SH3 binding  
 CC sequences can also be used, such as the fragment of  
 CC 3BP1 protein that binds to the SH3 of the Abl kinase (AAR60997), or  
 CC a sequence found in the SOS protein (AAR60999).  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 5 AA;  
 Query Match 50.0%; Score 3; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PPV 6  
 DB 1 PPV 3  
 RESULT 73  
 AAR83783  
 ID AAR83783 standard; peptide; 5 AA.  
 AC AAR83783;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 25-FEB-1996 (first entry)  
 XX  
 XX Monocyte cytotoxicity-inducing N-terminal peptide.  
 DE  
 XX Monocyte cytotoxicity inducing factor; treatment; diagnosis; cancer;  
 KW tumour; T-cell; malignancy.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US5434247-A.  
 PN  
 XX 18-JUL-1995.  
 PD  
 XX 17-JUN-1992; 92US-0901717.  
 PF  
 XX 17-JUN-1992; 92US-0901717.  
 PR 10-OCT-1986; 86US-0917983.  
 PR 04-OCT-1989; 89US-0417162.  
 PR 07-DEC-1990; 90US-0624053.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.

XX Jones CM;  
 PI  
 XX WPI; 1995-263281/34.  
 DR  
 XX  
 XX New peptide(s) which induce monocyte cytotoxicity - useful in  
 PT treatment of cancer and infectious diseases and for diagnosis e.g.  
 PT of T-cell malignancies  
 PT  
 XX  
 PS Claim 5; Column 37; 32pp; English.  
 XX  
 CC AAR83781-R83783 are N-terminal peptides of a new lymphokine molecule  
 CC known as the monocyte cytotoxicity inducing factor (MCF). Purified  
 CC MCF is capable of inducing human monocytes to a cytotoxic state. The  
 CC N-terminal peptides fragments of MCF are useful in the treatment of  
 CC cancer (leukaemia or solid tumours) and infectious disease partic.  
 CC those where the pathogen is present in phagocytes, e.g. tuberculosis  
 CC and leishmaniasis. Also antibodies may be raised to identify MCF in  
 CC blood for diagnosis or evaluation of T-cell malignancies. The  
 CC peptides have equivalent activity to MCF but are easier and less  
 CC expensive to prepare, penetrate tissue better and are less likely  
 CC to invoke an immune responses.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 5 AA;  
 Query Match 50.0%; Score 3; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSQ 3  
 DB 3 DSQ 5  
 RESULT 74  
 AAW29522  
 ID AAW29522 standard; peptide; 5 AA.  
 XX  
 XX AAW29522;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 22-APR-1998 (first entry)  
 XX  
 XX Platelet aggregation inhibitor pentapeptide SEQ ID NO:2.  
 DE  
 XX Platelet aggregation; inhibitor; pentapeptide; blood; barley.  
 KW  
 XX Hordeum vulgare.  
 OS  
 XX EP801074-A1.  
 PN  
 XX 15-OCT-1997.  
 PD  
 XX 03-JUN-1996; 96EP-0108882.  
 PF  
 XX 14-MAR-1996; 96US-0615888.  
 PR  
 XX (HAGI/) HAGIWARA Y.  
 PA  
 XX Badamchiam M, Hagiwara Y, Hagiwara H;  
 PI  
 XX WPI; 1997-491946/46.  
 DR  
 XX Penta:peptide(s) useful as platelet aggregation inhibitors - derived  
 PT from freeze-dried and ground green barley leaves  
 PT  
 XX Claim 2; Page 10; 22pp; English.  
 PS  
 XX A composition has been developed consisting of a pentapeptide. The  
 CC present sequence represents a specifically claimed pentapeptide derived  
 CC from freeze-dried and ground green barley leaves. The pentapeptide can  
 CC be used for inhibiting blood platelet aggregation in mammals, e.g. by

CC parental administration at doses of 0.1-10 mg/kg.  
 CC (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 5 AA;

Query Match 50.0%; Score 3; DB 18; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSQ 3

Db 2 DSQ 4

# RESULT 75

AAW81247

ID AAW81247 standard; peptide; 5 AA.

XX AC AAW81247;

XX AC AAW81247;

DT 25-MAR-2003 (updated)

DT 30-APR-1999 (first entry)

XX DE Human iNOS peptide fragment PS-5206.

XX DE Human iNOS peptide fragment PS-5206.

XX KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;

XX KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;

XX KW myocardial infarction; tissue rejection; transplantation; psoriasis;

XX KW autoimmune disease; multiple sclerosis.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Modified-site 5

FT FT /note= "His residue amidated"

XX PN WO9845710-A1.

XX PD 15-OCT-1998.

XX PF 11-APR-1997; 97WO-US06500.

XX PR 07-APR-1997; 97US-0833506.

XX PA (WEBB/) WEBBER R.

XX PI Webber R;

XX WPI; 1998-594495/50.

XX PT Detection of human inducible nitric oxide synthase - using an

PT immunoassay in which a sample is contacted with a specific binding

PT entity reactive with human iNOS or mimics.

XX PS Example 4; Page 38; 93pp; English.

XX CC This invention describes an immunoassay method where a sample with a

CC specific binding entity (e.g. a monoclonal antibody) reactive to human

CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used

CC to detect the presence of human iNOS protein in the sample. The method

CC can be used for the detection and quantitation of human iNOS in cells and

CC tissues for various pathological conditions such as sepsis, septic

CC shock, myocardial infarction, rejection of tissue in organs following

CC transplantation, monitoring "flare ups" in certain autoimmune diseases

CC such as lupus, psoriasis, and multiple sclerosis. This sequence

CC represents a peptide from human iNOS which is used in the method of the

CC invention.

CC (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 3; DB 19; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches

3; Conservative

0; Mismatches

0; Indels

0; Gaps

Qy 1 DSQ 3

Db 2 DSQ 4

Search completed: November 25, 2003, 18:15:57

Job time : 21.4362 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 11.9362 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-13

Perfect score: 6

Sequence: 1 DSQPPV 6

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
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- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	15	US-10-281-652-13
2	4	66.7	7	12	US-09-990-833C-10
3	4	66.7	8	10	US-09-984-245-148
4	4	66.7	8	11	US-09-966-262-148
5	4	66.7	8	11	US-09-983-966-148
6	4	66.7	8	12	US-09-933-767-1242
7	4	66.7	8	15	US-10-143-090-148
8	4	66.7	9	12	US-10-365-908-51
9	4	66.7	9	12	US-10-365-908-76
10	4	66.7	9	15	US-10-195-117-34
11	4	66.7	10	12	US-10-365-908-61
12	4	66.7	10	12	US-10-365-908-105
13	4	66.7	12	11	US-09-229-751A-34
14	4	66.7	12	11	US-09-229-751A-43
15	4	66.7	12	11	US-09-954-385-182
					Sequence 13, Appl
					Sequence 10, Appl
					Sequence 148, Appl
					Sequence 148, Appl
					Sequence 148, Appl
					Sequence 1242, Ap
					Sequence 148, Appl
					Sequence 51, Appl
					Sequence 76, Appl
					Sequence 34, Appl
					Sequence 61, Appl
					Sequence 105, Appl
					Sequence 34, Appl
					Sequence 43, Appl
					Sequence 182, Appl

16	4	66.7	12	12	US-10-116-275-65	Sequence 65, Appl
17	4	66.7	12	15	US-10-185-050-135	Sequence 135, Appl
18	4	66.7	12	15	US-10-185-815-19	Sequence 19, Appl
19	4	66.7	13	15	US-10-012-542-530	Sequence 530, Appl
20	4	66.7	14	11	US-09-030-061-12	Sequence 12, Appl
21	4	66.7	14	14	US-10-100-057-12	Sequence 12, Appl
22	4	66.7	15	12	US-10-294-891-17	Sequence 17, Appl
23	4	66.7	15	14	US-10-036-444-7	Sequence 7, Appl
24	4	66.7	18	9	US-09-864-761-48166	Sequence 48166, A
25	4	66.7	18	11	US-09-809-391-577	Sequence 577, App
26	4	66.7	18	12	US-09-882-171-577	Sequence 577, App
27	4	66.7	18	15	US-10-106-698-6748	Sequence 6748, Ap
28	4	66.7	18	15	US-10-225-567A-1779	Sequence 1779, Ap
29	4	66.7	19	9	US-09-864-761-36800	Sequence 36800, A
30	3	50.0	4	11	US-09-915-914B-24	Sequence 24, Appl
31	3	50.0	4	12	US-10-309-627-5	Sequence 5, Appl
32	3	50.0	4	15	US-10-096-986-12	Sequence 12, Appl
33	3	50.0	5	11	US-09-992-896-42	Sequence 42, Appl
34	3	50.0	5	14	US-10-014-485A-128	Sequence 128, App
35	3	50.0	5	14	US-10-014-485A-129	Sequence 129, App
36	3	50.0	5	14	US-10-099-895-12	Sequence 12, Appl
37	3	50.0	5	14	US-10-099-895-16	Sequence 16, Appl
38	3	50.0	5	14	US-10-099-895-28	Sequence 28, Appl
39	3	50.0	5	15	US-10-096-986-3	Sequence 3, Appl
40	3	50.0	5	15	US-10-096-986-13	Sequence 13, Appl
41	3	50.0	6	10	US-09-865-018-23	Sequence 23, Appl
42	3	50.0	6	10	US-09-727-963A-68	Sequence 68, Appl
43	3	50.0	6	11	US-09-992-896-41	Sequence 41, Appl
44	3	50.0	6	12	US-10-159-006-64	Sequence 64, Appl
45	3	50.0	6	12	US-10-161-791-249	Sequence 249, App
46	3	50.0	6	15	US-10-028-075B-141	Sequence 141, App
47	3	50.0	6	15	US-10-028-075B-141	Sequence 141, App
48	3	50.0	7	9	US-09-019-679-5	Sequence 5, Appl
49	3	50.0	7	9	US-09-879-957-203	Sequence 203, App
50	3	50.0	7	9	US-09-873-676-86	Sequence 86, Appl
51	3	50.0	7	9	US-09-832-723-16	Sequence 16, Appl
52	3	50.0	7	11	US-09-827-345-5	Sequence 5, Appl
53	3	50.0	7	11	US-09-827-345-21	Sequence 21, Appl
54	3	50.0	7	11	US-09-992-896-40	Sequence 40, Appl
55	3	50.0	7	11	US-09-954-385-46	Sequence 46, Appl
56	3	50.0	7	11	US-09-954-385-347	Sequence 347, App
57	3	50.0	7	12	US-10-052-578-301	Sequence 301, App
58	3	50.0	7	12	US-09-990-832C-27	Sequence 27, Appl
59	3	50.0	7	12	US-10-303-331-16	Sequence 16, Appl
60	3	50.0	7	12	US-10-293-371-53	Sequence 53, Appl
61	3	50.0	7	12	US-10-053-520-301	Sequence 301, App
62	3	50.0	7	12	US-10-062-109A-727	Sequence 727, App
63	3	50.0	7	12	US-10-286-457-92	Sequence 92, Appl
64	3	50.0	7	12	US-10-220-033-21	Sequence 21, Appl
65	3	50.0	7	12	US-10-005-480A-727	Sequence 727, App
66	3	50.0	7	12	US-10-053-498B-301	Sequence 301, App
67	3	50.0	7	12	US-10-291-241-67	Sequence 67, Appl
68	3	50.0	7	15	US-10-024-123-2	Sequence 2, Appl
69	3	50.0	7	15	US-10-024-123-6	Sequence 6, Appl
70	3	50.0	7	15	US-10-024-123-4	Sequence 4, Appl
71	3	50.0	7	15	US-10-281-652-1	Sequence 1, Appl
72	3	50.0	7	15	US-10-281-652-24	Sequence 24, Appl
73	3	50.0	7	15	US-10-028-075B-142	Sequence 142, App
74	3	50.0	7	15	US-10-028-075B-143	Sequence 143, App
75	3	50.0	7	15	US-10-029-206A-142	Sequence 142, App
76	3	50.0	7	15	US-10-029-206A-143	Sequence 143, App
77	3	50.0	8	7	US-08-344-824-263	Sequence 263, App
78	3	50.0	8	8	US-08-424-550B-491	Sequence 491, App
79	3	50.0	8	8	US-08-979-847-147	Sequence 147, App
80	3	50.0	8	8	US-08-979-847-154	Sequence 154, App
81	3	50.0	8	8	US-08-979-847-155	Sequence 155, App
82	3	50.0	8	8	US-08-979-847-156	Sequence 156, App
83	3	50.0	8	8	US-08-979-847-157	Sequence 157, App
84	3	50.0	8	8	US-08-979-847-158	Sequence 158, App
85	3	50.0	8	8	US-09-765-614B-6	Sequence 6, Appl
86	3	50.0	8	10	US-09-925-715-2	Sequence 2, Appl
87	3	50.0	8	10	US-09-925-715-2	Sequence 2, Appl
88	3	50.0	8	10	US-09-791-378-285	Sequence 285, App

89 3 50.0 8 10 US-09-826-290-124 Sequence 124, Appl  
90 3 50.0 8 10 US-09-910-553-35 Sequence 35, Appl  
91 3 50.0 8 11 US-09-992-896-39 Sequence 39, Appl  
92 3 50.0 8 11 US-09-999-724-58 Sequence 58, Appl  
93 3 50.0 8 12 US-10-052-578-97 Sequence 97, Appl  
94 3 50.0 8 12 US-10-348-504-71 Sequence 71, Appl  
95 3 50.0 8 12 US-10-283-423-61 Sequence 61, Appl  
96 3 50.0 8 12 US-10-053-520-97 Sequence 97, Appl  
97 3 50.0 8 12 US-10-365-908-98 Sequence 98, Appl  
98 3 50.0 8 12 US-09-829-382-11 Sequence 11, Appl  
99 3 50.0 8 12 US-10-213-821-61 Sequence 61, Appl  
100 3 50.0 8 12 US-10-053-498B-97 Sequence 97, Appl

## ALIGNMENTS

RESULT 1  
US-10-281-652-13  
; Sequence 13, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-13

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQPPV 6  
Db 1 DSQPPV 6

RESULT 2  
US-09-990-832C-10  
; Sequence 10, Application US/09990832C  
; Publication No. US20030149235A1  
; GENERAL INFORMATION:  
; APPLICANT: University Court of the University of Glasgow  
; TITLE OF INVENTION: Targeting peptides  
; FILE REFERENCE: PC/MC/JW/P11910US  
; CURRENT APPLICATION NUMBER: US/09/990,832C  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Targeting peptide sequence  
US-09-990-832C-10,

Query Match 66.7%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
Db 3 SQPP 6

RESULT 3  
US-09-984-245-148  
; Sequence 148, Application US/09984245  
; Patent No. US20020165374A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 87 Human Secreted Proteins  
; FILE REFERENCE: PZ004P1  
; CURRENT APPLICATION NUMBER: US/09/984,245  
; CURRENT FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/154,707  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: PCT/US98/05311  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: US 60/041,277  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/042,344  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,276  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,281  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/048,094  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,350  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,188  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,135  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/050,937  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,187  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,099  
; PRIOR FILING DATE: 1997-05-30  
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; PRIOR APPLICATION NUMBER: US 60/048,186  
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; PRIOR APPLICATION NUMBER: US 60/048,069  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,095  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,131  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,096  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,355  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,160  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,351  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,154  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/054,804  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: US 60/056,370  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: US 60/060,862  
; PRIOR FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 343

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 148  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-984-245-148

Query Match 66.7%; Score 4; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSQP 4  
Db 5 DSQP 8

## RESULT 4

US-09-966-262-148  
; Sequence 148, Application US/09966262  
; Publication No. US20030050461A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 87 Human Secreted Proteins  
; FILE REFERENCE: PZ004P1  
; CURRENT APPLICATION NUMBER: US/09/966,262  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: US 09/154,707  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: PCT/US98/05311  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: US 60/041,277  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/042,344  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,276  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,281  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/048,094  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,350  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,188  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,135  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/050,937  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,187  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,099  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,352  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,186  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,069  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,095  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,131  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,096  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,351  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,154  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/054,804

; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: US 60/056,370  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: US 60/060,862  
; PRIOR FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 343  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 148  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-966-262-148

Query Match 66.7%; Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSQP 4  
Db 5 DSQP 8

## RESULT 5

US-09-983-966-148  
; Sequence 148, Application US/09983966  
; Publication No. US20030060619A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 87 Human Secreted Proteins  
; FILE REFERENCE: PZ004P1  
; CURRENT APPLICATION NUMBER: US/09/983,966  
; CURRENT FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/154,707  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: PCT/US98/05311  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: US 60/041,277  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/042,344  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,276  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,281  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/048,094  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,350  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,188  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,135  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/050,937  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,187  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,099  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,352  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,186  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,069  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,095  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,131  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,096  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,355  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,160

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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 148
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-966-148

Query Match      66.7%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DSQP 4
Db      5 DSQP 8

RESULT 6
US-09-933-767-1242
; Sequence 1242, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882

; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
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; PRIOR APPLICATION NUMBER: 60/094,657  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1245  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1242  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-933-767-1242

Query Match 66.7%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||  
Db 5 DSQP 8

RESULT 7  
US-10-143-090-148  
; Sequence 148, Application US/10143090  
; Publication No. US20030069406A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 87 Human Secreted Proteins  
; FILE REFERENCE: P2004P1  
; CURRENT APPLICATION NUMBER: US/10/143,090  
; CURRENT FILING DATE: 2002-05-13  
; PRIOR APPLICATION NUMBER: 09/154,707  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 343  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 148  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-143-090-148

Query Match 66.7%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||  
Db 5 DSQP 8

RESULT 8  
US-10-365-908-51  
; Sequence 51, Application US/10365908  
; Publication No. US20030170268A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/214,202  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human papilloma virus  
US-10-365-908-51

Query Match 66.7%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||  
Db 1 DSQP 4

RESULT 9  
US-10-365-908-76  
; Sequence 76, Application US/10365908  
; Publication No. US20030170268A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/214,202  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 76  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human papilloma virus  
US-10-365-908-76

Query Match 66.7%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||  
Db 5 DSQP 8

RESULT 10  
US-10-195-117-34  
; Sequence 34, Application US/10195117  
; Publication No. US20030092083A1  
; GENERAL INFORMATION:  
; APPLICANT: In2Gen Co., Ltd.  
; APPLICANT: Jeoung, Doo-il  
; APPLICANT: Cho, Bomsoo  
; APPLICANT: Lim, Yoon  
; APPLICANT: Park, Saeyoung  
; APPLICANT: Lee, Daeyeon  
; APPLICANT: Bang, Yung-Jue  
; APPLICANT: Yang, Hankwang  
; APPLICANT: Kim, Dae-kee  
; TITLE OF INVENTION: CAGE Antigen  
; FILE REFERENCE: 59258-00002  
; CURRENT APPLICATION NUMBER: US/10/195,117  
; CURRENT FILING DATE: 2002-07-11  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 34  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(9)  
; OTHER INFORMATION:

US-10-195-117-34

Query Match  
Best Local Similarity 66.7%; Score 4; DB 15; Length 9;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
Db 5 DSQP 8

RESULT 11

US-10-365-908-61  
; Sequence 61, Application US/10365908  
; Publication No. US20030170268A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/214,202  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human papilloma virus  
US-10-365-908-61

Query Match  
Best Local Similarity 66.7%; Score 4; DB 12; Length 10;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
Db 6 DSQP 9

RESULT 12

US-10-365-908-105  
; Sequence 105, Application US/10365908  
; Publication No. US20030170268A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/214,202  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 105  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human papilloma virus  
US-10-365-908-105

Query Match  
Best Local Similarity 66.7%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
Db 2 DSQP 5

RESULT 13

US-09-229-751A-34  
; Sequence 34, Application US/09229751A  
; Publication No. US20030044838A1  
; GENERAL INFORMATION:  
; APPLICANT: Turnbough, Charles K  
; TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES  
; OF BACTERIAL CELLS  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glenna Hendricks  
; STREET: P.O. Box 2509  
; CITY: Fairfax  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22031  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/229,751A  
; FILING DATE: 14-Jan-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hendricks, Glenna M  
; REGISTRATION NUMBER: 32,535  
; REFERENCE/DOCKET NUMBER: turn  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 425-8405  
; TELEFAX: (703) 425-8406  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
US-09-229-751A-34

Query Match  
Best Local Similarity 66.7%; Score 4; DB 11; Length 12;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPV 6  
Db 7 QPPV 10

RESULT 14

US-09-229-751A-43  
; Sequence 43, Application US/09229751A  
; Publication No. US20030044838A1  
; GENERAL INFORMATION:  
; APPLICANT: Turnbough, Charles K  
; TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES  
; OF BACTERIAL CELLS  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glenna Hendricks  
; STREET: P.O. Box 2509

;  
; CITY: Fairfax  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22031  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/229,751A  
; FILING DATE: 14-Jan-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hendricks, Glenna M  
; REGISTRATION NUMBER: 32,535  
; REFERENCE/DOCKET NUMBER: turn  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 425-8405  
; TELEFAX: (703) 425-8406  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
US-09-229-751A-43

Query Match 66.7%; Score 4; DB 11; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPPV 6  
; ; ;  
; ; ;  
DB 7 QPPV 10

RESULT 15  
US-09-954-385-182  
; Sequence 182, Application US/09954385  
; Publication No. US20030100467A1  
; GENERAL INFORMATION:  
; APPLICANT: Ahle, Wolfgang  
; APPLICANT: Baldwin, Toby L.  
; APPLICANT: Van Gastel, Franciscus J.C.  
; APPLICANT: Janssen, Giselle G.  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Wang, Huaming  
; APPLICANT: Winetzkvy, Deborah S.  
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
; TITLE OF INVENTION: Complexes  
; FILE REFERENCE: GC690  
; CURRENT APPLICATION NUMBER: US/09/954,385  
; CURRENT FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 182  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: binding peptide  
US-09-954-385-182

Query Match 66.7%; Score 4; DB 11; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5

DB ; ; ; ;  
; 7 SQPP 10

RESULT 16  
US-10-116-275-65  
; Sequence 65, Application US/10116275  
; Publication No. US20030211476A1  
; GENERAL INFORMATION:  
; APPLICANT: Elan Pharmaceutical Technology  
; APPLICANT: O'Mahony, Daniel J.  
; APPLICANT: Brayden, David  
; APPLICANT: Byrne, Daragh  
; APPLICANT: Lambkin, Imelda  
; APPLICANT: Higgins, Lisa  
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and  
; Compositions Targeting Peyer's Patches and M Cell Receptors  
; FILE REFERENCE: E1067/20087  
; CURRENT APPLICATION NUMBER: US/10/116,275  
; CURRENT FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 349  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 65  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance U  
; OTHER INFORMATION: take Across the GIT"  
US-10-116-275-65

Query Match 66.7%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
; ; ; ;  
; ; ; ;  
DB 6 SQPP 9

RESULT 17  
US-10-185-050-135  
; Sequence 135, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 233  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/185,050  
; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 135:  
US-10-185-050-135,

Query Match 66.7%; Score 4; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
|||  
Db 2 SQPP 5

## RESULT 18

US-10-185-815-19  
Sequence 19, Application US/10185815  
Publication No. US20030096354A1  
GENERAL INFORMATION:  
APPLICANT: Elan Corporation, plc  
APPLICANT: O'Mahony, Daniel  
APPLICANT: Lambkin, Imelda  
APPLICANT: Higgins, Lisa  
TITLE OF INVENTION: Peyer's Patch And/or M-Cell Targeting Ligands  
FILE REFERENCE: E1067-20093  
CURRENT APPLICATION NUMBER: US/10/185,815  
CURRENT FILING DATE: 2002-10-09  
PRIOR APPLICATION NUMBER: 60/302,591  
PRIOR FILING DATE: 2001-07-02  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: polypeptide ligand  
US-10-185-815-19

Query Match 66.7%; Score 4; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
|||  
Db 6 SQPP 9

## RESULT 19

US-10-012-542-530  
Sequence 530, Application US/10012542  
Publication No. US20030044851A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 94 Human Secreted Proteins  
FILE REFERENCE: P2029p1  
CURRENT APPLICATION NUMBER: US/10/012,542  
CURRENT FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22  
NUMBER OF SEQ ID NOS: 532  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 530  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-012-542-530

Query Match 66.7%; Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||  
Db 9 DSQP 12

## RESULT 20

US-09-030-061-12  
Sequence 12, Application US/09030061  
Publication No. US20030095946A1  
GENERAL INFORMATION:  
APPLICANT: GILLISPIE, Matthew Todd  
APPLICANT: HORWOOD, Nicole JOY  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,061  
FILING DATE: 25-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 55,468/1997  
FILING DATE: 25-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: GILLISPIE-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal fragment  
US-09-030-061-12

Query Match 66.7%; Score 4; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||||  
Db 10 DSQP 13

## RESULT 21

US-10-100-057-12  
; Sequence 12, Application US/10100057  
; Publication No. US20020150555A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; HORWOOD, Nicole Joy  
; UDAGAWA, No. US20020150555A1uyuki  
; KURIMOTO, Maaashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/100,057  
; FILING DATE: 19-Mar-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal fragment  
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Query Match 66.7%; Score 4; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||||  
Db 10 DSQP 13

## RESULT 22

US-10-294-891-17  
; Sequence 17, Application US/10294891  
; Publication No. US20030166569A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; APPLICANT: GEMMEL, JACK  
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER  
; CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS

; FILE REFERENCE: 59003.000010  
; CURRENT APPLICATION NUMBER: US/10/294,891  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: 60/331,447  
; PRIOR FILING DATE: 2001-11-16  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-294-891-17

Query Match 66.7%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
|||||  
Db 5 SQPP 8

## RESULT 23

US-10-036-444-7  
; Sequence 7, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "NO. US20020142445A1el triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide derived  
; OTHER INFORMATION: from natural sequence, useful for antiserum  
; OTHER INFORMATION: production  
; US-10-036-444-7

Query Match 66.7%; Score 4; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
|||||  
Db 3 SQPP 6

## RESULT 24

US-09-864-761-48166  
; Sequence 48166, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761

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; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48166
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011229.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; US-09-864-761-48166

Query Match      66.7%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SQPP 5
Db      8 SQPP 11

RESULT 25
US-09-809-391-577
; Sequence 577, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US/09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598

; ORGANISM: Homo sapiens
; US-09-809-391-577

Query Match      66.7%; Score 4; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SQPP 5
Db      14 SQPP 17

RESULT 26
US-09-882-171-577
; Sequence 577, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/882,171
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
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; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,613  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,582  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,596  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,612  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,632  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,601  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,580  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,568  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,314  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,569  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,311  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,671  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,674  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,669  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,312  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,313  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,672  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,315  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/056,886  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,877  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,889  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,893  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,630  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,878  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,662  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,872  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,882  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,637  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,903  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,888  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,879  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,880  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,894  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,911  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,636  
; PRIOR FILING DATE: 1997-08-22

; PRIOR APPLICATION NUMBER: 60/056,874  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,910  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,864  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,631  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,845  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,892  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,761  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/047,595  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,599  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,588  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,585  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,586  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,590  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,594  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,589  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,593  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,614  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,578  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,576  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/047,501  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,670  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/056,632  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,664  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,876  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,881  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,909  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,875  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,862  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,887  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,908  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/057,650  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/056,884  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,669  
; PRIOR FILING DATE: 1997-09-05

Query Match 66.7%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
|||||  
Db 14 SQPP 17

RESULT 27  
US-10-106-698-6748  
; Sequence 6748, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 6748  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: MISC FEATURE  
; LOCATION: (7)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-106-698-6748

Query Match 66.7%; Score 4; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
|||||  
Db 12 DSQP 15

RESULT 28  
US-10-225-567A-1779  
; Sequence 1779, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1779  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-1779

Query Match 66.7%; Score 4; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4

Db 3 DSQP 6  
|||||

RESULT 29  
US-09-864-761-36800  
; Sequence 36800, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anncmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 36800  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC006840.13  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.67  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.83  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.88  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.66  
US-09-864-761-36800

Query Match 66.7%; Score 4; DB 9; Length 19;



Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4  
Db 16 DSQP 19

## RESULT 30

US-09-915-914B-24  
; Sequence 24, Application US/09915914B  
; Publication No. US20030119725A1  
; GENERAL INFORMATION:  
; APPLICANT: Divita, Gilles  
; APPLICANT: Fernandez, Joseph  
; APPLICANT: Heitz, Frederic  
; APPLICANT: Morris, May  
; APPLICANT: Mery, Jean  
; APPLICANT: Archdeacon, John  
; APPLICANT: Hornsdorff, Kyle  
; TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS  
; FILE REFERENCE: AM-00105.P.1.1  
; CURRENT APPLICATION NUMBER: US/09/915,914B  
; CURRENT FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: US 60/221,932  
; PRIOR FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic sequence  
US-09-915-914B-24

Query Match 50.0%; Score 3; DB 11; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
Db 2 SQP 4

## RESULT 31

US-10-309-627-5  
; Sequence 5, Application US/10309627  
; Publication No. US20030186427A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhou, Xiaochuan  
; APPLICANT: Gulari, Erdogan  
; TITLE OF INVENTION: A Device for Chemical and Biochemical Reactions Using  
; FILE REFERENCE: UN-07714  
; CURRENT APPLICATION NUMBER: US/10/309,627  
; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 10/157,442  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: 09/248,093  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 60/074,368  
; PRIOR FILING DATE: 1998-02-11  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-309-627-5

Query Match 50.0%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3  
Db 2 DSQ 4

## RESULT 32

US-10-096-986-12  
; Sequence 12, Application US/10096986  
; Publication No. US20030083464A1  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Richardson, Charles  
; APPLICANT: Chambers, James  
; APPLICANT: Causey, Stuart  
; APPLICANT: Pollock, Thomas J.  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Criesman, John W.  
; TITLE OF INVENTION: No. US20030083464A1 Peptides Comprising Repetitive  
; Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/096,986  
; FILING DATE: 12-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/444,791  
; FILING DATE: 22-No. US20030083464A1-1999  
; APPLICATION NUMBER: US 08/482,085  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-10-096-986-12

Query Match 50.0%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 1 PPV 3

## RESULT 33

US-09-992-896-42  
; Sequence 42, Application US/09992896  
; Publication No. US20030022158A1

## GENERAL INFORMATION:

; APPLICANT: Matti Sallberg

; TITLE OF INVENTION: PEPTIDES FROM THE TT VIRUS SEQUENCE AND

; FILE REFERENCE: TRIPEP.033CPI

; CURRENT APPLICATION NUMBER: US/09/992,896

; CURRENT FILING DATE: 2001-11-05

; PRIOR APPLICATION NUMBER: PCT/EP00/03958

; PRIOR FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: SE 19990001601

; PRIOR FILING DATE: 1999-05-04

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 42

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Peptide Immunogen

US-09-992-896-42

Query Match 50.0%; Score 3; DB 11; Length 5;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 3 PPV 5

## RESULT 34

US-10-014-485A-128

; Sequence 128, Application US/10014485A

; Publication No. US20020168684A1

## GENERAL INFORMATION:

; APPLICANT: Cell Signaling Technology, Inc.

; APPLICANT: COMB, Michael J.

; APPLICANT: ZHANG, Hui

; APPLICANT: TAN, Yi

; TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES

; FILE REFERENCE: CST-138 CIP2

; CURRENT APPLICATION NUMBER: US/10/014,485A

; CURRENT FILING DATE: 2002-03-18

; PRIOR APPLICATION NUMBER: US 09/148,712

; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: US 09/535,364

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 128

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (3)..(3)

; OTHER INFORMATION: PHOSPHORYLATION; serine at position 3 is phosphorylated

US-10-014-485A-128

Query Match

Best Local Similarity

Matches

3; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
|||  
Db 3 SQP 5

## RESULT 35

US-10-014-485A-129

; Sequence 129, Application US/10014485A

; Publication No. US20020168684A1

## GENERAL INFORMATION:

; APPLICANT: Cell Signaling Technology, Inc.

; APPLICANT: COMB, Michael J.

; APPLICANT: ZHANG, Hui

; APPLICANT: TAN, Yi

; TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES

; FILE REFERENCE: CST-138 CIP2

; CURRENT APPLICATION NUMBER: US/10/014,485A

; CURRENT FILING DATE: 2002-03-18

; PRIOR APPLICATION NUMBER: US 09/148,712

; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: US 09/535,364

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 129

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (3)..(3)

; OTHER INFORMATION: PHOSPHORYLATION; serine at position 3 is phosphorylated

US-10-014-485A-129

Query Match

Best Local Similarity

Matches

3; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 2 SQP 4  
|||  
Db 3 SQP 5

## RESULT 36

US-10-099-895-12

; Sequence 12, Application US/10099895

; Publication No. US2002017166A1

## GENERAL INFORMATION:

; APPLICANT: BERNDT, Michael C

; APPLICANT: STOMSKI, Frank C

; APPLICANT: LOPEZ, Angel F

; APPLICANT: GUTHRIE, Mark A

; TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR

; FILE REFERENCE: 3991/OK379

; CURRENT APPLICATION NUMBER: US/10/099,895

; CURRENT FILING DATE: 2002-03-14

; PRIOR APPLICATION NUMBER: PCT/AU00/01118

; PRIOR FILING DATE: 2000-09-15

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

; OTHER INFORMATION: PHOSPHORYLATION; serine at position 3 is phosphorylated

US-10-099-895-12

Query Match

Best Local Similarity

Matches

3; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

50.0%; Score 3; DB 14; Length 5;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
Db |||  
3 SQP 5

## RESULT 37

US-10-099-895-16  
; Sequence 16, Application US/10099895  
; Publication No. US20020177166A1

## ; GENERAL INFORMATION:

; APPLICANT: BERNDT, Michael C

; APPLICANT: STOMSKI, Frank C

; APPLICANT: LOPEZ, Angel F

; APPLICANT: GUTHRIDGE, Mark A

; TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR

; FILE REFERENCE: 3991/OK379

; CURRENT APPLICATION NUMBER: US/10/099,895

; PRIOR FILING DATE: 2002-03-14

; PRIOR APPLICATION NUMBER: PCT/AU00/01118

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-099-895-16

Query Match 50.0%; Score 3; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
Db |||  
3 SQP 5

## RESULT 38

US-10-099-895-28  
; Sequence 28, Application US/10099895  
; Publication No. US20020177166A1

## ; GENERAL INFORMATION:

; APPLICANT: BERNDT, Michael C

; APPLICANT: STOMSKI, Frank C

; APPLICANT: LOPEZ, Angel F

; APPLICANT: GUTHRIDGE, Mark A

; TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR

; FILE REFERENCE: 3991/OK379

; CURRENT APPLICATION NUMBER: US/10/099,895

; PRIOR FILING DATE: 2002-03-14

; PRIOR APPLICATION NUMBER: PCT/AU00/01118

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 28

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-099-895-28

Query Match 50.0%; Score 3; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
Db |||  
3 SQP 5

## RESULT 39

US-10-096-986-3  
; Sequence 3, Application US/10096986  
; Publication No. US20030083464A1

## ; GENERAL INFORMATION:

; APPLICANT: Ferrari, Franco A.

; Richardson, Charles

; Chambers, James

; Causey, Stuart

; Pollock, Thomas J.

; Cappello, Joseph

; Crissman, John W.

; TITLE OF INVENTION: No. US20030083464A1 Peptides Comprising Repetitive  
Units of Amino Acids and DNA Sequences Encoding the Same

; NUMBER OF SEQUENCES: 117

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: US

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/096,986

; FILING DATE: 12-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/444,791

; FILING DATE: 22-No. US20030083464A1-1999

; APPLICATION NUMBER: US 08/482,085

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/175,155

; FILING DATE: 29-DEC-1993

; APPLICATION NUMBER: US 08/053,049

; FILING DATE: 22-APR-1993

; APPLICATION NUMBER: US 07/114,618

; FILING DATE: 29-OCT-1987

; APPLICATION NUMBER: US 06/927,258

; FILING DATE: 04-NOV-1986

; ATTORNEY/AGENT INFORMATION:

; NAME: Trecartin, Richard P.

; REGISTRATION NUMBER: 31,801

; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-781-1989

; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-096-986-3

Query Match 50.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
Db |||  
1 PPV 3

## RESULT 40

US-10-096-986-13

; Sequence 13, Application US/10096986

; Publication No. US20030083464A1

; GENERAL INFORMATION:

; APPLICANT: Ferrari, Franco A.

; Richardson, Charles

Chambers, James  
Causey, Stuart  
Pollock, Thomas J.  
Cappello, Joseph  
Crissman, John W.  
TITLE OF INVENTION: No. US20030083464A1el Peptides Comprising Repetitive  
Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fiehr Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/096,986  
FILING DATE: 12-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/444,791  
FILING DATE: 22-No. US20030083464A1-1999  
APPLICATION NUMBER: US 08/482,085  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-096-986-13  
Query Match 50.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PPV 6  
DB 1 PPV 3  
RESULT 41  
US-09-865-018-23  
Sequence 23, Application US/09865018  
Patent No. US2002011086A1  
GENERAL INFORMATION:  
APPLICANT: Masseague, Joan  
Roberts, James M.  
Koff, Andrew  
Polyak, Kornelia  
TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS

Chambers, James  
Causey, Stuart  
Pollock, Thomas J.  
Cappello, Joseph  
Crissman, John W.  
TITLE OF INVENTION: No. US20030083464A1el Peptides Comprising Repetitive  
Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fiehr Hobbach Test Albritton & Herbert LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/096,986  
FILING DATE: 12-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/444,791  
FILING DATE: 22-No. US20030083464A1-1999  
APPLICATION NUMBER: US 08/482,085  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-096-986-13  
Query Match 50.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PPV 6  
DB 1 PPV 3  
RESULT 41  
US-09-865-018-23  
Sequence 23, Application US/09865018  
Patent No. US2002011086A1  
GENERAL INFORMATION:  
APPLICANT: Masseague, Joan  
Roberts, James M.  
Koff, Andrew  
Polyak, Kornelia  
TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS

NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/865,018  
FILING DATE: 24-May-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,039  
FILING DATE: 09-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-079.04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-865-018-23  
Query Match 50.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SQP 4  
DB 2 SQP 4  
RESULT 42  
US-09-727-963A-68  
Sequence 68, Application US/09727963A  
Patent No. US20020155106A1  
GENERAL INFORMATION:  
APPLICANT: V.I. Technologies, Inc.  
TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
FILE REFERENCE: 18242-505  
CURRENT APPLICATION NUMBER: US/09/727,963A  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557  
PRIOR FILING DATE: 1999-12-02  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 68  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand  
NAME/KEY: VARIANT  
LOCATION: (1)  
OTHER INFORMATION: wherein Xaa is D-phenylalanine  
US-09-727-963A-68  
Query Match 50.0%; Score 3; DB 10; Length 6;

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Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3
   |||
Db 4 DSQ 6

RESULT 43
US-09-992-896-41
; Sequence 41, Application US/0992896
; Publication No. US20030022158A1
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; TITLE OF INVENTION: PEPTIDES FROM THE TT VIRUS SEQUENCE AND
; TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES BINDING TO THE TT VIRUS
; FILE REFERENCE: TRIPEP 033CP1
; CURRENT APPLICATION NUMBER: US/09/992,896
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/EP00/03958
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: SE 19990001601
; PRIOR FILING DATE: 1999-05-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Immunogen
US-09-992-896-41

Query Match 50.0%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6
   |||
Db 4 PPV 6

RESULT 44
US-10-159-006-64
; Sequence 64, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Productivity
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 64
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-64

Query Match 50.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3
   |||
Db 2 DSQ 4

RESULT 45
US-10-161-791-249
; Sequence 249, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-249

Query Match 50.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6
   |||
Db 1 PPV 3

RESULT 46
US-10-227-353-7
; Sequence 7, Application US/10227353
; Publication No. US20030087383A1
; GENERAL INFORMATION:
; APPLICANT: CLARE, JEFFREY J.
; APPLICANT: ROMANOS, MICHAEL A.
```

TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
STREET: 2200 Clarendon Blvd., Suite 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/227,353  
FILING DATE: 26-Aug-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,269C  
FILING DATE: 02-Jun-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lebovitz, Richard M.  
REGISTRATION NUMBER: 37,067  
REFERENCE/DOCKET NUMBER: Popov-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 243-6333  
TELEFAX: (703) 243-6410  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-227-353-7

Query Match 50.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 3 QPP 5  
|||  
Db 4 QPP 6  
|||

## RESULT 47

US-10-028-075B-141  
; Sequence 141, Application US/10028075B  
; Publication No. US20030113733A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/028,075B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: EP 01203748.7  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 141  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN  
US-10-028-075B-141

Query Match 50.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 4 PPV 6  
|||  
Db 3 PPV 5  
|||

## RESULT 48

US-10-029-206A-141  
; Sequence 141, Application US/10029206A  
; Publication No. US20030119720A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; TITLE OF INVENTION: Oligopeptide treatment of anthrax  
; FILE REFERENCE: 2183-5222US  
; CURRENT APPLICATION NUMBER: US/10/029,206A  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/821,380  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 141  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN  
US-10-029-206A-141

Query Match 50.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 4 PPV 6  
|||  
Db 3 PPV 5  
|||

## RESULT 49

US-09-019-679-5  
; Sequence 5, Application US/09019679  
; Patent No. US20020012943A1  
; GENERAL INFORMATION:  
; APPLICANT: Fowlkes, Dana M  
; APPLICANT: Thorp, H. Holden  
; TITLE OF INVENTION: Electrochemical Probes for Detection of Molecular  
; FILE REFERENCE: 97082-B  
; CURRENT APPLICATION NUMBER: US/09/019,679  
; CURRENT FILING DATE: 1998-02-06  
; EARLIER APPLICATION NUMBER: 60/036,919  
; EARLIER FILING DATE: 1997-02-06  
; EARLIER APPLICATION NUMBER: 60/059,049  
; EARLIER FILING DATE: 1997-09-16  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Src SH3  
; OTHER INFORMATION: binding motif  
US-09-019-679-5

Query Match 50.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 4 PPV 6  
|||  
Db 2 PPV 4  
|||

RESULT 50  
US-09-879-957-203  
; Sequence 203, Application US/09879957  
; Patent No. US20020034755A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; HOFFMAN, No. US20020034755A1h  
; KAY, Brian K.  
; FOLKES, Dana M.  
; MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,957  
; FILING DATE: 13-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,915  
; FILING DATE: 03-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 203:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 203:  
US-09-879-957-203  
  
Query Match 50.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 PPV 6  
DB 2 PPV 4  
  
RESULT 51  
US-09-873-676-86  
; Sequence 86, Application US/09873676  
; Patent No. US20020077289A1  
; GENERAL INFORMATION:  
; APPLICANT: MacDonald, Nicholas J.  
; APPLICANT: Sim, Kim L.  
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use  
; FILE REFERENCE: 05213-0378 (43170-259333)  
; CURRENT APPLICATION NUMBER: US/09/873,676  
; CURRENT FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: US 60/209,065  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 60/289,387  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 86  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-09-873-676-86  
  
Query Match 50.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 QPP 5  
DB 2 QPP 4  
  
RESULT 52  
US-09-832-723-16  
; Sequence 16, Application US/09832723  
; Patent No. US20020098524A1  
; GENERAL INFORMATION:  
; APPLICANT: Estell, David A.  
; APPLICANT: Chen, Yiyou  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Tijerina, Pilar  
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
; FILE REFERENCE: GC617-2  
; CURRENT APPLICATION NUMBER: US/09/832,723  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; peptide library  
US-09-832-723-16  
  
Query Match 50.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 SQP 4  
DB 2 SQP 4  
  
RESULT 53  
US-09-827-345-5  
; Sequence 5, Application US/09827345  
; Publication No. US20030021800A1  
; GENERAL INFORMATION:  
; APPLICANT: CHERMANN, JEAN-CLAUDE  
; APPLICANT: LE CONTEL, CAROLE  
; APPLICANT: GALEA, PASCALE  
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN  
; INTRACELLULAR PHASE. COMPOSITION FOR THE TREATMENT AND  
; PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF  
; DIAGNOSIS  
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF  
; DIAGNOSIS  
; FILE REFERENCE: 065691-0216  
; CURRENT APPLICATION NUMBER: US/09/827,345  
; CURRENT FILING DATE: 2001-04-09

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; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-827-345-5

Query Match          50.0%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SQP 4
Db      1 SQP 3

RESULT 54
US-09-827-345-21
; Sequence 21, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: GALEA, PASCALE
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; FILE REFERENCE: 065691-0216
; CURRENT APPLICATION NUMBER: US/09/827,345
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-827-345-21

Query Match          50.0%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SQP 4
Db      1 SQP 3

RESULT 55
US-09-992-896-46
; Sequence 40, Application US/09992896
; Publication No. US20030022158A1
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; TITLE OF INVENTION: PEPTIDES FROM THE TT VIRUS SEQUENCE AND
; FILE REFERENCE: TRIPEP 033CP1
; CURRENT APPLICATION NUMBER: US/09/992,896
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/EP00/03958
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: SE 19990001601
; PRIOR FILING DATE: 1999-05-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Immunogen
; OTHER INFORMATION:
US-09-992-896-40

Query Match          50.0%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPV 6
Db      5 PPV 7

RESULT 56
US-09-954-385-46
; Sequence 46, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Ahle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gestel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-46

Query Match          50.0%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPV 6
Db      4 PPV 6

RESULT 57
US-09-954-385-347
; Sequence 347, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
```



APPLICANT: Ahle, Wolfgang  
APPLICANT: Baldwin, Toby L.  
APPLICANT: Van Gastel, Franciscus J.C.  
APPLICANT: Janssen, Giselle G.  
APPLICANT: Murray, Christopher J.  
APPLICANT: Wang, Huaming  
APPLICANT: Winetzkzy, Deborah S.  
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
FILE REFERENCE: GC690  
CURRENT APPLICATION NUMBER: US/09/954,385  
CURRENT FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 433  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 347  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: binding peptide  
US-09-954-385-347

Query Match 50.0%; Score 3; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 3 QPP 5  
DB 2 QPP 4

RESULT 58  
US-10-052-578-301  
Sequence 301, Application US/10052578  
Publication No. US20030134787A1  
GENERAL INFORMATION:  
APPLICANT: Sloan-Kettering Institute for Cancer Research  
APPLICANT: Rothman, James E.  
APPLICANT: Mayhew, Mark  
APPLICANT: Hoe, Mee H.  
APPLICANT: Houghton, Alan  
APPLICANT: Hartl, Ulrich  
APPLICANT: Querfelli, Ouathek  
APPLICANT: Moroi, Yoichi  
TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
FILE REFERENCE: 11746/46003  
CURRENT APPLICATION NUMBER: US/10/052,578  
CURRENT FILING DATE: 2002-01-17  
PRIOR APPLICATION NUMBER: 08/961,707  
PRIOR FILING DATE: 1997-10-31  
NUMBER OF SEQ ID NOS: 321  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 301  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: peptide in ml3 coliphage  
US-10-052-578-301

Query Match 50.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 4 PPV 6  
DB 5 PPV 7

RESULT 59  
US-09-990-832C-27  
Sequence 27, Application US/09990832C  
Publication No. US20030149235A1

GENERAL INFORMATION:  
APPLICANT: University Court of the University of Glasgow  
TITLE OF INVENTION: Targeting peptides  
FILE REFERENCE: PC/MC/JM/P11910US  
CURRENT APPLICATION NUMBER: US/09/990,832C  
CURRENT FILING DATE: 2003-01-27  
NUMBER OF SEQ ID NOS: 127  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 27  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Targeting peptide sequence  
US-09-990-832C-27

Query Match 50.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 2 SQP 4  
DB 3 SQP 5

RESULT 60  
US-10-303-331-16  
Sequence 16, Application US/10303331  
Publication No. US20030152976A1  
GENERAL INFORMATION:  
APPLICANT: Janssen, Giselle G.  
APPLICANT: Murray, Christopher J.  
APPLICANT: Winetzkzy, Deborah S.  
TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
FILE REFERENCE: GC617-3  
CURRENT APPLICATION NUMBER: US/10/303,331  
CURRENT FILING DATE: 2002-11-25  
PRIOR APPLICATION NUMBER: US 09/832,723  
PRIOR FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: US 60/197,259  
PRIOR FILING DATE: 2000-04-14  
NUMBER OF SEQ ID NOS: 125  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: peptides screened from a phage display random peptide library  
US-10-303-331-16

Query Match 50.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 2 SQP 4  
DB 2 SQP 4

RESULT 61  
US-10-293-371-53  
Sequence 53, Application US/10293371  
Publication No. US20030157522A1  
GENERAL INFORMATION:  
APPLICANT: BOUDREAU, ALAIN  
APPLICANT: KORNELUK, ROBERT G.  
APPLICANT: LACASSE, ERIC  
APPLICANT: LISTON, PETER  
TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
FILE REFERENCE: 07891/030002

; CURRENT APPLICATION NUMBER: US/10/293,371  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,934  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: US 60/332,300  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-293-371-53

Query Match 50.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4  
|||  
DB 1 SQP 3

RESULT 62  
US-10-053-520-301  
; Sequence 301, Application US/10053520  
; Publication No. US20030166530A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoes, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Querfelli, Ouathek  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES.  
; FILE REFERENCE: 11746/46004  
; CURRENT APPLICATION NUMBER: US/10/053,520  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: 08/961,707  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 301  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in ml3 coliphage  
US-10-053-520-301

Query Match 50.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
DB 5 PPV 7

RESULT 63  
US-10-062-109A-727  
; Sequence 727, Application US/10062109A  
; Publication No. US20030165505A1  
; GENERAL INFORMATION:  
; APPLICANT: Agensys  
; APPLICANT: Challita-Eid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.

; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; TITLE OF INVENTION: Cancer  
; FILE REFERENCE: 51158-20062.01  
; CURRENT APPLICATION NUMBER: US/10/062,109A  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 727  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-062-109A-727

Query Match 50.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3  
|||  
DB 4 DSQ 6

RESULT 64  
US-10-286-457-92  
; Sequence 92, Application US/10286457  
; Publication No. US20030166004A1  
; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: GPCI-P01-178  
; CURRENT APPLICATION NUMBER: US/10/286,457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 92  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, base  
; OTHER INFORMATION: ability to selectively bind to endothelial cells  
US-10-286-457-92

Query Match 50.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
DB 1 QPP 3

RESULT 65  
US-10-220-033-21  
; Sequence 21, Application US/10220033  
; Publication No. US20030186906A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlengersiepen, Karl-Hermann  
; APPLICANT: Schlengersiepen, Reimar  
; TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene  
; TITLE OF INVENTION: and a molecule binding to an expression product of that  
; TITLE OF INVENTION: gene  
; FILE REFERENCE: F68119U50  
; CURRENT APPLICATION NUMBER: US/10/220,033  
; CURRENT FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: PCT/EP01/02694

```
; PRIOR FILING DATE: 2001-03-10
; PRIOR APPLICATION NUMBER: EP00105190.3
; PRIOR FILING DATE: 2000-03-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; OTHER INFORMATION: Obtained by screening randomly synthesized
; OTHER INFORMATION: peptides
US-10-220-033-21

Query Match          50.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
   |||
Db 1 QPP 3

RESULT 66
US-10-005-480A-727
; Sequence 727, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 727
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-005-480A-727

Query Match          50.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3
   |||
Db 4 DSQ 6

RESULT 67
US-10-053-498B-301
; Sequence 301, Application US/10053498B
; Publication No. US2003019409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Quatchek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES

; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 301
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-301

Query Match          50.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6
   |||
Db 5 PPV 7

RESULT 68
US-10-291-241-67
; Sequence 67, Application US/10291241
; Publication No. US20030206905A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Paris
; APPLICANT: Rene S. Hubert
; APPLICANT: Wangmao Ge
; APPLICANT: Karen Jane Meyrick Morrison
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Pia M. Challita-Eld
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
; FILE REFERENCE: 51158-20062.20
; CURRENT APPLICATION NUMBER: US/10/291,241
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-291-241-67

Query Match          50.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3
   |||
Db 4 DSQ 6

RESULT 69
US-10-024-123-2
; Sequence 2, Application US/10024123
; Publication No. US2003002263A1
; GENERAL INFORMATION:
; APPLICANT: Kastan, Michael
```

APPLICANT: Canman, Christine  
APPLICANT: Kim, Seong-Tae  
APPLICANT: Lim, Dae-Sik  
APPLICANT: St. Jude Children's Research Hospital  
TITLE OF INVENTION: ATM Kinase Modulation for Screening and  
FILE REFERENCE: 2427/1F142  
CURRENT APPLICATION NUMBER: US/10/024,123  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 09/400,653  
PRIOR FILING DATE: 1999-09-21  
PRIOR APPLICATION NUMBER: 09/248,061  
PRIOR FILING DATE: 1999-02-10  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PHOSPHORYLATION  
LOCATION: 4  
OTHER INFORMATION: Xaa at position seven is any amino acid.  
US-10-024-123-2

Query Match 50.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSQ 3  
Db 3 DSQ 5

RESULT 70  
US-10-024-123-4  
Sequence 4, Application US/10024123  
Publication No. US20030022263A1  
GENERAL INFORMATION:  
APPLICANT: Kastan, Michael  
APPLICANT: Canman, Christine  
APPLICANT: Kim, Seong-Tae  
APPLICANT: Lim, Dae-Sik  
APPLICANT: St. Jude Children's Research Hospital  
TITLE OF INVENTION: ATM Kinase Modulation for Screening and  
FILE REFERENCE: 2427/1F142  
CURRENT APPLICATION NUMBER: US/10/024,123  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 09/400,653  
PRIOR FILING DATE: 1999-09-21  
PRIOR APPLICATION NUMBER: 09/248,061  
PRIOR FILING DATE: 1999-02-10  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PHOSPHORYLATION  
LOCATION: 4  
OTHER INFORMATION: Xaa at position seven is any amino acid.  
US-10-024-123-4

Query Match 50.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4  
Db 4 SQP 6

RESULT 71  
US-10-024-123-6  
Sequence 6, Application US/10024123  
Publication No. US20030022263A1  
GENERAL INFORMATION:  
APPLICANT: Kastan, Michael  
APPLICANT: Canman, Christine  
APPLICANT: Kim, Seong-Tae  
APPLICANT: Lim, Dae-Sik  
APPLICANT: St. Jude Children's Research Hospital  
TITLE OF INVENTION: ATM Kinase Modulation for Screening and  
FILE REFERENCE: 2427/1F142  
CURRENT APPLICATION NUMBER: US/10/024,123  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 09/400,653  
PRIOR FILING DATE: 1999-09-21  
PRIOR APPLICATION NUMBER: 09/248,061  
PRIOR FILING DATE: 1999-02-10  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PHOSPHORYLATION  
LOCATION: 4  
OTHER INFORMATION: Xaa at position seven is any amino acid.  
US-10-024-123-6

Query Match 50.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4  
Db 4 SQP 6

RESULT 72  
US-10-281-652-1  
Sequence 1, Application US/10281652  
Publication No. US20030091606A1  
GENERAL INFORMATION:  
APPLICANT: STANTON, G. John  
APPLICANT: HUGHES, Thomas K.  
APPLICANT: BOLDOGH, Istvan  
TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
FILE REFERENCE: 265.00220101  
CURRENT APPLICATION NUMBER: US/10/281,652  
CURRENT FILING DATE: 2002-10-28  
PRIOR APPLICATION NUMBER: US/09/641,803  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: 60/149,310  
PRIOR FILING DATE: 1999-08-17  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: peptide  
US-10-281-652-1

Query Match 50.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 2 QPP 4

## RESULT 73

US-10-281-652-24  
; Sequence 24, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOCH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281.652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641.803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-24

Query Match 50.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 5 QPP 7

## RESULT 74

US-10-028-075B-142  
; Sequence 142, Application US/10028075B  
; Publication No. US20030113733A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/028,075B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: EP 01203748.7  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 142  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN  
US-10-028-075B-142

Query Match 50.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 3 PPV 5

## RESULT 75

US-10-028-075B-143  
; Sequence 143, Application US/10028075B  
; Publication No. US20030113733A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/028,075B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: EP 01203748.7  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 143  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN  
US-10-028-075B-143

Query Match 50.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 4 PPV 6

Search completed: November 25, 2003, 20:25:40  
Job time : 12.9362 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 6.54255 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-13

Perfect score: 6

Sequence: 1 DSQPPV 6

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*

5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pcp.\*

6: /cgn2\_6/ptodata/1/iaa/backfileei.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	4	US-09-641-803-13
2	4	66.7	7	6	5284931-35
3	4	66.7	9	3	US-08-664-962B-15
4	4	66.7	9	3	US-09-311-743-15
5	4	66.7	13	2	US-08-919-724-1
6	4	66.7	13	4	US-09-461-325-530
7	4	66.7	14	3	US-08-832-198-4
8	4	66.7	14	4	US-09-819-902-4
9	4	66.7	14	4	US-09-752-510-4
10	4	66.7	15	1	US-08-002-024B-1
11	4	66.7	18	4	US-09-149-476-577
12	4	66.7	20	2	US-08-484-530-17
13	4	66.7	20	2	US-08-827-618A-17
14	4	66.7	20	3	US-08-483-952A-17
15	4	66.7	20	4	US-08-476-501-17
16	3	50.0	4	1	US-08-160-317-3
17	3	50.0	4	1	US-08-351-147-3
18	3	50.0	4	1	US-08-471-154-3
19	3	50.0	4	1	US-08-477-509B-12
20	3	50.0	4	1	US-08-482-085B-12
21	3	50.0	4	3	US-08-810-720-12
22	3	50.0	4	4	US-09-444-791A-12
23	3	50.0	4	4	US-09-248-093-9
24	3	50.0	5	1	US-07-901-717-3
25	3	50.0	5	1	US-08-615-888-2
26	3	50.0	5	1	US-08-477-509B-3
27	3	50.0	5	1	US-08-477-509B-13
28	3	50.0	3	3	US-08-472-453-27
29	3	50.0	3	3	US-08-482-085B-3
30	3	50.0	3	3	US-08-482-085B-13
31	3	50.0	3	3	US-08-774-354B-2
32	3	50.0	3	3	US-08-882-046-107
33	3	50.0	3	3	US-09-444-791A-3
34	3	50.0	3	3	US-09-444-791A-13
35	3	50.0	3	3	US-09-082-358B-31
36	3	50.0	3	3	US-08-634-332A-68
37	3	50.0	3	3	US-09-119-507B-4
38	3	50.0	3	3	US-09-119-507B-6
39	3	50.0	3	3	US-08-897-556A-4
40	3	50.0	3	3	US-08-897-556A-6
41	3	50.0	3	3	US-08-877-605-294
42	3	50.0	3	3	US-08-877-605-294
43	3	50.0	3	3	US-08-127-499A-22
44	3	50.0	3	3	US-08-482-847-22
45	3	50.0	3	3	US-08-237-716-7
46	3	50.0	3	3	US-08-704-170-89
47	3	50.0	3	3	US-08-209-261B-6
48	3	50.0	3	3	US-08-472-453-11
49	3	50.0	3	3	US-08-472-453-16
50	3	50.0	3	3	US-08-472-453-18
51	3	50.0	3	3	US-08-472-453-19
52	3	50.0	3	3	US-08-472-453-28
53	3	50.0	3	3	US-08-472-453-40
54	3	50.0	3	3	US-08-472-453-42
55	3	50.0	3	3	US-08-472-453-50
56	3	50.0	3	3	US-08-472-453-53
57	3	50.0	3	3	US-08-804-439A-66
58	3	50.0	3	3	US-08-944-479-11
59	3	50.0	3	3	US-08-720-229-66
60	3	50.0	3	3	US-08-819-101-11
61	3	50.0	3	3	US-08-602-999A-249
62	3	50.0	3	3	US-08-460-269C-7
63	3	50.0	3	3	US-09-211-013-6
64	3	50.0	3	3	US-08-854-039B-23
65	3	50.0	3	3	US-09-500-124-249
66	3	50.0	3	3	US-09-301-593-64
67	3	50.0	3	3	US-09-301-593-64
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79	3	50.0	3	3	US-09-301-593-64
80	3	50.0	3	3	US-09-301-593-64
81	3	50.0	3	3	US-09-301-593-64
82	3	50.0	3	3	US-09-301-593-64
83	3	50.0	3	3	US-09-301-593-64
84	3	50.0	3	3	US-09-301-593-64
85	3	50.0	3	3	US-09-301-593-64
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87	3	50.0	3	3	US-09-301-593-64
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99	3	50.0	3	3	US-09-301-593-64
100	3	50.0	3	3	US-09-301-593-64

## ALIGNMENTS

RESULT 1  
US-09-641-803-13  
; Sequence 13, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-13

Query Match 100.0%; Score 6; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSQPPV 6  
Db 1 DSQPPV 6

RESULT 2  
5284931-35  
; Patent No. 5284931  
; APPLICANT: SPRINGER, TIMOTHY A.; ROTHLEIN, ROBERT; MARLIN,  
; STEVEN D.; DUSTIN, MICHAEL L.  
; TITLE OF INVENTION: INTERCELLULAR ADHESION MOLECULES AND  
; THEIR BINDING LIGANDS  
; NUMBER OF SEQUENCES: 41  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/515,478  
; FILING DATE: 27-APR-1990  
; SEQ ID NO: 35  
; LENGTH: 7  
5284931-35

Query Match 66.7%; Score 4; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSQP 4  
Db 3 DSQP 6

RESULT 3  
US-08-664-962B-15  
; Sequence 15, Application US/08664962B  
; Patent No. 6218162  
; GENERAL INFORMATION:  
; APPLICANT: Krystal, Gerald  
; TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MERCHANT & GOULD  
; STREET: 3100 No. 6218162west Center, 90 South Seventh Street  
; CITY: Minneapolis  
; STATE: Minnesota  
; COUNTRY: U.S.A.  
; ZIP: 55402-4131  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/664,962B  
; FILING DATE: 14-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Douglas P.  
; REGISTRATION NUMBER: 30,300  
; REFERENCE/DOCKET NUMBER: M&G 7933.49-US-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-664-962B-15

Query Match 66.7%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SQPP 5  
Db 3 SQPP 6

RESULT 4  
US-09-311-743-15  
; Sequence 15, Application US/09311743  
; Patent No. 6238903  
; GENERAL INFORMATION:  
; APPLICANT: Krystal, Gerald  
; TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BERESKIN & PARR  
; STREET: 40 King Street West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/311,743  
; FILING DATE: 14-May-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gravelle, Micheline  
; REGISTRATION NUMBER: 40,261  
; REFERENCE/DOCKET NUMBER: 7771-32  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 416-364-7311  
; TELEFAX: 416-361-1398  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:



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; ; LENGTH: 9 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: peptide
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-311-743-15

Query Match          66.7%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SQPP 5
Db      3 SQPP 6
      |||||

RESULT 5
US-08-919-724-1
; Sequence 1, Application US/08919724
; Patent No. 5919746
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Haikier, Torben
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5919746 No. 5919746disk of No. 5919746th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,724
; FILING DATE: 28-August-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A.
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4406.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Botryosphaeria ribis
; STRAIN: CBS 504.94
US-08-919-724-1

Query Match          66.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 QPPV 6
Db      6 QPPV 9
      |||||

RESULT 6
US-09-461-325-530
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; Sequence 530, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029Pl
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 530
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-461-325-530

Query Match          66.7%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DSQP 4
Db      9 DSQP 12
      |||||

RESULT 7
US-08-832-198-4
; Sequence 4, Application US/08832198
; Patent No. 6242255
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitsukiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste: 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,198
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-832-198-4

Query Match 66.7%; Score 4; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4
Db 10 DSQP 13

RESULT 8
US-09-819-902-4
; Sequence 4, Application US/09819902
; Patent No. 6403079
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsuakiyo
; TANIMOTO, Tadao
; KURIMOTO, Masaashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/819,902
; FILING DATE: 29-Mar-2001
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/832,798
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-819-902-4

Query Match 66.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQP 4
Db 10 DSQP 13

RESULT 9
US-09-752-510-4
; Sequence 4, Application US/09752510
; Patent No. 6441138
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; NUKADA, Yoshiyuki
; FUJII, Mitsuakiyo
; TANIMOTO, Tadao
; KURIMOTO, Masaashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; PRODUCTION BY IMMUNOCOMPETENT CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,510
; FILING DATE: 03-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-752-510-4
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EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048, 974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056, 886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057, 761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047, 595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 590  
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047, 594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043, 578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047, 501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043, 670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056, 632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048, 964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057, 650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056, 884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057, 669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049, 610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061, 060  
EARLIER FILING DATE: 1997-10-02

Query Match 66.7%; Score 4; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
Db 14 SQPP 17

RESULT 12

US-08-484-530-17  
Sequence 17, Application US/08484530  
Patent No. 5846740  
GENERAL INFORMATION:  
APPLICANT: Tobin, Allan J  
APPLICANT: Erlander, Mark G  
APPLICANT: Kaufman, Daniel L.  
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111-4187

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/484,530  
APPLICATION NUMBER: US/08/484,530  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 17:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-530-17

Query Match 66.7%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
Db 15 SQPP 18

RESULT 13  
US-08-827-618A-17  
Sequence 17, Application US/08827618A  
Patent No. 5998366  
GENERAL INFORMATION:  
APPLICANT: Tobin, Allan J  
APPLICANT: Erlander, Mark G  
APPLICANT: Kaufman, Daniel L.  
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase  
NUMBER OF SEQUENCES: 60  
CURRENT APPLICATION DATA:  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,618A  
FILING DATE: 09-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,725  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/716,909  
FILING DATE: 18-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/586,536  
FILING DATE: 21-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-827-618A-17

Query Match 66.7%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
Db 15 SQPP 18

RESULT 14  
US-08-483-952A-17  
Sequence 17, Application US/08483952A  
Patent No. 6011139  
GENERAL INFORMATION:  
APPLICANT: Tobin, Allan J  
APPLICANT: Erlander, Mark G  
APPLICANT: Kaufman, Daniel L.  
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase  
NUMBER OF SEQUENCES: 60  
CURRENT APPLICATION DATA:  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,952A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/123,859  
FILING DATE: 17-SEP-1993  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/716,909  
FILING DATE: 18-JUN-1991  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/586,536  
FILING DATE: 21-SEP-1990  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-60780-7/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-483-952A-17

Query Match 66.7% Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
|||  
DB 15 SQPP 18

RESULT 15

US-08-476-501-17

Sequence 17, Application US/08476501

Patent No. 6455267

GENERAL INFORMATION:

APPLICANT: TOBIN, Allan J.

APPLICANT: ERLANDER, Mark G.

APPLICANT: KAUFMAN, Daniel L.

TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton &amp; Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: US

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,501

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I.

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A60780-10/BIR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-476-501-17

Query Match 66.7% Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPP 5  
|||  
DB 15 SQPP 18

RESULT 16

US-08-160-317-3

Sequence 3, Application US/08160317

Patent No. 5468639

GENERAL INFORMATION:

APPLICANT: FASANO, Alessio

APPLICANT: LEVINE, Myron M.

APPLICANT: NORIEGA, Fernando

APPLICANT: NATARO, James P.

TITLE OF INVENTION: ENTEROTOXINS OF SHIGELLA FLEXNERI 2a

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK &amp; SEAS

STREET: 2100 Pennsylvania Avenue, N.W., Suite 800

CITY: Washington, D.C.

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/160,317

FILING DATE: 02-DEC-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/984,774

FILING DATE: 05-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764

REFERENCE/DOCKET NUMBER: A-6259

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060

TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal fragment

US-08-160-317-3

Query Match 50.0% Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
DB 2 PPV 4

RESULT 17

US-08-351-147-3

Sequence 3, Application US/08351147

Patent No. 5589380

GENERAL INFORMATION:

APPLICANT: FASANO, Alessio

APPLICANT: LEVINE, Myron M.

APPLICANT: NORIEGA, Fernando

APPLICANT: NATARO, James P.

TITLE OF INVENTION: ENTEROTOXINS OF SHIGELLA FLEXNERI 2a

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK &amp; SEAS

STREET: 2100 Pennsylvania Avenue, N.W., Suite 800

CITY: Washington, D.C.

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/351,147

FILING DATE: -NOV-1994

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,317  
FILING DATE: 02-DEC-1993  
APPLICATION NUMBER: US 07/984,774  
FILING DATE: 05-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: KIT, Gordon  
REGISTRATION NUMBER: 30,764  
REFERENCE/DOCKET NUMBER: A-6468  
TELEPHONE: (202) 293-7860  
TELEFAX: (202) 293-7860  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal fragment  
US-08-351-147-3

Query Match 50.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 2 PPV 4

RESULT 18  
US-08-471-154-3  
Sequence 3, Application US/08471154  
Patent No. 5686580  
GENERAL INFORMATION:  
APPLICANT: FASANO, Alessio  
APPLICANT: LEVINE, Myron M.  
APPLICANT: NORIEGA, Fernando  
APPLICANT: NATARO, James P.  
TITLE OF INVENTION: ENTEROTOXINS OF SHIGELLA FLEXNERI 2a  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800  
CITY: Washington, D.C.  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,154  
FILING DATE: -NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,317  
FILING DATE: 02-DEC-1993  
APPLICATION NUMBER: US 07/984,774  
FILING DATE: 05-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: KIT, Gordon  
REGISTRATION NUMBER: 30,764  
REFERENCE/DOCKET NUMBER: A-6468  
TELEPHONE: (202) 293-7860  
TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal fragment  
US-08-471-154-3

Query Match 50.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 2 PPV 4

RESULT 19  
US-08-477-509B-12  
Sequence 12, Application US/08477509B  
Patent No. 5770697  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W  
APPLICANT: Dorman, Mary A  
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
UNITS OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,509B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-509B-12

Query Match 50.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
Db 1 PPV 3

## RESULT 20

US-08-482-085B-12  
; Sequence 12, Application US/08482085B  
; Patent No. 6018030  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Richardson, Charles  
; APPLICANT: Chambers, James  
; APPLICANT: Causey, Stuart  
; APPLICANT: Pollock, Thomas J.  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W.  
; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482.085B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-482-085B-12

Query Match 50.0%; Score 3; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
Db 1 PPV 3

## RESULT 21

US-08-810-720-12  
; Sequence 12, Application US/08810720  
; Patent No. 6037527  
; GENERAL INFORMATION:  
; APPLICANT: Barton, Kenneth A.  
; APPLICANT: Umbeck, Paul F.  
; TITLE OF INVENTION: INSECTICIDAL COTTON PLANTS (AS AMENDED)  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nicholas J. Seay  
; STREET: One South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810,720  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seay, Nicholas J.  
; REGISTRATION NUMBER: 27,386  
; REFERENCE/DOCKET NUMBER: 670513.90163  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608/251-5000  
; TELEFAX: 608/251-9166  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-810-720-12

Query Match 50.0%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
Db 2 QPP 4

## RESULT 22

US-09-444-791A-12  
; Sequence 12, Application US/09444791A  
; Patent No. 6355776  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Richardson, Charles  
; APPLICANT: Chambers, James  
; APPLICANT: Causey, Stuart  
; APPLICANT: Pollock, Thomas J.  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W.  
; TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 117



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fiehr Hobbach Test Albritton & Herbert LLP  
;; STREET: Four Embarcadero Center, Suite 3400  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: US  
;; ZIP: 94111  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/444,791A  
;; FILING DATE: 22-Nov. 6355776-1999  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/482,085  
;; FILING DATE: 07-JUN-1995  
;; APPLICATION NUMBER: US 08/175,155  
;; FILING DATE: 29-DEC-1993  
;; APPLICATION NUMBER: US 08/053,049  
;; FILING DATE: 22-APR-1993  
;; APPLICATION NUMBER: US 07/114,618  
;; FILING DATE: 29-OCT-1987  
;; APPLICATION NUMBER: US 06/927,258  
;; FILING DATE: 04-NOV-1986  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Trecartin, Richard F.  
;; REGISTRATION NUMBER: 31,801  
;; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-781-1989  
;; TELEFAX: 415-398-3249  
;;  
;; INFORMATION FOR SEQ ID NO: 12:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-444-791A-12  
  
Query Match 50.0%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 PPV 6  
Db 1 PPV 3  
  
RESULT 23  
US-09-248-093-9  
; Sequence 9, Application US/09248093  
; Patent No. 6426184  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Xiaolian  
; APPLICANT: Zhou, Xiaochuan  
; APPLICANT: Gulari, Erdogan  
; TITLE OF INVENTION: Method and Apparatus for Chemical and Biochemical  
; FILE REFERENCES: UM-04389  
; CURRENT APPLICATION NUMBER: US/09/248,093  
; CURRENT FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

;; OTHER INFORMATION: Synthetic  
US-09-248-093-9  
  
Query Match 50.0%; Score 3; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DSQ 3  
Db 2 DSQ 4  
  
RESULT 24  
US-07-901-717-3  
; Sequence 3, Application US/07901717  
; Patent No. 5434247  
; GENERAL INFORMATION:  
; APPLICANT: C. Michael Jones  
; TITLE OF INVENTION: Proteins and Peptides for Inducing  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/901,717  
; FILING DATE: 19920617  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSH:170  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512-320-7200  
; TELEFAX: 512-474-7577  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-901-717-3  
  
Query Match 50.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DSQ 3  
Db 3 DSQ 5  
  
RESULT 25  
US-08-615-888-2  
; Sequence 2, Application US/08615888  
; Patent No. 5705486  
; GENERAL INFORMATION:  
; APPLICANT: MAHNAZ BADAMCHIAN, ET AL.  
; TITLE OF INVENTION: ISOLATION OF NOVEL PEPTIDES FROM GREEN  
; TITLE OF INVENTION: BARLEY LEAF EXTRACT AND USE OF SAME TO INHIBIT HUMAN  
; TITLE OF INVENTION: PLATELET AGGREGATION  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Office of Sherman and Shalloway

STREET: 413 N. Washington Street  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: Dell System 210; Intel 80 286 Microprocessor  
OPERATING SYSTEM: MS DOS 6.2  
SOFTWARE: Word Perfect, Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/615,888  
FILING DATE: March 14, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard A. Steinberg  
REGISTRATION NUMBER: 26,588  
REFERENCE/DOCKET NUMBER: HAG-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 549-2282  
TELEFAX: (703) 836-0106  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal fragment  
FEATURE:  
NAME/KEY: MB-F14  
LOCATION: 1-5  
IDENTIFICATION METHOD: amino acid sequence analysis  
OTHER INFORMATION: extracted from green leaves of barley  
OTHER INFORMATION: plants  
PUBLICATION INFORMATION:  
RELEVANT RESIDUES IN SEQ ID NO: from 1 to 5  
US-08-615-888-2

Query Match 50.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSQ 3  
Db 2 DSQ 4  
RESULT 26  
US-08-477-509B-3  
Sequence 3, Application US/08477509B  
Patent No. 5770697  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W  
APPLICANT: Dorman, Mary A  
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,509B  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,358  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-509B-3  
Query Match 50.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PPV 6  
Db 1 PPV 3  
RESULT 27  
US-08-477-509B-13  
Sequence 13, Application US/08477509B  
Patent No. 5770697  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W  
APPLICANT: Dorman, Mary A  
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,509B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
TELEPHONE: 415-398-3249  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-509B-13

Query Match 50.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 1 PPV 3

RESULT 28  
US-08-472-453-27  
Sequence 27, Application US/08472453  
Patent No. 5831002  
GENERAL INFORMATION:  
APPLICANT: Haupt, Andreas  
APPLICANT: Emiling, Franz  
APPLICANT: Romerdahl, Cynthia  
TITLE OF INVENTION: No. 5831002el Compounds, The Preparation and Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patricia Granahan, Esq., Hamilton, Brook, Smith &  
ADDRESSEE: Reynolds, P.C.  
STREET: Two Milita Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,453  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/431,795  
FILING DATE: 05-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/985,696  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/885,788  
FILING DATE: 20-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia.  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BBC-029C  
TELEPHONE: 781 8616240

TELEFAX: 781 8619540  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-472-453-27

Query Match 50.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 3 PPV 5

RESULT 29  
US-08-482-085B-3  
Sequence 3, Application US/08482085B  
Patent No. 6018030  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
APPLICANT: Richardson, Charles  
APPLICANT: Chambers, James  
APPLICANT: Causey, Stuart  
APPLICANT: Pollock, Thomas J.  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W.  
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,085B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK  
TELEPHONE: 415-398-3249  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-085B-3

Query Match 50.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 1 PPV 3

RESULT 30  
US-08-482-085B-13  
; Sequence 13, Application US/08482085B  
; Patent No. 6018030  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Richardson, Charles  
; APPLICANT: Chambers, James  
; APPLICANT: Causey, Stuart  
; APPLICANT: Pollock, Thomas J.  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W.  
; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,085B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
PRIOR APPLICATION DATA: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA: US 08/175,155  
FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-6/RPT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-085B-13

Query Match 50.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 1 PPV 3

RESULT 31  
US-08-774-354B-2  
; Sequence 2, Application US/08774354B  
; Patent No. 6063427  
; GENERAL INFORMATION:  
; APPLICANT: Michiko WATANABE  
; TITLE OF INVENTION: METHOD FOR PRODUCING A  
; TITLE OF INVENTION: HYPOALLERGENIC WHEAT FLOUR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 2033 K Street, N.W., Suite 800  
; CITY: Washington, D.C.  
; STATE:  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1+  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,354B  
FILING DATE: December 27, 1996  
CLASSIFICATION: 426  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER: 653-96F029US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 721-8200  
TELEFAX: (202) 721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
US-08-774-354B-2

Query Match 50.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 3 QPP 5

RESULT 32  
US-08-882-046-107

; Sequence 107, Application US/08882046  
; Patent No. 6136952  
; GENERAL INFORMATION:  
; APPLICANT: Li, Linheng  
; APPLICANT: Hood, Leroy  
; APPLICANT: Krantz, Ian D.  
; APPLICANT: Spinner, Nancy B.  
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding  
; TITLE OF INVENTION: Nucleic Acids and Methods of Use  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/882,046  
; FILING DATE: 25-JUN-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UW 2637  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 107:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-882-046-107

Query Match 50.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSQ 3  
Db 1 DSQ 3

RESULT 33  
US-09-444-791A-3  
; Sequence 3, Application US/09444791A  
; Patent No. 6355776  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; Richardson, Charles  
; Causey, Stuart  
; Pollock, Thomas J.  
; Cappello, Joseph  
; Crissman, John W.  
; TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive  
; Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/444,791A  
; FILING DATE: 22-NOV-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/482,085  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-444-791A-3

Query Match 50.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6  
Db 1 PPV 3

RESULT 34  
US-09-444-791A-13  
; Sequence 13, Application US/09444791A  
; Patent No. 6355776  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; Richardson, Charles  
; Chambers, James  
; Causey, Stuart  
; Pollock, Thomas J.  
; Cappello, Joseph  
; Crissman, John W.  
; TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive  
; Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/444,791A  
FILING DATE: 22-JUN-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,085  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-444-791A-13

Query Match 50.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 1 PPV 3

RESULT 35  
US-09-082-358B-31  
Sequence 31, Application US/09082358B  
Patent No. 6469153  
GENERAL INFORMATION:  
APPLICANT: Goff, Stephen P.  
TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,  
TITLE OF INVENTION: EIP-1, and EIP-3  
FILE REFERENCE: 0575/54804  
CURRENT APPLICATION NUMBER: US/09/082,358B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 5  
TYPE: PRT  
ORGANISM: murine  
US-09-082-358B-31

Query Match 50.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 2 QPP 4

RESULT 36  
US-08-634-332A-68  
Sequence 68, Application US/08634332A  
Patent No. 6531578

GENERAL INFORMATION:  
APPLICANT: ROBERT WEBBER  
TITLE OF INVENTION: IMMUNOASSAY METHOD EMPLOYING  
MONOCLONAL ANTIBODY REACTIVE TO HUMAN INOS  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIELEN, PETERSON & LAMPE  
STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720  
CITY: WALNUT CREEK  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94596  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: MICROSOFT WORD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,332A  
FILING DATE: 12-Apr-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NONE  
FILING DATE: NONE  
ATTORNEY/AGENT INFORMATION:  
NAME: THEODORE J. BIELEN, JR.  
REGISTRATION NUMBER: 27,420  
REFERENCE/DOCKET NUMBER: 12280  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (925) 937-1515  
TELEFAX: (925) 937-1529  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
NAME/KEY: HUMAN INOS (997-1002)  
LOCATION: CARBOXY TERMINAL WITH AMIDE  
IDENTIFICATION METHOD: AMINO ACID ANALYSIS  
OTHER INFORMATION:  
SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-08-634-332A-68

Query Match 50.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSQ 3  
|||  
Db 2 DSQ 4

RESULT 37  
US-09-119-507B-4  
Sequence 4, Application US/09119507B  
Patent No. 6548642  
GENERAL INFORMATION:  
APPLICANT: Kieliszewski, Marcia J.  
TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums  
FILE REFERENCE: OHU-03417  
CURRENT APPLICATION NUMBER: US/09/119,507B  
CURRENT FILING DATE: 1998-07-20  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
FEATURE:  
NAME/KEY: SITE

; LOCATION: (2)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
US-09-119-507B-4

Query Match 50.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 1 PPV 3

## RESULT 38

US-09-119-507B-6  
; Sequence 6, Application US/09119507B  
; Patent No. 6548642  
; GENERAL INFORMATION:  
; APPLICANT: KIELSZESKI, Marcia J.  
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums  
; FILE REFERENCE: OHU-03417  
; CURRENT APPLICATION NUMBER: US/09/119,507B  
; CURRENT FILING DATE: 1998-07-20  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; FEATURE:  
; LOCATION: (4)  
; OTHER INFORMATION: xaa can be Thr, Glu, hydroxyproline, Pro, His and  
; OTHER INFORMATION: Ile.  
US-09-119-507B-6

Query Match 50.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 1 PPV 3

## RESULT 39

US-08-897-556A-4  
; Sequence 4, Application US/08897556A  
; Patent No. 6570062  
; GENERAL INFORMATION:  
; APPLICANT: KIELSZESKI, MARCIA J.  
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER  
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/897,556A  
; FILING DATE: 21-JUL-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: OHU-02908  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 2  
; OTHER INFORMATION: /note= "The proline at this  
; OTHER INFORMATION: position is a hydroxyproline."  
US-08-897-556A-4

Query Match 50.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 1 PPV 3

## RESULT 40

US-08-897-556A-6  
; Sequence 6, Application US/08897556A  
; Patent No. 6570062  
; GENERAL INFORMATION:  
; APPLICANT: KIELSZESKI, MARCIA J.  
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER  
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/897,556A  
; FILING DATE: 21-JUL-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: OHU-02908  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FEATURE:

```
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /note= "The Proline at this
; OTHER INFORMATION: position is a hydroxyproline."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Xaa can be Thr, Glu,
; OTHER INFORMATION: hydroxyproline, Pro, His and Ile."
; US-08-897-556A-6

Query Match          50.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPV 6
Db      1 PPV 3

RESULT 41
US-08-877-605-294
; Sequence 294, Application US/08877605
; Patent No. 6582965
; GENERAL INFORMATION:
; APPLICANT: Robert Townsend
; APPLICANT: Raj Parekh
; APPLICANT: Sally Prime
; APPLICANT: Nick Webb
; TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
; FILE REFERENCE: 9195-004
; CURRENT APPLICATION NUMBER: US/08/877,605
; CURRENT FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 294
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Z Library
; US-08-877-605-294

Query Match          50.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPV 6
Db      2 PPV 4

RESULT 42
PCT-US94-01840-13
; Sequence 13, Application PC/TUS9401840
; GENERAL INFORMATION:
; APPLICANT: Christopher E. Rudd
; APPLICANT: Prasad Kanteti
; APPLICANT: Lewis Cantley
; TITLE OF INVENTION: CD4 MEDIATED MODULATION OF
; TITLE OF INVENTION: LIPID KINASES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
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; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,915
; FILING DATE: February 26, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/063001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; PCT-US94-01840-13

Query Match          50.0%; Score 3; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPV 6
Db      1 PPV 3

RESULT 43
US-08-127-499A-22
; Sequence 22, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-127-499A-22
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Query Match 50.0%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
DB 2 QPP 4

RESULT 44  
US-08-482-847-22  
; Sequence 22, Application US/08482847  
; Patent No. 5556757  
; GENERAL INFORMATION:  
; APPLICANT: VAN ALSTYNE, Diane  
; APPLICANT: SHARMA, Lawrence Rajendra  
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR  
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR  
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,847  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/127,499  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 51916/104/INBI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
US-08-482-847-22

Query Match 50.0%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
DB 2 QPP 4

RESULT 45  
US-08-237-716-7  
; Sequence 7, Application US/08237716  
; Patent No. 5583384  
; GENERAL INFORMATION:  
; APPLICANT: LIPSCOMBE, Martin J  
; APPLICANT: CHARLES, Ian G  
; APPLICANT: FAIRWEATHER, Neil F

; TITLE OF INVENTION: FUSION PROTEINS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderhye, P.C.  
; STREET: 1100 No. 5583384th Glebe Road, 8th Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/237,716  
; FILING DATE: 02-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/896,003  
; FILING DATE: 11-JUN-1992  
; APPLICATION NUMBER: GB 9112553.4  
; FILING DATE: 11-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mary J  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 117-157  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-237-716-7

Query Match 50.0%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
DB 4 QPP 6

RESULT 46  
US-08-704-170-89  
; Sequence 89, Application US/08704170  
; Patent No. 5707626  
; GENERAL INFORMATION:  
; APPLICANT: Douvas, Angeline  
; APPLICANT: Takehana, Yoshi  
; APPLICANT: Ehresmann, Glenn  
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR  
; TITLE OF INVENTION: IMMUNOINFECTIVE CLUSTER VIRUS INFECTIONS  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Robbins, Berliner & Carson  
; STREET: 201 No. 5707626th Figueroa Street, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/704,170

;; FILING DATE: 424  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION NUMBER: US 08/029,850  
;; FILING DATE: 11-MAR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Spitals, John P.  
;; REGISTRATION NUMBER: 29,215  
;; REFERENCE/DOCKET NUMBER: 1920-331  
;; TELEPHONE: (213) 977-1001  
;; TELEFAX: (213) 977-1003  
;; INFORMATION FOR SEQ ID NO: 89:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-704-170-89

Query Match 50.0%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
Db 2 QPP 4

RESULT 47  
US-08-209-261B-6  
; Sequence 6, Application US/08209261B  
; Patent No. 5789152  
; GENERAL INFORMATION:  
; APPLICANT: Black, Christopher  
; APPLICANT: Tosi, Pierre-Francois  
; APPLICANT: Atkin, Andrew  
; APPLICANT: Lazarte, Jaime E.  
; APPLICANT: Nicolson, Yves Claude  
; TITLE OF INVENTION: Diagnostic Device and Method  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew  
; STREET: 191 Peachtree Street, Ste. 3700  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303-1769  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/209,261B  
; FILING DATE: 16-MAR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stults, Larry W.  
; REGISTRATION NUMBER: 34,025  
; REFERENCE/DOCKET NUMBER: 05213-0061  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 818-3700  
; TELEFAX: (404) 818-3799  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-209-261B-6

Query Match 50.0%; Score 3; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PPV 6  
Db 4 PPV 6

RESULT 48  
US-08-472-453-11  
; Sequence 11, Application US/08472453  
; Patent No. 5831002  
; GENERAL INFORMATION:  
; APPLICANT: Haupt, Andreas  
; APPLICANT: Romerdahl, Cynthia  
; TITLE OF INVENTION: No. 5831002el Compounds, The Preparation and Use  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patricia Granahan, Esq., Hamilton, Brook, Smith &  
; ADDRESSEE: Reynolds, P.C.  
; STREET: Two Milita Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,453  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER: US 08/431,795  
; FILING DATE: 05-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/985,696  
; FILING DATE: 25-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/885,788  
; FILING DATE: 20-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia.  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: BBC-029C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781 8616240  
; TELEFAX: 781 8619540  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-472-453-11

Query Match 50.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
Db 3 PPV 5

RESULT 49  
US-08-472-453-16  
; Sequence 16, Application US/08472453

Patent No. 5831002  
GENERAL INFORMATION:  
APPLICANT: Haupt, Andreas  
APPLICANT: Emling, Franz  
APPLICANT: Romerdahl, Cynthia  
TITLE OF INVENTION: No. 5831002el Compounds, The Preparation and Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patricia Granahan, Esq., Hamilton, Brook, Smith &  
ADDRESSEE: Reynolds, P.C.  
STREET: Two Milita Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,453  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/431,795  
FILING DATE: 05-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/985,696  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/885,788  
FILING DATE: 20-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia.  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BBC-029C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781 8616240  
TELEFAX: 781 8619540  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-472-453-16

Query Match 50.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6  
Db 4 PPV 6

RESULT 50  
US-08-472-453-18  
Sequence 18, Application US/08472453  
Patent No. 5831002  
GENERAL INFORMATION:  
APPLICANT: Haupt, Andreas  
APPLICANT: Emling, Franz  
APPLICANT: Romerdahl, Cynthia  
TITLE OF INVENTION: No. 5831002el Compounds, The Preparation and Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patricia Granahan, Esq., Hamilton, Brook, Smith &  
ADDRESSEE: Reynolds, P.C.

STREET: Two Milita Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,453  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/431,795  
FILING DATE: 05-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/985,696  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/885,788  
FILING DATE: 20-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia.  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BBC-029C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781 8616240  
TELEFAX: 781 8619540  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-472-453-18

Query Match 50.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6  
Db 4 PPV 6

RESULT 51  
US-08-472-453-19  
Sequence 19, Application US/08472453  
Patent No. 5831002  
GENERAL INFORMATION:  
APPLICANT: Haupt, Andreas  
APPLICANT: Emling, Franz  
APPLICANT: Romerdahl, Cynthia  
TITLE OF INVENTION: No. 5831002el Compounds, The Preparation and Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patricia Granahan, Esq., Hamilton, Brook, Smith &  
ADDRESSEE: Reynolds, P.C.  
STREET: Two Milita Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,453  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/431,795  
FILING DATE: 05-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/985,696  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/885,788  
FILING DATE: 20-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia.  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BBC-029C  
TELEPHONE: 781 8616240  
TELEFAX: 781 8619540  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-472-453-19

Query Match 50.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
DB 4 PPV 6

RESULT 52  
US-08-472-453-28  
Sequence 28, Application US/08472453  
Patent No. 5831002  
GENERAL INFORMATION:  
APPLICANT: Haupt, Andreas  
APPLICANT: Emiling, Franz  
APPLICANT: Romerdahl, Cynthia  
TITLE OF INVENTION: No. 5831002el Compounds, The Preparation and Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patricia Granahan, Esq., Hamilton, Brook, Smith &  
ADDRESSEE: Reynolds, P.C.  
STREET: Two Milita Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,453  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/431,795  
FILING DATE: 05-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/985,696  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/885,788

FILING DATE: 20-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia.  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BBC-029C  
TELEPHONE: 781 8616240  
TELEFAX: 781 8619540  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-472-453-28  
Query Match 50.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PPV 6  
DB 3 PPV 5  
RESULT 53  
US-08-472-453-40  
Sequence 40, Application US/08472453  
Patent No. 5831002  
GENERAL INFORMATION:  
APPLICANT: Haupt, Andreas  
APPLICANT: Emiling, Franz  
APPLICANT: Romerdahl, Cynthia  
TITLE OF INVENTION: No. 5831002el Compounds, The Preparation and Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patricia Granahan, Esq., Hamilton, Brook, Smith &  
ADDRESSEE: Reynolds, P.C.  
STREET: Two Milita Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,453  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/431,795  
FILING DATE: 05-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/985,696  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/885,788  
FILING DATE: 20-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia.  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BBC-029C  
TELEPHONE: 781 8616240  
TELEFAX: 781 8619540  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids

; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-472-453-40

Query Match 50.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 4 PPV 6

RESULT 54  
US-08-472-453-42  
; Sequence 42, Application US/08472453  
; Patent No. 5831002  
; GENERAL INFORMATION:  
; APPLICANT: Haupt, Andreas  
; APPLICANT: Emling, Franz  
; APPLICANT: Romerdahl, Cynthia  
; TITLE OF INVENTION: No. 5831002el Compounds, The Preparation and Use  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patricia Granahan, Esq., Hamilton, Brook, Smith &  
; ADDRESSEE: Reynolds, P.C.  
; STREET: Two Milita Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,453  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/431,795  
; FILING DATE: 05-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/985,696  
; FILING DATE: 25-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia.  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: BBC-029C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781 8616240  
; TELEFAX: 781 8619540  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-472-453-42

Query Match 50.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6

Db |||  
4 PPV 6

RESULT 55  
US-08-472-453-50  
; Sequence 50, Application US/08472453  
; Patent No. 5831002  
; GENERAL INFORMATION:  
; APPLICANT: Haupt, Andreas  
; APPLICANT: Emling, Franz  
; APPLICANT: Romerdahl, Cynthia  
; TITLE OF INVENTION: No. 5831002el Compounds, The Preparation and Use  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patricia Granahan, Esq., Hamilton, Brook, Smith &  
; ADDRESSEE: Reynolds, P.C.  
; STREET: Two Milita Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,453  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/431,795  
; FILING DATE: 05-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/985,696  
; FILING DATE: 25-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/885,788  
; FILING DATE: 20-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia.  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: BBC-029C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781 8616240  
; TELEFAX: 781 8619540  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-472-453-50

Query Match 50.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6  
|||  
Db 4 PPV 6

RESULT 56  
US-08-472-453-53  
; Sequence 53, Application US/08472453  
; Patent No. 5831002  
; GENERAL INFORMATION:  
; APPLICANT: Haupt, Andreas  
; APPLICANT: Emling, Franz



```
;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-944-479-11

Query Match          50.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6
Db 4 PPV 6

RESULT 59
US-08-720-229-66
; Sequence 66, Application US/08720229
; Patent No. 6022542
; GENERAL INFORMATION:
; APPLICANT: Rose, Timothy M.
; APPLICANT: Bosch, Marnix L.
; APPLICANT: Strand, Kurt
; TITLE OF INVENTION: GLYCOPROTEIN B OF THE RPHV/KSHV
; TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,229
; FILING DATE: 26-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 29938-20002.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-720-229-66

Query Match          50.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4
Db 4 SQP 6

RESULT 60
US-08-819-101-11
; Sequence 11, Application US/08819101
; Patent No. 6103698
; GENERAL INFORMATION:
; APPLICANT: Barlozzari, Teresa
; APPLICANT: Haupt, Andreas
; TITLE OF INVENTION: Dolastatin-15 Derivatives in Combination

;
; TITLE OF INVENTION: With Taxanes
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,101
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BBC-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-101-11

Query Match          50.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6
Db 4 PPV 6

RESULT 61
US-08-602-999A-249
; Sequence 249, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
```

```
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mierock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; - TELEPHONE: (212) 790-9090
;; - TELEFAX: (212) 869-9741/8864
;; - TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 249:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-602-999A-249

Query Match 50.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6
DB 1 PPV 3

RESULT 62
US-08-460-269C-7
; Sequence 7, Application US/08460269C
; Patent No. 6197548
; GENERAL INFORMATION:
; APPLICANT: CLARE, JEFFREY J.
; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd., Suite 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER/READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,269C
; FILING DATE: 02-Jun-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: Popov-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 243-6333
; TELEFAX: (703) 243-6410
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-460-269C-7

Query Match 50.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5
DB |||
```

```
DB 4 QPP 6

RESULT 63
US-09-211-013-6
; Sequence 6, Application US/09211013
; Patent No. 6248865
; GENERAL INFORMATION:
; APPLICANT: AMBERG, Wilhelm; BERNARD, Harold; BUSCHMANN,
; APPLICANT: ERNST, HAUPT, Andreas; JANITSCHKE, Lothar;
; APPLICANT: JANSSEN, Bernd; KARL, Ulrich; KLING, Andreas;
; APPLICANT: MUELLER, Stefan; DE POTZOLLI, Bernd; RITTER,
; APPLICANT: KURT, THYES, Marco; and ZIERKE, Thomas
; TITLE OF INVENTION: NOVEL TETRAPEPTIDES, THEIR
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER/READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM AT-compatible, Pentium processor
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/211,013
; FILING DATE: 15-DEC-1998
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: Amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-211-013-6

Query Match 50.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPV 6
DB 4 PPV 6

RESULT 64
US-08-854-039B-23
; Sequence 23, Application US/08854039B
; Patent No. 6355774
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: POLYAK, Kornelia
; TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHOD FOR ITS
; PRODUCTION AND USE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER/READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```



;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/854.039B  
;; FILING DATE: 09-MAY-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Vincent, Matthew P.  
;; REGISTRATION NUMBER: 36,709  
;; REFERENCE/DOCKET NUMBER: MIV-079.04  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-832-1000  
;; TELEFAX: 617-832-7000  
;; INFORMATION FOR SEQ ID NO: 23:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-854-039B-23

Query Match 50.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4  
Db 2 SQP 4

RESULT 65  
US-09-500-124-249  
; Sequence 249, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 249:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids

;;  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-09-500-124-249

Query Match 50.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6  
Db 1 PPV 3

RESULT 66  
US-09-301-593-64  
; Sequence 64, Application US/09301593A  
; Patent No. 6455677  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652.1890001  
; CURRENT APPLICATION NUMBER: US/09/301,593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-301-593-64

Query Match 50.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSQ 3  
Db 2 DSQ 4

RESULT 67  
PCT-US94-02631-89  
; Sequence 89, Application PC/TUS9402631  
; GENERAL INFORMATION:  
; APPLICANT: Douvas, Angeline  
; APPLICANT: Takehana, Yoshi  
; APPLICANT: Ehresmann, Glenn  
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR  
; TITLE OF INVENTION: IMMUNOINFECTIVE CLUSTER VIRUS INFECTIONS  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Robbins, Berliner & Carson  
; STREET: 201 North Figueroa Street, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/02631  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/029,850  
FILING DATE: 11-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Spitaler, John P.  
REGISTRATION NUMBER: 29,215  
REFERENCE/DOCKET NUMBER: 1920-331  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US94-02631-89

Query Match 50.0%; Score 3; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
Db 2 QPP 4

RESULT 68  
US-08-205-938A-20  
Sequence 20, Application US/08205938A  
Patent No. 5466671  
GENERAL INFORMATION:  
APPLICANT: TEMPEST, PAUL  
APPLICANT: CASTEELS, PETER  
TITLE OF INVENTION: APIRACIN-TYPE PEPTIDE ANTIBIOTICS WITH  
TITLE OF INVENTION: IMPROVED ACTIVITIES AND/OR DIFFERENT  
TITLE OF INVENTION: ANTIBACTERIAL SPECTRUM  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: COOPER & DUNHAM LLP  
STREET: 1185 AVENUE OF THE AMERICAS  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/205,938A  
FILING DATE: 02-MAR-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: WHITE, JOHN P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-205-938A-20

Query Match 50.0%; Score 3; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4  
Db 1 SQP 3

RESULT 69  
US-08-169-524-3  
Sequence 3, Application US/08169524  
Patent No. 5496706  
GENERAL INFORMATION:  
APPLICANT: Kuusela, Pentti  
APPLICANT: Hilden, Pekka  
TITLE OF INVENTION: Methods and Materials for the  
TITLE OF INVENTION: Detection of  
TITLE OF INVENTION: Staphylococcus Aureus  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray &  
ADDRESSES: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/169,524  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: 36,989  
REFERENCE/DOCKET NUMBER: 28113/31832  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-169-524-3

Query Match 50.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPP 5  
Db 1 QPP 3

RESULT 70  
US-08-081-539-113  
Sequence 113, Application US/08081539  
Patent No. 5501962  
GENERAL INFORMATION:  
APPLICANT: Braford-Goldberg, Sarah R.  
APPLICANT: Easton, Alan M.  
APPLICANT: Klein, Barbara K.  
APPLICANT: McKeen, John P.  
APPLICANT: Olin, Peter O.  
TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine  
TITLE OF INVENTION: Chimeric Hybrid Polypeptides

NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate  
ADDRESSEE: Patent Dept.  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/081,539  
FILING DATE: 19930621  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanady, Mary J.  
REGISTRATION NUMBER: 28623  
REFERENCE/DOCKET NUMBER: 2724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708)470-6501  
TELEFAX: (708)470-6881  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-081-539-113

Query Match 50.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 1 QPP 3

RESULT 71  
US-08-127-499A-3  
; Sequence 3, Application US/08127499A  
; Patent No. 5510264  
; GENERAL INFORMATION:  
; APPLICANT: VAN ALSTYNE, Diane  
; APPLICANT: SHARMA, Lawrence Rajendra  
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/127,499A  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399  
TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
US-08-127-499A-3

Query Match 50.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 3 QPP 5

RESULT 72  
US-08-127-499A-7  
; Sequence 7, Application US/08127499A  
; Patent No. 5510264  
; GENERAL INFORMATION:  
; APPLICANT: VAN ALSTYNE, Diane  
; APPLICANT: SHARMA, Lawrence Rajendra  
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/127,499A  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
US-08-127-499A-7

Query Match 50.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 3 QPP 5

RESULT 73  
US-08-127-499A-10  
; Sequence 10, Application US/08127499A  
; Patent No. 5510264

GENERAL INFORMATION:  
APPLICANT: VAN ALSTYNE, Diane  
APPLICANT: SHARMA, Lawrence Rajendra  
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,499A  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 51916/102/INBI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-08-127-499A-10

Query Match 50.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 3 QPP 5

RESULT 74  
US-08-127-499A-25  
; Sequence 25, Application US/08127499A  
; Patent No. 5510264  
; GENERAL INFORMATION:  
; APPLICANT: VAN ALSTYNE, Diane  
; APPLICANT: SHARMA, Lawrence Rajendra  
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/127,499A  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-466-647-113

REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 51916/102/INBI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-08-127-499A-25

Query Match 50.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPP 5  
|||  
Db 3 QPP 5

RESULT 75  
US-08-466-647-113  
; Sequence 113, Application US/08466647  
; Patent No. 5543141  
; GENERAL INFORMATION:  
; APPLICANT: Braford-Goldberg, Sarah R.  
; APPLICANT: Easton, Alan M.  
; APPLICANT: Klein, Barbara K.  
; APPLICANT: McKearn, John P.  
; APPLICANT: Olins, Peter O.  
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine  
; TITLE OF INVENTION: Chimeric Hybrid Polypeptides  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate  
; ADDRESSEE: Patent Dept.  
; STREET: P. O. Box 5110  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60680  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,647  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US 08/081,539  
; FILING DATE: 21-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanady, Mary J.  
; REGISTRATION NUMBER: 28623  
; REFERENCE/DOCKET NUMBER: 2724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (708)470-6501  
; TELEFAX: (708)470-6881  
; INFORMATION FOR SEQ ID NO: 113:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-466-647-113

Query Match 50.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

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Matches	3;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	3	Qpp	5						
Db	1	Qpp	3						

Search completed: November 25, 2003, 20:16:10  
Job time : 7.54255 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 6.44149 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-14

Perfect score: 7

Sequence: 1 DPPPFQS 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	57.1	7	S71299	ICL2 protein - Par
2	4	57.1	10	A36454	trypsin-modulating
3	4	57.1	11	D45900	complement C3b rec
4	4	57.1	13	D39690	neural cell adhesi
5	4	57.1	15	PT0037	light harvesting c
6	4	57.1	17	S57991	hydroxyproline-ric
7	4	57.1	17	S59481	hydroxyproline-ric
8	3	42.9	11	F33098	214K exoantigen (v
9	3	42.9	12	S07436	tachykinin - Afric
10	3	42.9	12	C39109	hypothetical 1.2K
11	3	42.9	12	PN0663	dystrophin-associa
12	3	42.9	12	B39690	neural cell adhesi
13	3	42.9	13	S21152	tryptophyllin-rela
14	3	42.9	13	A05174	tryptophyllin-l3 -
15	3	42.9	13	S09716	2S albumin large c
16	3	42.9	14	C33098	223K exoantigen -
17	3	42.9	14	S12904	protein kinase (EC
18	3	42.9	14	S11129	phosphoprotein, bo
19	3	42.9	15	PA0014	seed storage prote
20	3	42.9	15	PN0173	seed storage prote
21	3	42.9	15	S71300	ICL3 protein - Par
22	3	42.9	16	JH0517	insulin-like growt
23	3	42.9	16	PH0763	T-cell receptor be
24	3	42.9	16	PH0759	T-cell receptor be
25	3	42.9	17	A42920	fatty acid ethyl e
26	3	42.9	18	PC2280	prolylendopeptidase
27	3	42.9	18	A54195	Na+/K+-exchanging
28	3	42.9	19	G56819	PS I complex subun
29	3	42.9	19	PH1352	Ig heavy chain DJ

30	3	42.9	19	2	A61377	endometrial secret
31	3	42.9	19	2	S25715	hypothetical prote
32	3	42.9	20	2	A33878	myosin light chain
33	3	42.9	20	2	S46205	comosain (EC 3.4.2
34	3	42.9	20	2	S46204	anana (EC 3.4.22
35	3	42.9	20	2	C45164	chromogranin-B - r
36	3	42.9	20	2	A05313	apolipoprotein A-I
37	3	42.9	20	2	S78763	ribosomal protein
38	3	42.9	20	2	A42267	J-kappa recombinat
39	3	42.9	20	2	A31516	lectin, galactose/
40	2	28.6	4	2	I51049	metallothionein-A
41	2	28.6	5	2	B60274	major protein anti
42	2	28.6	5	2	B37988	acid proteinase 11
43	2	28.6	5	2	A60803	neuropeptide - sea
44	2	28.6	6	2	A37765	hypothetical prote
45	2	28.6	6	2	S29637	jacalin beta-II ch
46	2	28.6	6	2	A19780	transferrin - bovi
47	2	28.6	6	2	PT0709	T-cell receptor be
48	2	28.6	7	2	A61081	tryptophyllin, bas
49	2	28.6	7	2	PT0087	ribulose-bisphosph
50	2	28.6	7	2	S70335	endospem protein,
51	2	28.6	7	2	PT0283	Ig heavy chain CRD
52	2	28.6	7	2	E30608	Ig kappa chain V-I
53	2	28.6	8	2	B24749	neuropeptide B - b
54	2	28.6	8	2	B39745	endoglycosylcerami
55	2	28.6	8	2	S16324	hypothetical prote
56	2	28.6	8	2	S21288	lectin - potato (f
57	2	28.6	8	2	A46306	spasmogenic toxin
58	2	28.6	8	2	JS0316	leucokinin VI - Ma
59	2	28.6	8	2	JS0317	leucokinin VII - M
60	2	28.6	8	2	E47393	neuropeptide calla
61	2	28.6	8	2	S71919	alcohol dehydrogen
62	2	28.6	8	2	S10783	enamelin f - bovin
63	2	28.6	8	2	PT0559	T-cell receptor be
64	2	28.6	8	2	I49404	prealbumin - waste
65	2	28.6	8	2	I64832	Ca2+-transporting
66	2	28.6	9	2	B45796	dihydrolipoamide S
67	2	28.6	9	2	D58503	translation elonga
68	2	28.6	9	2	A61358	bradykinin-like pe
69	2	28.6	9	2	A61057	Thr-6 bradykinin -
70	2	28.6	9	2	A26744	bradykinin-like pe
71	2	28.6	9	2	A61363	bradykinin - commo
72	2	28.6	9	2	A60579	bradykinin-like pe
73	2	28.6	9	2	B60246	ornitho-kinin - ch
74	2	28.6	9	2	B41983	orf dowstream to b
75	2	28.6	9	2	C36730	hutu protein - Kle
76	2	28.6	9	2	A60108	exotoxin A - Srep
77	2	28.6	9	2	S36898	ribosomal protein
78	2	28.6	9	2	S65433	bradykinin - horn
79	2	28.6	9	2	A41978	calliFERamide 1 -
80	2	28.6	9	2	PT0080	60K Ca binding pro
81	2	28.6	9	2	G58978	collagen alpha 1(I
82	2	28.6	9	2	S28508	collagen alpha 2(V
83	2	28.6	9	2	PD0443	3-oxoacid CoA-tran
84	2	28.6	9	2	B30572	T-cell receptor be
85	2	28.6	9	2	A43065	hydroxyproline-3-b
86	2	28.6	10	1	XAVI6B	angiotensin-conver
87	2	28.6	10	1	XASNPC	angiotensin-conver
88	2	28.6	10	1	ECLQ3M	tachykinin III - m
89	2	28.6	10	1	GMR042	leucosulfakinin-II
90	2	28.6	10	1	S33844	alpha-2-macroglobu
91	2	28.6	10	2	PC2171	triacylglycerol li
92	2	28.6	10	2	S39030	lysyl-bradykinin -
93	2	28.6	10	2	A24407	amicyanin - Paraco
94	2	28.6	10	2	S18396	probable glucose-6
95	2	28.6	10	2	C35389	urease (EC 3.5.1.5
96	2	28.6	10	2	S70336	napin small chain
97	2	28.6	10	2	JN0440	peptide-N4-(N-acet
98	2	28.6	10	2	B59272	peptide-N4-(N-acet
99	2	28.6	10	2	H28027	protein P11 - curl
100	2	28.6	10	2	S19296	16K protein - poul

## ALIGNMENTS

```
RESULT 1
S71299
ICU2 protein - Paramesidium tetraurelia (fragment)
C;Species: Paramesidium tetraurelia
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
C;Accession: S71299
R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Eur. J. Biochem. 238, 121-128, 1996
A;Title: Characterization of centrin genes in Paramesidium.
A;Reference number: S71298; MUID:96248429; PMID:8665928
A;Accession: S71299
A;Molecule type: protein
A;Residues: 1-7 <MAD>
A;Experimental source: strain d4-2
C;Genetics:
A;Genetic code: SGC5

Query Match          57.1%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPQ 6
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Db 3 PPPQ 6

RESULT 2
A36454
trypsin-modulating oostatic factor - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-May-1996
C;Accession: A36454; A61630
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
FASEB J. 4, 3015-3020, 1990
A;Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi
A;Reference number: A36454; MUID:90367888; PMID:2394318
A;Accession: A36454
A;Molecule type: protein
A;Residues: 1-10 <BOR>
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A;Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost
A;Reference number: A61630; MUID:93357794; PMID:8353526
A;Accession: A61630
A;Molecule type: protein
A;Residues: 1-10 <BO2>
A;Note: none of the amino acids is modified
C;Function:
A;Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep
C;Keywords: hormone

Query Match          57.1%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5
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Db 5 PPPP 8

RESULT 3
D45900
complement C3b receptor type 2 - mouse (clone 12) (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: D45900
R;Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.
J. Immunol. 144, 3581-3591, 1990
A;Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gen
A;Reference number: A45900; MUID:90229754; PMID:2139460

A;Accession: D45900
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr.
A;Molecule type: mRNA
A;Residues: 1-11 <KUR>

Query Match          57.1%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 4
   ||||
Db 8 DPPP 11

RESULT 4
D39690
neural cell adhesion molecule, cardiac splice form +,-,-,+ - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C;Accession: D39690
R;Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1854-1861, 1991
A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule m
A;Reference number: A39690; MUID:91141516; PMID:1396115
A;Accession: D39690
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr.
A;Molecule type: mRNA
A;Residues: 1-13 <REY>
A;Cross-references: GB:M63970
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
C;Keywords: cardiac muscle; cell adhesion; heart

Query Match          57.1%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPQ 6
   ||||
Db 6 PPPQ 9

RESULT 5
PT0037
light harvesting complex chain III/b, photosystem I - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C;Accession: PT0037; PS0205
R;Uchiyama, Y.; Tsugita, A.
submitted to JIPID, June 1991
A;Reference number: PS0189
A;Accession: PT0037
A;Molecule type: protein
A;Residues: 1-15 <UCH>

Query Match          57.1%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5
   ||||
Db 8 PPPP 11

RESULT 6
S57991
hydroxyproline-rich protein - Sesbania rostrata (fragment)
C;Species: Sesbania rostrata
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 11-Jan-2000
C;Accession: S57991
R;Goormachtig, S.; Valerio-Lepiniec, M.; Szczygłowski, K.; van Montagu, M.; Holsters, M.
submitted to the EMBL Data Library, March 1995
A;Description: Use of differential display to identify novel Sesbania rostrata genes en
A;Reference number: S57991
```



A;Accession: S57991  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-17 <GOO>  
A;Cross-references: EMBL:Z48673; NID:G899484; PID:G899485  
C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 57.1%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
DB 10 PPPP 13

## RESULT 7

S59481  
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)  
C;Species: Phaseolus vulgaris (kidney bean)  
C;Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998  
A;Accession: S59481

R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A;Title: Specificity in the immobilisation of cell wall proteins in response to different  
A;Reference number: S59481; MUID:96011753; PMID:7548825

A;Accession: S59481

A;Molecule type: protein

A;Residues: 1-17 <WOJ>

C;Keywords: glycoprotein; hydroxyproline

F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 57.1%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
DB 8 PPPP 11

## RESULT 8

F33098  
214K exoantigen (version 3) - malaria parasite (Plasmodium falciparum) (fragments)  
C;Species: Plasmodium falciparum  
C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
A;Accession: F33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: F33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIC>

Query Match 42.9%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
DB 4 PQS 6

## RESULT 9

S07436  
tachykinin - African tree frog (Kassina maculata)  
N;Alternate names: hylambatin  
C;Species: Kassina maculata

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 02-Sep-2000

A;Accession: S07436

R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.

Biomed. Res. 2, 613-617, 1981

A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in  
A;Reference number: S07436  
A;Accession: S07436  
A;Molecule type: protein  
A;Residues: 1-12 <YAS>  
A;Experimental source: skin  
A;Note: the source is designated as Hylambates maculatus  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
F;12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 42.9%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPP 3  
DB 1 DPP 3

## RESULT 10

C39109  
hypothetical 1.2K protein - hepatitis C virus

N;Alternate names: hypothetical protein 3

C;Species: hepatitis C virus

C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
A;Accession: C39109; JQ1586

R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp

Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identificat

A;Reference number: A39109; MUID:91156678; PMID:1705704

A;Accession: C39109

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-12 <HAN>

A;Cross-references: GB:M58406

R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

A;Title: Cloning and sequencing of the structural region and expression of putative cor

A;Reference number: JQ1584; MUID:92300349; PMID:1318944

A;Accession: JQ1586

A;Molecule type: genomic RNA

A;Residues: 1-12 <KUM>

A;Experimental source: strain U.K.

Query Match 42.9%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
DB 8 PPQ 10

## RESULT 11

PN0663  
dystrophin-associated glycoprotein A3a-II - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

A;Accession: PN0663

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0663

A;Molecule type: protein

A;Residues: 1-12 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 42.9%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 42.9%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 5 PPP 7

RESULT 12  
B39690  
neural cell adhesion molecule, cardiac splice form +, -, - - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
C;Accession: B39690  
R;Reyes, A.A.; Small, S.J.; Akesson, R.  
Mol. Cell. Biol. 11, 1654-1661, 1991  
A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA  
A;Reference number: A39690; MUID: 91141516; PMID: 19961115  
A;Accession: B39690  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-12 <REV>  
A;Cross-references: GB:M63970  
C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 42.9%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 6 PPP 8

RESULT 13  
S21152  
tryptophyllin-related peptide - two-colored leaf frog  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000  
C;Accession: S21152  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of the two-colored leaf frog  
A;Reference number: S21152; MUID: 92339502; PMID: 1633846  
A;Accession: S21152  
A;Molecule type: protein  
A;Residues: 1-13 <MIC>  
A;Experimental source: skin  
C;Superfamily: unassigned animal peptides

Query Match 42.9%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 7 PPP 9

RESULT 14  
A05174  
tryptophyllin-13 - Rohde's leaf frog  
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C;Date: 05-Jun-1997 #sequence\_revision 05-Jun-1997 #text\_change 18-Aug-2000  
C;Accession: A05174  
R;Montecucchi, P.C.; Gozzini, L.; Erspamer, V.  
Int. J. Pept. Protein Res. 27, 175-182, 1986  
A;Reference number: A05174  
A;Accession: A05174  
A;Molecule type: protein  
A;Residues: 1-13 <MON>  
C;Superfamily: unassigned animal peptides  
C;Keywords: pyroglutamic acid; skin  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 7 PPP 9

RESULT 15  
S09716  
2S albumin large chain (1 and 2) nII - rape (fragments)  
N;Alternate names: 2S albumin large chain nII  
C;Species: Brassica napus (rape)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Aug-1998  
C;Accession: S09716; S09718; S09717  
R;Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.  
FEBS Lett. 263, 209-212, 1990  
A;Title: beta-Turns as structural motifs for the proteolytic processing of seed protein  
A;Reference number: S09720; MUID: 90242974; PMID: 2185951  
A;Accession: S09716  
A;Molecule type: protein  
A;Residues: 1-9;10-13 <MON>  
A;Experimental source: seed  
A;Note: 3-Ser was also found  
A;Accession: S09718  
A;Molecule type: protein  
A;Residues: 1-9;10-13 <MO2>  
A;Experimental source: seed  
A;Accession: S09717  
A;Molecule type: protein  
A;Residues: 1-9;10-13 <MO3>  
A;Experimental source: seed

Query Match 42.9%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
DB 8 PPP 10

RESULT 16  
C33098  
223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C;Species: Plasmodium falciparum  
C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C;Accession: C33098  
R;Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A;Reference number: A33098  
A;Accession: C33098  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-14 <NIC>

Query Match 42.9%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
DB 3 PPQ 5

RESULT 17  
S12904  
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)  
C;Species: Pisaster ochraceus  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997  
C;Accession: S12904  
R;Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Palech, S.L.

FEBS Lett. 273, 223-226, 1990

A;Title: Identification of the sites in myelin basic protein that are phosphorylated by  
A;Reference number: S12904; MUID:91032186; PMID:1699809  
A;Accession: S12904  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-14 <SAN>  
C;Keywords: phosphotransferase

Query Match 42.9%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 8 PPP 10

#### RESULT 18

S11129  
phosphoprotein, bone - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 25-Oct-1996  
C;Accession: S11129  
R;Mikuni-Takagaki, Y.; Glincher, M.J.  
Biochem. J. 268, 585-591, 1990

A;Title: Post-translational processing of chicken bone phosphoproteins. Identification of  
A;Reference number: S11127; MUID:90303246; PMID:2363696  
A;Accession: S11129  
A;Status: preliminary

A;Molecule type: protein  
A;Residues: 1-14 <MIK>  
C;Keywords: phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 5 PPP 7

#### RESULT 19

PA0014  
seed storage protein 12S 3 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995  
C;Accession: PA0014  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A;Reference number: PA0001  
A;Accession: PA0014  
A;Molecule type: protein  
A;Residues: 1-15 <KAM>  
A;Experimental source: seed

C;Keywords: seed; storage protein

Query Match 42.9%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
|||  
Db 7 PPQ 9

#### RESULT 20

PN0173  
seed storage protein 12S4 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 22-Dec-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Mar-2001

C;Accession: PN0173

R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.  
submitted to JIPID, December 1995

A;Description: Two dimensional electrophoresis of plant proteins and standardization of

A;Reference number: PN0173

A;Accession: PN0173

A;Molecule type: protein

A;Residues: 1-15 <TSU>

A;Experimental source: seeds

Query Match 42.9%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
|||  
Db 7 PPQ 9

#### RESULT 21

S71300  
ICL3 protein - Paramacium tetraurelia (fragment)

C;Species: Paramacium tetraurelia

C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999

C;Accession: S71300

R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.

Eur. J. Biochem. 238, 121-128, 1996

A;Title: Characterization of centrin genes in Paramacium.

A;Reference number: S71298; MUID:96248429; PMID:8665928

A;Accession: S71300

A;Molecule type: protein

A;Residues: 1-15 <MAD>

A;Experimental source: strain d4-2

C;Genetics:

A;Genetic code: SGCS

Query Match 42.9%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POS 7  
|||  
Db 2 POS 4

#### RESULT 22

JH0517

insulin-like growth factor-binding protein 4 - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 23-Mar-1995

C;Accession: JH0517

R;Coleman, M.E.; Pan, Y.C.E.; Ehterton, T.D.

Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991

A;Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth

A;Reference number: JH0515; MUID:92109718; PMID:1722398

A;Accession: JH0517

A;Molecule type: protein

A;Residues: 1-16 <COL>

A;Experimental source: serum

Query Match 42.9%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 7 PPP 9

#### RESULT 23

PH0763

T-cell receptor beta chain (F15) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C;Accession: PH0763

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-II allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0763

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>

A;Cross-references: EMBL:X60857; NID:G50933; PIDN:CAA43247.1; PID:G50934

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 42.9%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6

Db 5 PPQ 7

#### RESULT 24

PH0759

T-cell receptor beta chain (QB7.3.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C;Accession: PH0759

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-II allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0759

A;Molecule type: mRNA

A;Residues: 1-16 <CAS>

A;Cross-references: EMBL:X60854; NID:G53878; PIDN:CAA43244.1; PID:G53879

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 42.9%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6

Db 5 PPQ 7

#### RESULT 25

A42920

fatty acid ethyl ester synthase-II - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995

C;Accession: A42920

R;Bora, P.S.; Wu, X.; Spilburg, C.A.; Lange, L.G.

J. Biol. Chem. 267, 13217-13221, 1992

A;Title: Purification and characterization of fatty acid ethyl ester synthase-II from human liver.

A;Reference number: A42920; MUID:92317032; PMID:1618826

A;Accession: A42920

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-17 <BOR>

A;Experimental source: myocardium

A;Note: sequence extracted from NCBI backbone (NCBIP:107742)

Query Match 42.9%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPP 3

Db 1 DPP 3

Db 2 DPP 4

#### RESULT 26

PC2280

prolylendopeptidase-inhibiting peptide - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 28-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-May-1997

C;Accession: PC2280

R;Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.

Biochem. Biophys. Res. Commun. 202, 809-815, 1994

A;Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.

A;Reference number: PC2280; MUID:94324971; PMID:8048952

A;Accession: PC2280

A;Molecule type: protein

A;Residues: 1-18 <OHM>

A;Experimental source: brain

C;Superfamily: cytoskeletal keratin

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

Db 2 PPP 4

#### RESULT 27

A54195

Na+/K+-exchanging ATPase (BC 3.6.3.9) - spiny dogfish (fragment)

C;Species: Squalus acanthias (spiny dogfish)

C;Date: 13-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 19-Apr-2002

C;Accession: A54195

R;Esmann, M.; Karlsh, S.J.; Sottrup-Jensen, L.; Marsh, D.

Biochemistry 33, 8044-8050, 1994

A;Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase

A;Reference number: A54195; MUID:94297020; PMID:8025109

A;Accession: A54195

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <ESM>

A;Experimental source: rectal gland

A;Note: sequence extracted from NCBI backbone (NCBIP:149363)

C;Keywords: hydrolase

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

Db 8 PPP 10

#### RESULT 28

G56819

PS I complex subunit 6 - cucumber (fragment)

C;Species: Cucumis sativus (cucumber)

C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996

C;Accession: G56819

R;Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.

Biochim. Biophys. Acta 1059, 141-148, 1991

A;Title: Characterization of genes that encode subunits of cucumber PS I complex by N-terminal sequencing.

A;Reference number: A56819; MUID:91355209; PMID:1863835

A;Accession: G56819

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <IWA>

A;Note: sequence extracted from NCBI backbone (NCBIP:58604)

Query Match 42.9%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 6 PPP 8

RESULT 29  
PH1352  
IG heavy chain DJ region (Clone C100-115) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1352  
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1352  
A:Molecule type: DNA  
A:Residues: 1-19 <WAS>  
A>Note: the authors translated the stop codon for residue 2 as X  
C:Keywords: heterotrimer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 7 PPP 9

RESULT 30  
A61377  
endometrial secretory protein - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 17-Mar-1999  
C:Accession: A61377  
R;Vallet, J.L.; Barker, P.J.; Lamming, G.E.; Skinner, N.; Huskisson, N.S.  
J. Endocrinol. 130, R1-R4, 1991  
A:Title: A low molecular weight endometrial secretory protein which is increased by ovariectomy  
A:Reference number: A61377; MUID:92013712; PMID:1919388  
A:Accession: A61377  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-19 <VAL>

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPP 3  
|||  
Db 13 DPP 15

RESULT 31  
S25715  
hypothetical protein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S25715; S21390  
R;Bowtell, D.; Fu, P.; Simon, M.; Senior, P.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6511-6515, 1992  
A:Title: Identification of murine homologues of the Drosophila Son of sevenless gene: pDrosophila  
A:Reference number: S25714; MUID:92335328; PMID:1631150  
A:Accession: S25715  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-19 <BOW>  
A:Cross-references: EMBL:Z11578; NID:G54132; PTDN:CAA77665.1; PID:G54133  
R;Bowtell, D.D.; Fu, P.; Simon, M.A.; Senior, P.V.  
submitted to the EMBL Data Library, January 1992

A:Description: Identification of murine homologues of the Drosophila Son of sevenless gene  
A:Reference number: S21390  
A:Accession: S21390  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-19 <BO2>  
A:Cross-references: EMBL:Z11578; NID:G54132; PTDN:CAA77665.1; PID:G54133

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
|||  
Db 2 PPP 4

RESULT 32  
A33878  
myosin light chain kinase, smooth muscle - turkey (fragment)  
C:Species: Meleagris gallopavo (common turkey)  
C:Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 07-Nov-1997  
C:Accession: A33878  
R;Ikebe, M.; Maruta, S.; Reardon, S.  
J. Biol. Chem. 264, 6967-6971, 1989  
A:Title: Location of the inhibitory region of smooth muscle myosin light chain kinase.  
A:Reference number: A33878; MUID:89214114; PMID:2708351  
A:Accession: A33878  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <IKE>  
C:Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat homology  
C:Keywords: smooth muscle

Query Match 42.9%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
|||  
Db 14 PPQ 16

RESULT 33  
S46205  
comosain (EC 3.4.22.-) - pineapple (fragment)  
C:Species: Ananas comosus (pineapple)  
C:Date: 16-Feb-1995 #sequence\_revision 01-Nov-1996 #text\_change 07-May-1999  
C:Accession: S46205  
R;Napper, A.D.; Bennett, S.P.; Borowski, M.; Holdridge, M.B.; Leonard, M.J.C.; Rogers, B.  
Biochem. J. 301, 727-735, 1994  
A:Title: Purification and characterization of multiple forms of the pineapple-stem-derived  
A:Reference number: S46204; MUID:94330946; PMID:8053898  
A:Accession: S46205  
A:Molecule type: protein  
A:Residues: 1-20 <NAP>  
C:Superfamily: papain  
C:Keywords: cysteine proteinase; hydrolase

Query Match 42.9%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
|||  
Db 2 PQS 4

RESULT 34  
S46204  
ananain (EC 3.4.22.31) - pineapple (fragment)  
C:Species: Ananas comosus (pineapple)  
C:Date: 16-Feb-1995 #sequence\_revision 01-Nov-1996 #text\_change 07-May-1999

C;Accession: S46204  
 R;Mapper, A.D.; Bennett, S.P.; Borowski, M.; Holdridge, M.B.; Leonard, M.J.C.; Rogers, B.  
 Biochem. J. 301, 727-735, 1994  
 A;Title: Purification and characterization of multiple forms of the pineapple-stem-derived  
 C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-May-1997  
 C;Accession: C49164  
 R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.  
 Endocrinology 129, 3147-3156, 1991  
 A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th  
 A;Reference number: A49164; MUID:92063871; PMID:1954895  
 A;Accession: C49164  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-20 <NIE>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:66369)  
 C;Superfamily: chromogranin B precursor

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
 ||||  
 Db 2 PQS 4

RESULT 35  
 C49164  
 Chromogranin-B - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-May-1997  
 C;Accession: C49164  
 R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.  
 Endocrinology 129, 3147-3156, 1991  
 A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th  
 A;Reference number: A49164; MUID:92063871; PMID:1954895  
 A;Accession: C49164  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-20 <NIE>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:66369)  
 C;Superfamily: chromogranin B precursor

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
 ||||  
 Db 2 PQS 4

RESULT 36  
 A05313  
 apolipoprotein A-I - red guenon (fragment)  
 N;Alternate names: apo-A-I  
 C;Species: Erythrocebus patas (red guenon, hussar)  
 C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 11-May-2000  
 C;Accession: A05313  
 R;Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.  
 Biochemistry 15, 1928-1933, 1976  
 A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus  
 A;Reference number: A90395; MUID:76184721; PMID:178359  
 A;Accession: A05313  
 A;Molecule type: protein  
 A;Residues: 1-20 <MAH>  
 C;Superfamily: apolipoprotein A-I  
 C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipid

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
 ||||  
 Db 3 PPQ 5

RESULT 37

S78763  
 ribosomal protein MRP-S18, mitochondrial - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C;Accession: S78763  
 R;Graack, H.R.  
 submitted to the Protein Sequence Database, July 1999  
 A;Reference number: S78760  
 A;Accession: S78763  
 A;Molecule type: protein  
 A;Residues: 1-20 <GRA>  
 C;Keywords: mitochondrial  
 F;1-20/Product: ribosomal protein MRP-S18 (fragment) #status experimental <MAT>

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPP 3  
 ||||  
 Db 6 DPP 8

RESULT 38  
 A42267  
 J-kappa recombination sequence-binding protein RBP-2N - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C;Accession: A42267; S23798  
 R;Kawauchi, M.; Oka, C.; Shibayama, S.; Koromilas, A.E.; Matsunami, N.; Hamaguchi, Y.;  
 J. Biol. Chem. 267, 4016-4022, 1992  
 A;Title: Genomic organization of mouse J-kappa recombination signal binding protein (RB  
 A;Reference number: A42267; MUID:92156146; PMID:1740450  
 A;Accession: A42267  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-20 <KAW>  
 A;Cross-references: GB:M81866

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
 ||||  
 Db 13 PPP 15

RESULT 39  
 A31516  
 lectin, galactose/N-acetylgalactosamine-specific - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993  
 C;Accession: A31516  
 R;Ii, M.; Kawasaki, T.; Yamashina, I.  
 Biochem. Biophys. Res. Commun. 155, 720-725, 1988  
 A;Title: Structural similarity between the macrophage lectin specific for galactose/N-a  
 A;Reference number: A31516; MUID:88339956; PMID:3421964  
 A;Accession: A31516  
 A;Molecule type: protein  
 A;Residues: 1-20 <IIX>

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
 ||||  
 Db 16 PPP 18

RESULT 40  
 I51049

metallothionein-A - rainbow trout (fragment)  
 C:Species: Oncorhynchus mykiss (rainbow trout)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
 C:Accession: I51049  
 R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.  
 Eur. J. Biochem. 230, 344-349, 1995  
 A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) metallothionein-A  
 A:Reference number: I51049; MUID:95324545; PMID:7601121  
 A:Accession: I51049  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-4 <OLS>  
 A:Cross-references: EMBL:X80181; NID:g1019799; PID:CAA56466.1; PID:g379328

Query Match 28.6%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
 ||  
 2 DP 3

## RESULT 41

B60274  
 major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993  
 C:Accession: B60274  
 R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.  
 Infect. Immun. 59, 372-382, 1991  
 A:Title: Isolation and partial characterization of major protein antigens in the culture supernatant of Mycobacterium tuberculosis  
 A:Reference number: A60274; MUID:91099989; PMID:1898889  
 A:Accession: B60274  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <NAG>

Query Match 28.6%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
 ||  
 1 DP 2

## RESULT 42

B37988  
 acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
 C:Species: Physarum polycephalum  
 C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
 C:Accession: B37988  
 R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Ogino, J.  
 J. Biol. Chem. 265, 19898-19903, 1990  
 A:Title: Purification and characterization of a novel intracellular acid proteinase from Physarum polycephalum  
 A:Reference number: A37988; MUID:91060608; PMID:2246266  
 A:Accession: B37988  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <MUR>

Query Match 28.6%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 ||  
 3 PP 4

## RESULT 43

A60803

neuropeptide - sea anemone (Anthopleura elegantissima)  
 C:Species: Anthopleura elegantissima  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: A60803  
 R:Graff, D.; Grimmelikhuijzen, C.J.P.  
 Brain Res. 442, 354-358, 1988  
 A:Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2>, a novel neuropeptide from sea anemones.  
 A:Reference number: A60803; MUID:88222764; PMID:2897223  
 A:Accession: A60803  
 A:Molecule type: protein  
 A:Residues: 1-5 <GRA>  
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F:5/Modified site: pyroglutamic acid (Gln) #status experimental  
 F:5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QS 7  
 ||  
 1 QS 2

## RESULT 44

A37765  
 hypothetical protein (csma 5' region) - Chloroflexus aurantiacus (fragment)  
 C:Species: Chloroflexus aurantiacus  
 C:Date: 31-May-1991 #sequence\_revision 31-May-1991 #text\_change 30-Sep-1993  
 C:Accession: A37765  
 R:Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.  
 J. Bacteriol. 172, 4497-4504, 1990  
 A:Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantiacus  
 A:Reference number: A37765; MUID:90330558; PMID:2376566  
 A:Accession: A37765  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-6 <THE>  
 A:Cross-references: GB:M33964

Query Match 28.6%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQ 6  
 ||  
 1 PQ 2

## RESULT 45

S29637  
 jacalin beta-II chain - Artocarpus champeden (fragment)  
 C:Species: Artocarpus champeden  
 C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
 C:Accession: S29637  
 R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.  
 Biochim. Biophys. Acta 1156, 219-222, 1993  
 A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kDa precursor  
 A:Reference number: S29637; MUID:93152601; PMID:8427879  
 A:Accession: S29637  
 A:Molecule type: protein  
 A:Residues: 1-6 <NGO>  
 A:Experimental source: seed  
 C:Complex: heterotetramer; two alpha and two beta chains  
 C:Function:  
 A:Description: seed storage protein  
 A>Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine  
 C:Keywords: heterotetramer; lectin; seed; storage protein

Query Match 28.6%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QS 7  
||  
Db 3 QS 4

## RESULT 46

A19780  
transferrin - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 18-Jun-1993  
C:Accession: A19780  
R:Brook, J.H.; Esparza, I.; Oliver, R.A.; Spooner, R.L.  
Biochem. Genet. 18, 851-860, 1980  
A:Title: Electrophoretic mobility of N- and C-terminal monoferric fragments of bovine transferrin  
A:Reference number: A19780; PMID:81183891; PMID:7225082  
A:Accession: A19780  
A:Molecule type: protein  
A:Residues: 1-6 <BRO>

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
||  
Db 1 DP 2

## RESULT 47

PT0709  
T-cell receptor beta chain V-D-J region (161-2K) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0709  
R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; PMID:91277601; PMID:1711558  
A:Accession: PT0709  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-6 <FEB>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
||  
Db 4 DP 5

## RESULT 48

A61081  
cryptophyllin, basic - Rohde's leaf frog  
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000  
C:Accession: A61081  
R:Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.  
Int. J. Pept. Protein Res. 33, 391-395, 1989  
A:Title: Isolation, structure determination and synthesis of a novel tryptophan-containing peptide  
A:Reference number: A61081  
A:Accession: A61081  
A:Molecule type: protein  
A:Residues: 1-7 <MO>  
A:Comment: The biological activity of this peptide was not determined.  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; hydroxyproline; skin  
F:3/Modified site: 4-hydroxyproline (Pro) #status experimental  
F:7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 49

PT0087  
ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - Arabidopsis thaliana (fraternalis)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 10-Apr-1996 #sequence\_revision 24-May-1996 #text\_change 24-Nov-1999  
C:Accession: PT0087  
R:Tsuigita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.  
submitted to JIPID, December 1995  
A:Description: Two dimensional electrophoresis of plant proteins and standardization of A:Reference number: PN0173  
A:Accession: PT0087  
A:Molecule type: protein  
A:Residues: 1-7 <TSU>  
A:Experimental source: leaf  
C:Keywords: acetylated amino end; carbon-carbon lyase; carboxy-lyase  
F:1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQ 6  
||  
Db 2 PQ 3

## RESULT 50

S70335  
endosperm protein, 40K - rye (fragment)  
C:Species: Secale cereale (rye)  
C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
C:Accession: S70335  
R:Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.  
Biochim. Biophys. Acta 1295, 13-22, 1996  
A:Title: Identification of major rye scallins as coeliac immunoreactive proteins.  
A:Reference number: S70327; PMID:96283789; PMID:8679669  
A:Accession: S70335  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <ROC>

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QS 7  
||  
Db 5 QS 6

## RESULT 51

PT0283  
Ig heavy chain CDR3 region (clone 4-94B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0283  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A:Reference number: PT0222; PMID:9108337; PMID:1899102  
A:Accession: PT0283  
A:Molecule type: DNA  
A:Residues: 1-7 <YAM>  
A:Experimental source: B lymphocyte



C;Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 2 PP 3  
||  
Db 6 PP 7

#### RESULT 52

E30608  
Ig kappa chain V-III region (Gag) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 16-Aug-1996  
C;Accession: E30608  
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soldo  
J. Immunol. 142, 3158-3163, 1989  
A;Title: Structural and idiotypic characterization of the L chains of human Igm autoanti  
A;Reference number: A30601; MUID:89215279; PMID:2496160  
A;Accession: E30608

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <GON>  
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 6 QS 7  
||  
Db 6 QS 7

#### RESULT 53

B24749  
neuropeptide B - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Aug-2000  
C;Accession: B24749  
R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.  
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985  
A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b  
A;Reference number: A94074; MUID:86067985; PMID:3865193  
A;Accession: B24749

A;Molecule type: protein  
A;Residues: 1-8 <YAN>  
C;Superfamily: unassigned animal peptides  
C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 5 PQ 6  
||  
Db 5 PQ 6

#### RESULT 54

B39745  
endoglycosylceramidase (EC 3.2.1.123) I - Rhodococcus sp. (fragment)  
C;Species: Rhodococcus sp.  
C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 31-Dec-1993  
C;Accession: B39745  
R;Ito, M.; Ikegami, Y.; Yamagata, T.  
J. Biol. Chem. 266, 7919-7926, 1991.  
A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosylceramidases. El  
ble using these activator proteins.  
A;Reference number: A39745; MUID:91210321; PMID:1850427  
A;Accession: B39745

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <ITO>  
C;Keywords: glycosidase; hydrolase

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 2 PP 3  
||  
Db 2 PP 3

#### RESULT 55

S16324  
hypothetical protein 2 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000  
C;Accession: S16324  
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.  
EMBO J. 10, 1787-1791, 1991  
A;Title: A novel class of plant proteins containing a homeodomain with a closely linked  
A;Reference number: S16323; MUID:91266907; PMID:1675603  
A;Accession: S16324

A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-8 <RUB>  
A;Cross-references: EMBL:X58821; NID:916327; PIDN:CAA41624.1; PID:9579259

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 2 PP 3  
||  
Db 7 PP 8

#### RESULT 56

S21288  
lectin - potato (fragment)  
C;Species: Solanum tuberosum (potato)  
C;Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 05-Dec-1998  
C;Accession: S21288  
R;Willar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.  
Biochem. J. 283, 813-821, 1992  
A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizati  
A;Reference number: S21288; MUID:92272683; PMID:1590771  
A;Accession: S21288

A;Molecule type: protein  
A;Residues: 1-8 <ML>  
A;Experimental source: var. Ulster Sceptre  
C;Function:  
A;Description: may be involved in defence mechanism of the plant  
C;Keywords: hydroxyproline; lectin

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 2 PP 3  
||  
Db 7 PP 8

#### RESULT 57

A46306  
spasmogenic toxin PNVI - spider (Phoneutria nigriventer) (fragment)  
C;Species: Phoneutria nigriventer  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 17-Mar-1999  
C;Accession: A46306  
R;Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J

Toxinon 31, 377-384, 1993  
 A;Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide  
 A;Reference number: A46306; MUID:93276439; PMID:8503129  
 A;Accession: A46306  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-8 <MAR>

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QS 7  
 ||  
 Db 6 QS 7

## RESULT 58

JS0316  
 leucokinin VI - Madeira cockroach  
 C;Species: Leucophaea maderae (Madeira cockroach)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C;Accession: JS0316  
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic  
 A;Reference number: JS0315  
 A;Accession: JS0316  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act  
 F;Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid  
 F;Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QS 7  
 ||  
 Db 1 QS 2

## RESULT 59

JS0317  
 leucokinin VII - Madeira cockroach  
 C;Species: Leucophaea maderae (Madeira cockroach)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C;Accession: JS0317  
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 31-34, 1987  
 A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fir  
 A;Reference number: JS0317  
 A;Accession: JS0317  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act  
 F;Keywords: amidated carboxyl end; cephalomyotropic peptide  
 F;Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
 ||  
 Db 1 DP 2

## RESULT 60

E47393  
 neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)

C;Species: Calliphora vomitoria  
 C;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 03-Mar-1995  
 C;Accession: E47393  
 R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993  
 A;Title: Callatostatin: neuroptides from the blowfly Calliphora vomitoria with sequ  
 A;Reference number: A47393; MUID:93211980; PMID:8460157  
 A;Accession: E47393  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-8 <DUV>  
 A;Experimental source: whole flies  
 A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 ||  
 Db 2 PP 3

## RESULT 61

S71919  
 alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)  
 C;Species: Ctenopharyngodon idella (grass carp)  
 C;Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 07-May-1999  
 C;Accession: S71919  
 R;Tsui, H.T.; Mock, W.Y.; Lau, K.K.; Fong, W.P.  
 Biochim. Biophys. Acta 1296, 41-46, 1996  
 A;Title: Prophys. activation of grass carp (Ctenopharyngodon idellus) liver alcohol d  
 A;Reference number: S71919; MUID:96350418; PMID:8765227  
 A;Accession: S71919  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-8 <TSU>  
 A;Note: the source is designated Ctenopharyngodon idellus  
 C;Keywords: NAD; oxidoreductase

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
 ||  
 Db 2 DP 3

## RESULT 62

S10783  
 enamelin f - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
 C;Accession: S10783  
 R;Strawich, E.; Glimcher, M.J.  
 Eur. J. Biochem. 191, 47-56, 1990  
 A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is alb  
 A;Reference number: S10780; MUID:90336641; PMID:2379503  
 A;Accession: S10783  
 A;Molecule type: protein  
 A;Residues: 1-8 <STR>  
 C;Keywords: enamel; phosphoprotein

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 ||  
 Db 4 PP 5

## RESULT 63

PT0559  
T-cell receptor beta chain V-D-J region (126-18H) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0559  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0559  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-8 <FES>  
A;Experimental source: day 18 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
4 PP 5

Db

## RESULT 64

I49404  
prenalbumin - western wild mouse (fragment)  
C;Species: Mus spretus (western wild mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C;Accession: I49404  
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.  
Mamm. Genome 5, 349-355, 1994  
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
A;Accession: I49404  
A;Reference number: I48934; MUID:94319082; PMID:8043949  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-8 <RES>  
A;Cross-references: EMBL:U05689; NID:G497008; PIDN:AAB60461.1; PID:G642825

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQ 6  
||  
6 PQ 7

Db

## RESULT 65

I64832  
Ca2+-transporting ATPase (EC 3.6.3.8) - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 19-Apr-2002  
C;Accession: I64832  
R;Wu, K.

Am. J. Physiol. 264, 333-341, 1993  
A;Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase  
A;Reference number: I51892  
A;Accession: I64832  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-8 <RES>  
A;Cross-references: GB:M99223; NID:G203644; PIDN:AAA40992.1; PID:G203646  
C;Genetics:  
A;Gene: SERCA1b  
C;Keywords: hydrolase

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
||  
Db 1 DP 2

## RESULT 66

B45796  
dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) - Pseudomonas fluorescens (fragment)  
C;Species: Pseudomonas fluorescens  
C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 05-May-2000  
C;Accession: B45796  
R;Benen, J.A.E.; Van Berkel, W.J.H.; Van Dongen, W.M.A.M.; Mueller, F.; De Kok, A.  
J. Gen. Microbiol. 135, 1787-1797, 1989  
A;Title: Molecular cloning and sequence determination of the lpd gene encoding lipoamid.  
A;Reference number: A45796; MUID:90132584; PMID:2515251  
A;Accession: B45796  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-9 <BN>  
A;Cross-references: GB:M28356; NID:G151343; PIDN:AAA99233.1; PID:G151344  
C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology  
C;Keywords: acyltransferase; coenzyme A; lipoamide; tricarboxylic acid cycle

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
||  
Db 1 DP 2

## RESULT 67

DS8503  
translation elongation factor EF-Tu - unidentified bacterium (fragment)  
C;Species: unidentified bacterium  
C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 28-May-1999  
C;Accession: DS8503  
R;Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A;Description: The proteins of kidney and gallbladder stones.  
A;Reference number: A58501  
A;Accession: DS8503  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <BIN>  
A;Experimental source: human bile and stones  
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homol  
C;Keywords: GTP binding

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQ 6  
||  
4 PQ 5

Db

## RESULT 68

A61358  
bradykinin-like peptide I - Japanese pond frog  
C;Species: Rana nigromaculata (Japanese pond frog)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 02-Sep-2000  
C;Accession: A61358  
R;Nakajima, T.  
Chem. Pharm. Bull. 16, 769-770, 1968  
A;Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin  
A;Reference number: A61358; MUID:68412013; PMID:5677638  
A;Accession: A61358  
A;Status: preliminary  
A;Molecule type: protein

A;Residues: 1-9 <NAK>  
A;Status: preliminary  
C;Superfamily: unassigned animal peptides  
C;Keywords: skin

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 69

A61057  
Thr-6 bradykinin - scollid wasp (Colpa interrupta)  
C;Species: Colpa interrupta  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Aug-2000  
C;Accession: A61057  
R;Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.  
Comp. Biochem. Physiol. C 96, 157-162, 1990  
A;Title: Threonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynap  
A;Reference number: A61057; MUID:91130217; PMID:1980872

A;Accession: A61057  
A;Molecule type: protein  
A;Residues: 1-9 <PIE>

C;Superfamily: unassigned animal peptides  
C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 70

A26744  
bradykinin-like peptide - garden dagger wasp  
N;Alternate names: Thr-6-bradykinin  
C;Species: Megascollia flavifrons (garden dagger wasp)  
C;Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 18-Aug-2000  
C;Accession: A26744  
R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.  
Toxicol 25, 527-535, 1987  
A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary was  
A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: A26744  
A;Molecule type: protein  
A;Residues: 1-9 <YAS>  
C;Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 71

A61363  
bradykinin - common frog  
C;Species: Rana temporaria (common frog)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
C;Accession: A61363  
R;Anastasi, A.; Erspamer, V.; Bertaccini, G.  
Comp. Biochem. Physiol. A 14, 43-52, 1965  
A;Title: Occurrence of bradykinin in the skin of Rana temporaria.  
A;Reference number: A61363

A;Accession: A61363  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <ANA>  
C;Superfamily: unassigned animal peptides  
C;Keywords: skin

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 72

A60579  
bradykinin-like peptide - slider turtle  
C;Species: Pseudemys scripta (slider)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
C;Accession: A60579  
R;Conlon, J.M.; Hicks, J.W.; Smith, D.D.  
Endocrinology 126, 985-991, 1990  
A;Title: Isolation and biological activity of a novel kinin ([Thr(6)]bradykinin) from t  
A;Reference number: A60579; MUID:90126625; PMID:2298179

A;Accession: A60579  
A;Molecule type: protein  
A;Residues: 1-9 <CON>

C;Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammalian  
C;Superfamily: unassigned animal peptides  
C;Keywords: plasma

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 73

B60246  
ornitho-kinin - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 18-Aug-2000  
C;Accession: B60246  
R;Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.  
Adv. Exp. Med. Biol. 247A, 359-367, 1989  
A;Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemical  
A;Reference number: A60246; MUID:90102072; PMID:2603803

A;Accession: B60246  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <KIM>  
C;Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
||  
Db 2 PP 3

## RESULT 74

B41983  
orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)  
C;Species: Azotobacter vinelandii  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C;Accession: B41983

R;Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.  
Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992  
A;Title: Unification of the ferritin family of proteins.  
A;Reference number: A41983; MUID:92196129; PMID:1549605  
A;Accession: B41983  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid; protein  
A;Residues: 1-9 <GRO>  
A;Cross-references: GB:M83692; NID:gl42297; PIDN:AAA22122.1; PID:gl42299  
A;Note: sequence extracted from NCBI backbone (NCBIP:88442)

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
DB 3 PP 4

## RESULT 75

C36730  
hutU protein - Klebsiella pneumoniae (fragment)  
C;Species: Klebsiella pneumoniae  
C;Date: 19-Apr-1991 #sequence\_revision 19-Apr-1991 #text\_change 08-Oct-1999  
C;Accession: C36730  
R;Schwacha, A.; Bender, R.A.  
J;Bacteriol 172, 5477-5481, 1990  
A;Title: Nucleotide sequence of the gene encoding the repressor for the histidine utilization  
A;Reference number: A36730; MUID:90368611; PMID:2203754  
A;Accession: C36730  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-9 <SCH>  
A;Cross-references: GB:M34504; NID:gl49203; PIDN:AAA25076.1; PID:gl49206

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QS 7  
DB 3 QS 4

Search completed: November 25, 2003, 18:28:23  
Job time : 7.44149 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 3.3883 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-14

Perfect score: 7

Sequence: 1 DPPPPQS 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47036705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	71.4	15	1 PRP_MYCBO	P80149 mycobacteri
2	4	57.1	10	1 TMOF_ABDAA	P19425 aedes aegypt
3	3	42.9	10	1 AH3_PRUSE	P29261 prunus sero
4	3	42.9	12	1 FIF1_SARBU	P83349 sarcophaga
5	3	42.9	12	1 TKN2_KASMA	P08614 kassina mac
6	3	42.9	13	1 AH4_PRUSE	P29262 prunus sero
7	3	42.9	13	1 TY13_PHYRO	P04096 phyllomedus
8	3	42.9	15	1 AH2_PRUSE	P29260 prunus sero
9	3	42.9	15	1 UP01_METAN	P83440 metarhizium
10	3	42.9	16	1 AF2S_MALPA	P83142 malva parvi
11	3	42.9	16	1 AH1_PRUSE	P29259 prunus sero
12	3	42.9	16	1 IBP1_PIG	P24854 sus scrofa
13	3	42.9	17	1 APID_BOMPA	P81464 bombus pasc
14	3	42.9	19	1 AL22_HORSE	P81217 equus cabal
15	3	42.9	19	1 PSAE_CUCSA	P42047 eucymis sat
16	3	42.9	20	1 APA1_ERYPA	P18647 erythrocebu
17	3	42.9	20	1 M117_BOVIN	P35451 bos taurus
18	3	42.9	20	1 AL14_CARMA	P81807 carcinus ma
19	2	28.6	7	1 FARI_HELTI	P41871 helisoma tr
20	2	28.6	7	1 TPFY_PACDA	P83455 pachymedusa
21	2	28.6	7	1 UF04_MOUSE	P38642 mus musculu
22	2	28.6	7	1 UH11_RAT	P56576 rattus norv
23	2	28.6	8	1 AL15_CALVO	P41841 calliphora
24	2	28.6	8	1 FARI_PANRE	P41872 panagrellus
25	2	28.6	8	1 LCK1_LEUMA	P21140 leucophaea
26	2	28.6	8	1 LCK2_LEUMA	P21141 leucophaea
27	2	28.6	8	1 LCK6_LEUMA	P19988 leucophaea
28	2	28.6	8	1 LCK7_LEUMA	P19989 leucophaea
29	2	28.6	8	1 NP8_BOVIN	P15507 bos taurus
30	2	28.6	8	1 PPK2_PERAM	P82692 periplaneta
31	2	28.6	8	1 UH09_RAT	P56575 rattus norv
32	2	28.6	9	1 AL10_CARMA	P81813 carcinus ma
33	2	28.6	9	1 FARI_CALVO	P41856 calliphora

34	2	28.6	9	1 FAR2_PANRE	P41873 panagrellus
35	2	28.6	9	1 HUTU_KLEAE	P12381 klebsiella
36	2	28.6	9	1 KNL3_BOMVA	P83058 bombina var
37	2	28.6	9	1 OXYT_BURE	P42995 bufo regula
38	2	28.6	9	1 OXYT_RAJCL	P42994 raja clavac
39	2	28.6	9	1 YBPR_AZOVI	P25825 azotobacter
40	2	28.6	10	1 AMPN_HELAM	P81731 helicoverpa
41	2	28.6	10	1 BPP2_BOTIN	P30422 bothrops in
42	2	28.6	10	1 BPP2_BOTJA	P01022 bothrops ja
43	2	28.6	10	1 BPP8_BOTIN	P30426 bothrops in
44	2	28.6	10	1 BPP_VIPAS	P31351 vipera aspi
45	2	28.6	10	1 BRK_ONCMY	P9821 oncorhynch
46	2	28.6	10	1 FAR6_PANRE	P22660 panagrellus
47	2	28.6	10	1 LPR2_LOCM1	P41488 locusta mig
48	2	28.6	10	1 LSK2_LEUMA	P09039 leucophaea
49	2	28.6	10	1 MALE_KLEPN	P05564 klebsiella
50	2	28.6	10	1 NS1_MYCTU	P81135 mycobacteri
51	2	28.6	10	1 TKL3_LOCM1	P30449 locusta mig
52	2	28.6	10	1 TKU1_UREUN	P40751 urechis uni
53	2	28.6	10	1 UPA2_HUMAN	P30088 homo sapien
54	2	28.6	10	1 URE3_MORMO	P17339 morganella
55	2	28.6	11	1 BPP3_BOTIN	P30423 bothrops in
56	2	28.6	11	1 BPP4_BOTIN	P30424 bothrops in
57	2	28.6	11	1 BPPB_AKGHA	P01021 agkistrodon
58	2	28.6	11	1 BPP_AKGHP	P12797 megascolia
59	2	28.6	11	1 BRK_MEGFL	P22790 achatina fu
60	2	28.6	11	1 CEP1_ACHFU	P81018 oncorhynch
61	2	28.6	11	1 LADD_ONCMY	P81163 homo sapien
62	2	28.6	11	1 MORN_HUMAN	P08951 rana pipien
63	2	28.6	11	1 RANC_RANPI	P82026 uperoleia i
64	2	28.6	11	1 TKN1_UPEIN	P08612 uperoleia r
65	2	28.6	11	1 TKN1_UPERU	P08616 uperoleia r
66	2	28.6	11	1 TKN2_UPERU	P19850 gallus gall
67	2	28.6	11	1 TKNA_CHICK	P28498 gadus morhu
68	2	28.6	11	1 TKNA_GADMO	P01290 equus cabal
69	2	28.6	11	1 TKNA_HORSE	P08615 physalaemus
70	2	28.6	11	1 TKN_PHYFU	P50983 conus imper
71	2	28.6	12	1 CXA1_CONIM	P83322 peneaus mon
72	2	28.6	12	1 FAR7_PENMO	P83176 carcinus ma
73	2	28.6	12	1 HCY1_CARVA	P01371 tremella me
74	2	28.6	12	1 TAL0_TREME	P42991 pseudophryn
75	2	28.6	13	1 BOWL_PSEGU	P01020 bothrops ja
76	2	28.6	13	1 BPP1_BOTJA	P42717 parapolymbia
77	2	28.6	13	1 BRK_FARID	P31832 rana escul
78	2	28.6	13	1 CRTC_RANES	P80941 lymantria d
79	2	28.6	13	1 ECDE_LYMDI	P28525 hordeum vul
80	2	28.6	13	1 GER1_HORVU	P28526 hordeum vul
81	2	28.6	13	1 GER2_HORVU	P81532 microplitis
82	2	28.6	13	1 MPl_MICOC	P41536 rana tempor
83	2	28.6	13	1 NEUT_RANTE	P01370 tremella me
84	2	28.6	13	1 TAL3_TREME	P56535 canis fami
85	2	28.6	13	1 UHA3_CANFA	P56535 canis fami
86	2	28.6	14	1 CX1A_CONBE	P56535 canis fami
87	2	28.6	14	1 GLGS_SPIOL	P55335 spinacia ol
88	2	28.6	14	1 PH1_PRUSE	P29263 streptomyc
89	2	28.6	14	1 SODN_STRGR	P80732 streptomyc
90	2	28.6	14	1 TAT_HV1W2	P12509 human immun
91	2	28.6	14	1 TAT_HV1W8	P12511 human immun
92	2	28.6	14	1 UN07_CLOPA	P81352 clostridium
93	2	28.6	15	1 AF1L_MALPA	P83141 malva parvi
94	2	28.6	15	1 AFP3_MALPA	P83137 malva parvi
95	2	28.6	15	1 CH11_PEA	P21225 pisum sativ
96	2	28.6	15	1 CXA2_CONAL	P56640 conus aulic
97	2	28.6	15	1 HS11_PINPS	P81083 pinus pinas
98	2	28.6	15	1 LEC1_PSOSC	P22582 psophocarpu
99	2	28.6	15	1 LEC2_PSOSC	P22585 psophocarpu
100	2	28.6	15	1 LEC3_PSOSC	P22583 psophocarpu

## ALIGNMENTS

RESULT 1

```

PRP MYCBO
ID PRP MYCBO STANDARD; PRT; 15 AA.
AC P80149;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Proline-rich protein (Fragment).
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / Paris 1173 P2;
RX MEDLINE=93281750; PubMed=8506381;
RA Romain F., Augier J., Pescher P., Marchal G.A.;
RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-
RT type hypersensitivity reactions only in guinea pigs immunized with
RT living mycobacteria.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).
CC -/- SUBCELLULAR LOCATION: Secreted.
CC -/- DISEASE: IMMUNODOMINANT FOR DELAYED-TYPE HYPERSENSITIVITY
CC REACTIONS IN GUINEA PIGS.
FT NON TER 15
FT SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;
SQ
Query Match 71.4%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6
DB 7 PPPPQ 11

RESULT 2
TMOF AEDAE
ID TMOF AEDAE STANDARD; PRT; 10 AA.
AC F19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating
RT trypsin-like enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -/- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCTYE
CC DEVELOPMENT.
CC -/- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
CC 36 HRS AND STOPS AT 56 HRS.
DR PIR; A36454; A36454.
KW Hormone.
FT DOMAIN 3 10 POLY-PRO.

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FT VARIANT 1 2 YD -> DY (IN TMFO(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;

Query Match 57.1%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5
DB 5 PPPP 8

RESULT 3
AH3 PRUSE
ID AH3 PRUSE STANDARD; PRT; 10 AA.
AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -/- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -/- SUBUNIT: Monomer.
CC -/- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -/- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON TER 10
FT SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;
SQ
Query Match 42.9%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.8e-02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPP 3
DB 2 DPP 4

RESULT 4
FIF1 SARBU
ID FIF1 SARBU STANDARD; PRT; 12 AA.
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FIRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meeusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G

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RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DPP 6
DB 2 PPO 4

RESULT 5
TKN2_KASMA STANDARD; PRT; 12 AA.
AC P08614;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hylambatin.
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8414;
RN [1]
RP SEQUENCE
RC TISSUE=Skin secretion;
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus.";
RL Biomed. Res. 2:613-617(1981).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1441 MW; 32B7CD2FDD40AB7 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPP 3
DB 1 DPP 3

RESULT 6
AH4_PRUSE STANDARD; PRT; 13 AA.
AC P29262;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II' (EC 3.2.1.117) (Amygdalin hydrolase

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DE isozyme II') (AH II') (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eуроsids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -1- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -1- SUBUNIT: Monomer.
CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -1- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1417 MW; F7CC4FA321B9D051 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPP 3
DB 2 DPP 4

RESULT 7
TY13_PHYRO STANDARD; PRT; 13 AA.
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-13.
OS Phyllosticta rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllostictinae; Phyllosticta.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RA Montecucchi P.C., Gozzini L., Erspamer V.;
RT "Primary structure determination of a tryptophan-containing
RT tridecapeptide from Phyllosticta rohdei.";
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
DR PIR; A05174; A05174.
KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9

RESULT 8
AH2_PRUSE STANDARD; PRT; 15 AA.
AC P29260;
DT 01-DEC-1992 (Rel. 24, Created)

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DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Amygdalin beta-glucosidase I' (EC 3.2.1.117) (Amygdalin hydrolase  
 DE Isozyme I') (AH I') (Fragment).  
 OS Prunus serotina (Black cherry).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OS eurosid I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OC NCBI\_TaxID=23207;  
 OX [1]  
 RN  
 RP  
 RQ  
 RZ  
 RX TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -1- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-  
 CC glucose.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 CC EMBRYONAL TISSUES.  
 CC -1- PTM: GLYCOSYLATED.  
 CC KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1650 MW; F7CC4FA321E12EC4 CRC64;  
 Query Match 42.9%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DPP 3  
 DB 4 DPP 6  
 RESULT 9  
 UP01\_METAN  
 ID UP01\_METAN STANDARD; PRT; 15 AA.  
 AC P8340;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Unknown protein (Fragment).  
 OS Metarhizium anisopliae.  
 OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OS Hypocreomycetidae; Hypocreales; Clavicipitaceae;  
 OS mitosporic Clavicipitaceae; Metarhizium.  
 OC NCBI\_TaxID=5530;  
 OX [1]  
 RN  
 RP  
 RQ  
 RZ  
 RX STRAIN=54A-1b;  
 RA MEDLINE=22343006; PubMed=12455610;  
 RA Kamp A.M., Bidochna M.J.;  
 RT "Protein analysis in a plasmorphically deteriorated strain of the  
 RT insect-pathogenic fungus Metarhizium anisopliae.";  
 RL Can. J. Microbiol. 48:787-792(2002).  
 CC -1- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-  
 CC glucose.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 CC EMBRYONAL TISSUES.  
 CC -1- PTM: GLYCOSYLATED.  
 CC KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1651 MW; FBD76D669E1F0F4F CRC64;  
 Query Match 42.9%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DPP 3  
 DB 2 DPP 4  
 RESULT 10  
 AF2S\_MALPA  
 ID AF2S\_MALPA STANDARD; PRT; 16 AA.  
 AC P83142;

DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antifungal protein 2 small subunit (CW-2) (Fragment).  
 OS Malva parviflora (Little mallow) (Cheeseweed).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OS eurosid II; Malvales; Malvaceae; Malvoideae; Malva.  
 OC NCBI\_TaxID=145753;  
 OX [1]  
 RN  
 RP  
 RQ  
 RZ  
 RX TISSUE=Seed;  
 RA MEDLINE=20568734; PubMed=11118343;  
 RA Wang X., Bunkers G.J.;  
 RT "Potent heterologous antifungal proteins from cheeseweed (Malva  
 RT parviflora).";  
 RL Biochem. Biophys. Res. Commun. 279:669-673(2000).  
 CC -1- FUNCTION: Possesses antifungal activity against P.infestans but  
 CC not F.graminearum.  
 CC -1- SUBUNIT: Heterodimer of a large and a small subunit.  
 CC -1- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
 CC concentration.  
 CC GO: GO:0003799; F:antifungal peptide activity; IDA.  
 CC KW Fungicide; Antibiotic.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 2027 MW; 9998D9E8F8FB7EE65 CRC64;  
 Query Match 42.9%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DPP 3  
 DB 8 DPP 10  
 RESULT 11  
 AH1\_PRUSE  
 ID AH1\_PRUSE STANDARD; PRT; 16 AA.  
 AC P29259;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Amygdalin beta-glucosidase I (EC 3.2.1.117) (Amygdalin hydrolase  
 DE Isozyme I) (AH I) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OS eurosid I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OC NCBI\_TaxID=23207;  
 OX [1]  
 RN  
 RP  
 RQ  
 RZ  
 RX TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -1- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-  
 CC glucose.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 CC EMBRYONAL TISSUES.  
 CC -1- PTM: GLYCOSYLATED.  
 CC KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1693 MW; 86E7CC4FA321E129 CRC64;  
 Query Match 42.9%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DPP 3

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Db      4 DPP 6
RESULT 12
IBP4_PIG
ID      IBP4_PIG      STANDARD;      PRT;      16 AA.
AC      P24854;
DT      01-MAR-1992 (Rel. 21, Created)
DT      01-MAR-1992 (Rel. 21, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE      (IGF-binding protein 4) (fragment)
GN      IGFBP4.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=92109718; PubMed=1722398;
RA      Coleman M.E., Pan Y.-C.E., Etherton T.D.;
RT      "Identification and NH2-terminal amino acid sequence of three
RT      insulin-like growth factor-binding proteins in porcine serum.";
RL      Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC      -!- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFS
CC      AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC      PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE
CC      INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: Contains 1 IGFBP domain.
CC      -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
DR      PIR; JH0517; JH0517.
DR      InterPro; IPR000867; Insl_gro_fac_pr.
DR      InterPro; IPR000716; Thyroglobulin_1.
DR      PROSITE; PS00222; IGF_BINDING, PARTIAL.
DR      PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW      Growth factor binding.
FT      NON TER 16
FT      NON TER 16
SQ      SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match      42.9%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPP 4
DB      7 PPP 9

RESULT 13
APID_BOMPA
ID      APID_BOMPA      STANDARD;      PRT;      17 AA.
AC      P81464;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Apidaecin.
OS      Bombus pascuorum (Brown bumble bee).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC      Apidae; Bombus.
OX      NCBI_TaxID=65598;
RN      [1]
RP      SEQUENCE.
RX      TISSUE=Hemolymph;
RX      MEDLINE=97362903; PubMed=9219367;
RA      Rees J.A., Moniatte M., Bulet P.;
RT      "Novel antibacterial peptides isolated from a European bumblebee,
RT      Bombus pascuorum (Hymenoptera, Apoidea).";
RL      Insect Biochem. Mol. Biol. 27:413-422(1997).
CC      -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC      BACTERIA.
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CC      -!- INDUCTION: By bacterial infection.
DR      InterPro; IPR004828; Apidaecin.
DR      Pfam; PF08007; Apidaecin; 1.
KW      Insect immunity; Antibiotic; Hemolymph.
SQ      SEQUENCE 17 AA; 1963 MW; CD1D0D02C8BC23D1 CRC64;

Query Match      42.9%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPP 4
DB      8 PPP 10

RESULT 14
AL22_HORSE
ID      AL22_HORSE      STANDARD;      PRT;      19 AA.
AC      P81217;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Dander allergen Equ c 2.0102 (fragment).
OS      Equus caballus (Horse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX      NCBI_TaxID=9796;
RN      [1]
RP      SEQUENCE.
RX      TISSUE=Skin;
RX      MEDLINE=98237590; PubMed=9578478;
RA      Bulone V., Krogstad-Johnsen T., Smeestad-Paulsen B.;
RT      "Separation of horse dander allergen proteins by two-dimensional
RT      electrophoresis-- molecular characterisation and identification of
RT      Equ c 2.0101 and Equ c 2.0102 as lipocalin proteins.";
RL      Eur. J. Biochem. 253:202-211(1998).
RN      [2]
RP      MASS SPECTROMETRY.
RC      TISSUE=Hair dandruff;
RC      MEDLINE=21257838; PubMed=11358533;
RX      Goubiran Botros H., Poncet P., Rabillon J., Fontaine T., Laval J.-M.,
RA      David B.;
RT      "Biochemical characterization and surfactant properties of horse
RT      allergens.";
RL      Eur. J. Biochem. 268:3126-3136(2001).
CC      -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC      -!- MASS SPECTROMETRY: MW=16000; METHOD=Electrospray.
CC      -!- MISCELLANEOUS: Allergen of horse dander.
CC      -!- SIMILARITY: Belongs to the lipocalin family.
CC      -!- CAUTION: C 2.0101 AND C 2.0102 MIGHT BE TWO VARIANTS OF THE
CC      SAME PROTEIN.
DR      InterPro; IPR000566; Lipocalin_cytFABP.
DR      PROSITE; PS00213; LIPOCALIN_PARTIAL.
KW      Transport; Lipocalin; Allergen.
FT      NON TER 19
FT      NON TER 19
SQ      SEQUENCE 19 AA; 2195 MW; A8EE6FAFC9322C26 CRC64;

Query Match      42.9%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 POS 7
DB      4 POS 6

RESULT 15
PSAE_CUCA
ID      PSAE_CUCA      STANDARD;      PRT;      19 AA.
AC      P42047;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
```

DE Photosystem I reaction center subunit IV (PSI-E) (Photosystem I 19.5  
DE kDa protein) (PS I subunit 6) (Fragment).

GN PSAE.  
OS Cucumis sativus (Cucumber).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;  
OC eusoids I; Cucurbitales; Cucurbitaceae; Cucumis.

OX NCBI\_TaxID=3659;

RN [1]

RP SEQUENCE.

RC TISSUE=Cotyledon; PubMed=1883835;

RX MEDLINE=91355209; Pubmed=1883835;

RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;

RT "Characterization of genes that encode subunits of cucumber PS I

complex by N-terminal sequencing.";

RL Biochim. Biophys. Acta 1059:141-148 (1991).

CC -1- FUNCTION: Stabilizes the interaction between psac and the PSI

core, assists the docking of the ferredoxin to PSI and interacts

with ferredoxin-NADP oxidoreductase (By similarity).

CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.

CC -1- SIMILARITY: BELONGS TO THE PSAE FAMILY.

DR PIR; G56819; G56819.

KW Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.

FT NON TER 19 19

SQ SEQUENCE 19 AA; 1810 MW; A93E8BDD089FB738 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4

DB 6 PPP 8

RESULT 16

APAL\_ERYPA

ID APAL\_ERYPA STANDARD; PRT; 20 AA.

AC P18647;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Apolipoprotein A-I (Apo-AI) (Fragment).

GN APOA1.

OS Erythrocybus patas (Red guenon) (Hussar).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Erythrocybus.

OX NCBI\_TaxID=9538;

RN [1]

RP SEQUENCE.

RX MEDLINE=76184721; PubMed=178359;

RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;

RT "Characterization of the plasma lipoproteins and apoproteins of the

Erythrocybus patas monkey.";

RL Biochemistry 15:1928-1933 (1976).

CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF

CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING

CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR

THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN

CHYLOMICRONS.

CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

DR PIR; A05313; A05313.

KW Plasma; Lipid transport; HDL; Cholesterol metabolism.

FT NON TER 20 20

SQ SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 42.9%; Score 3; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 8.6e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6

DB 3 PPQ 5

RESULT 17

MIL7\_BOVIN

ID MIL7\_BOVIN STANDARD; PRT; 20 AA.

AC P35451;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE 17 kDa milk glycoprotein (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE.

RC TISSUE=Milk; PubMed=8320368;

RX MEDLINE=93308294; Pubmed=8320368;

RA Soerensen E.S., Petersen T.B.;

RT "Purification and characterization of three proteins isolated from

the protease fraction of bovine milk.";

RL J. Dairy Res. 60:189-197 (1993).

CC -1- PTM: N-GLYCOSYLATED.

CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.

KW Glycoprotein; Milk.

FT NON TER 1 1

SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C7 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 8.6e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POS 7

DB 5 POS 7

RESULT 18

ALL4\_CARMA

ID ALL4\_CARMA STANDARD; PRT; 7 AA.

AC P81807;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Carcinustatin 4.

OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

OC Eubrachyura; Portunioidea; Portunidae; Carcinus.

OX NCBI\_TaxID=6759;

RN [1]

RP SEQUENCE.

RC TISSUE=Cerebral ganglion, and Thoracic ganglion;

RX MEDLINE=98121193; PubMed=9461295;

RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,

RA Thorpe A.;

RT "Isolation and identification of multiple neuropeptides of the

allatostatin superfamily in the shore crab Carcinus maenas.";

RL Eur. J. Biochem. 250:727-734 (1997).

CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

KW Neuropeptide; Multigene family.

FT NON TER 20 20

SQ SEQUENCE 7 AA; 782 MW; 672879CDBC476AC0 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
DB 1 DP 2

RESULT 19  
FAR1\_HELTI STANDARD; PRT; 7 AA.  
ID FAR1\_HELTI  
AC P41871;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRPamide-like neuropeptide GDPFLRF-amide.  
OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC Lymnaeidae; Planorbidae; Helisoma.  
OX NCBI\_TaxID=27815;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRPamide-related peptides from the kidney of the snail, Helisoma  
trivolvis";  
RL Peptides 15:31-36(1994).  
CC -1- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING  
THE KIDNEY, MANTLE AND SKIN.  
CC -1- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEWOLYMPH.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
FAMILY.  
CC Neuropeptide; Amidation.  
KW Neuropeptide; Amidation.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 851 MW; 65D40729D76AA810 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
DB 2 DP 3

RESULT 20  
TPFY\_PACDA STANDARD; PRT; 7 AA.  
ID TPFY\_PACDA  
AC P83455;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Trypophyllin-1 (pdt-1).  
OS Pachymedusa dancicolor (Giant mexican leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Phyllomedusinae; Pachymedusa.  
OX NCBI\_TaxID=75988;  
RN [1]  
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
PRO-7.  
RC TISSUE=Skin secretion;  
RA Chen T.B., Orr D.F., Shaw C.;  
RT "Pachymedusa dancicolor tryptophyllin-1 (pdt-1): structural  
characterization, pharmacological activity and cloning of precursor  
cDNA";  
RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
smooth muscle.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.  
DR GO: 0005576; C:extracellular; NAS.  
DR GO: 0045986; P:negative regulation of smooth muscle contra. .; NAS.  
KW Amphibian defense peptide; Amidation; Hydroxylation.

FT MOD RES 3 3 HYDROXYLATION.  
FT MOD RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
DB 2 PP 3

RESULT 21  
UF04\_MOUSE STANDARD; PRT; 7 AA.  
ID UF04\_MOUSE  
AC F38642;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
using preparative two-dimensional gel electrophoresis";  
RL Electrophoresis 15:735-745(1994).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 5.0, ITS MW IS: 46 kDa.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
DB 3 PP 4

RESULT 22  
UH11\_RAT STANDARD; PRT; 7 AA.  
ID UH11\_RAT  
AC P56576;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Heart;  
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
Jungblut P.R.;  
RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 8.5, ITS MW IS: 42 kDa.  
FT UNSURE 2  
FT NON TER 2 OR A.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 775 MW; 686DB040DC5A6B0 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QS 7  
DB 1 QS 2

## RESULT 23

ALL5\_CALVO  
ID ALL5\_CALVO STANDARD; PRT; 8 AA.  
AC P41841;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Callatostatin 5 (Met-callatostatin 1) (Hyp3]Met-callatostatin).  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RN SEQUENCE.

RP MEDLINE=93211980; PubMed=8460157;  
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
RA Thorpe A.;  
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria  
with sequence homology to cockroach allatostatins."  
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
RN [2]  
RN CHARACTERIZATION, AND HYDROXYLATION.  
RC TISSUE=Head;  
RX MEDLINE=94342269; PubMed=8063725;  
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;  
RT "[Hyp3]Met-callatostatin. Identification and biological properties of  
a novel neuropeptide from the blowfly Calliphora vomitoria."  
RL J. Biol. Chem. 269:21059-21066(1994).  
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY  
A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
CC -1- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.  
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
DR PIR; E47393; E47393.  
KW Neuropeptide; Amidation; Hydroxylation.  
FT MOD RES 3 3 HYDROXYLATION (20%).  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB47768 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
DB 2 PP 3

## RESULT 24

FAR1\_PANRE  
ID FAR1\_PANRE STANDARD; PRT; 8 AA.  
AC P41872;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE FMRamide-like neuropeptide pP1 (SDPNFLRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RN SEQUENCE.  
RX MEDLINE=93027659; PubMed=1408999;

RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
RA Garrison R.D., Williams J.F., Friedman A.R.;  
RT "Two FMRamide-like peptides from the free-living nematode  
Panagrellus redivivus."  
RL Peptides 13:209-214(1992).  
CC -1- FUNCTION: MYOACTIVE.  
CC -1- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
CAUDALLY TO THE BASE OF THE PHARYNX.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
DB 2 DP 3

## RESULT 25

LCK1\_LEUMA  
ID LCK1\_LEUMA STANDARD; PRT; 8 AA.  
AC P21110;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 01-MAY-1991 (Rel. 18, Last annotation update)  
DE Leucokinin I (L-I).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RN SEQUENCE AND SYNTHESIS.  
RC TISSUE=Head;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure and synthesis of two neuropeptides  
from Leucophaea maderae: members of a new family of  
Cephalomyotropins."  
RL Comp. Biochem. Physiol. 84C:205-211(1986).  
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
KW Neuropeptide; Amidation.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2  
DB 1 DP 2

## RESULT 26

LCK2\_LEUMA  
ID LCK2\_LEUMA STANDARD; PRT; 8 AA.  
AC P21141;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DE FMRamide-like neuropeptide pP1 (SDPNFLRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;

RN SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of two neuropeptides  
 from Leucophaea maderae: members of a new family of  
 Cephalomyotropins.";  
 RL Comp. Biochem. Physiol. 84C:205-211 (1986).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8  
 SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;  
  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 DP 2  
 Db 1 DP 2  
  
 RESULT 27  
 LCK6 LEUMA  
 ID LCK6 LEUMA STANDARD; PRT; 8 AA.  
 AC P19988;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leucokinin VI (L-VI).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberoidea; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Head;  
 RX MEDLINE=87052651; PubMed=2877794;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
 RT myotropic peptides of Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 88C:27-30 (1987).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND  
 CC HELIOTHIS ZEA ADIPOKINETIC HORMONE.  
 DR PIR; JS0316;  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;  
  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 QS 7  
 Db 1 QS 2  
  
 RESULT 28  
 LCK7 LEUMA  
 ID LCK7 LEUMA STANDARD; PRT; 8 AA.  
 AC P19989;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Leucokinin VII (L-VII).  
 OS Leucophaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberoidea; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of leucokinin VII and  
 RT VIII: the final members of this new family of cephalomyotrophic  
 RT peptides isolated from head extracts of Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 88C:31-34 (1987).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
 DR PIR; JS0317; JS0317.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9C76A CRC64;  
  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 DP 2  
 Db 1 DP 2  
  
 RESULT 29  
 NPB BOVIN  
 ID NPB BOVIN STANDARD; PRT; 8 AA.  
 AC P15507;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuropeptide B.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=86667985; PubMed=3865193;  
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;  
 RT "Isolation, sequencing, synthesis, and pharmacological  
 RT characterization of two brain neuropeptides that modulate the action  
 RT of morphine.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761 (1985).  
 CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.  
 DR PIR; B24749; B24749.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1083 MW; 87D416C776D9C729 CRC64;  
  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 PQ 6  
 Db 5 PQ 6  
  
 RESULT 30  
 PPK2 PERAM  
 ID PPK2 PERAM STANDARD; PRT; 8 AA.  
 AC P82692;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pyrokinin-2 (Pep-PK-2) (FXPRL-amide).  
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OX Blattidae; Periplaneta.  
RN NCBI\_TaxID=6978;  
[1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Corporalcardiaca;  
RX MEDLINE=9733923; PubMed=9210163;  
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;  
RT "Isolation and structural elucidation of two pyrokinins from the  
RT retrocerebral complex of the American cockroach.";  
RL Peptides 18:473-478(1997).  
RN [2]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
RT the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro: IPR001484; Pyrokinin.  
DR PROSITE: PS00539; PYROKININ; FALSE\_NEG.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 8 8  
FT AMIDATION.  
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 PP 3  
DB 2 PP 3  
  
RESULT 31  
UH09 RAT  
ID UH09 RAT STANDARD; PRT; 8 AA.  
AC P56575;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Heart;  
RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
RA Jungblut P.R.;  
RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.  
FT NON TER 8 8  
FT  
SQ SEQUENCE 8 AA; 1029 MW; 9E0775AC64140B06 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 QS 7  
DB 5 QS 6

RESULT 32  
AL10 CARMA  
ID AL10 CARMA STANDARD; PRT; 9 AA.  
AC P81813;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 10.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunodea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 9 9  
FT AMIDATION.  
SQ SEQUENCE 9 AA; 963 MW; 372D79CDB4776C7 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 PQ 6  
DB 2 PQ 3  
  
RESULT 33  
FAR1 CALVO  
ID FAR1 CALVO STANDARD; PRT; 9 AA.  
AC P41856;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CallifMRamide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated callifMRamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
CC SALIVARY GLAND OF CALLIPHORA.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; A41978; A41978.  
KW Neuropeptide; Amidation.  
FT MOD RES 9 9  
FT AMIDATION.  
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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QY      5 PQ 6
DB      2 PQ 3

RESULT 34
ID_FAR2_PANRE STANDARD; PRT; 9 AA.
AC P41873;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide PF2 (SADPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RA Garrison R.D., Williams J.F., Friedman A.R.;
RT "Two FMRamide-like peptides from the free-living nematode
RL Panagrellus redivivus.";
RL Peptides 13:209-214(1992).
CC -!- FUNCTION: MYOACTIVE.
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
CC CAUDALLY TO THE BASE OF THE PHARYNX.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DP 2
DB      3 DP 4

RESULT 35
ID_HUTU_KLEAE STANDARD; PRT; 9 AA.
AC P12381;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate
DE hydrolase) (Fragment).
GN HUTU.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88198018; PubMed=2834335;
RA Nieuwkoop A.J., Baldauf S.A., Hudspeeth M.E.S., Bender R.A.;
RT "Bidirectional promoter in the hut(P) region of the histidine
RT utilization (hut) operons from Klebsiella aerogenes.";
RL J. Bacteriol. 170:2240-2246(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90368611; PubMed=2203754;
RA Schwacha A., Bender R.A.;
RT "Nucleotide sequence of the gene encoding the repressor for the
RT histidine utilization genes of Klebsiella aerogenes.";
RL J. Bacteriol. 172:5477-5481(1990).
CC -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-yl)propanoate = urocanate + H(2)O.
CC

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CC -!- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -!- PATHWAY: Histidine degradation; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
CC
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DR EMBL; M19665; AAA25078.1; -
DR EMBL; M34604; AAA25076.1; -
DR HAMAP; MF_00577; -; 1.
DR InterPro; IPR000193; Urocanase.
DR PROSITE; PS01233; UROCANASE; PARTIAL.
KW Histidine metabolism; Lyase; NAD.
FT NON TER 9
SQ SEQUENCE 9 AA; 1140 MW; 970FC41B5325A6C5 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QS 7
DB      3 QS 4

RESULT 36
KNL3_BOMVA STANDARD; PRT; 9 AA.
ID KNL3_BOMVA
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE-Skin secretion;
RA Chen T.B., Orr D.F., Bjorson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PP 3
DB      2 PP 3

RESULT 37
OXYT_BUPRE STANDARD; PRT; 9 AA.
ID OXYT_BUPRE
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC

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DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Seritocin ((ser5,11e8]-oxytocin)).  
 OC Bufo regularis (Leopard toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;  
 OC Bufo.  
 NCBI\_TaxID=8390;

RN [1]  
 RX TISSUE=pituitary neurointermediate lobe;  
 RX MEDLINE=96059313; PubMed=7591488;  
 RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;  
 RT "A new neurohypophyseal peptide, seritocin ((ser5,11e8]-oxytocin),  
 RT identified in a dryness-resistant African toad, Bufo regularis.";  
 RL Int. J. Pept. Protein Res. 45:482-487(1995).  
 CC -|- FUNCTION: Devoid of oxytocic activity.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR InterPro; IPR000981; Neurohyp\_horm.  
 DR Pfam; PF00220; hormone4; 1  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; FALSE\_NEG.  
 KW Hormone; Amidation.

FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 983 MW; 17FF476EASAD04B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 QS 7  
 DB 4 QS 5

RESULT 38  
 ID OXYT\_RAJCL STANDARD; PRT; 9 AA.  
 AC P42994;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Glutitocin.  
 OS Raja clavata (Thornback ray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squala; Hyphosqualea; Pristiogalea; Batoidae;  
 OC Rajiformes; Rajidae; Raja.  
 OC NCBI\_TaxID=7781;  
 RN [1]  
 RX SEQUENCE  
 RX MEDLINE=66123415; PubMed=5880565;  
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
 RT "Phylogeny of neurohypophyseal peptides: isolation of a new hormone,  
 RT Glutitocin (Ser 4-gln 8-oxytocin) present in a cartilaginous fish,  
 RT the ray (Raja clavata).";  
 RL Blochim. Biophys. Acta 107:393-396(1965).  
 CC -|- FUNCTION: ANTIURETIC HORMONE.  
 CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR InterPro; IPR000981; Neurohyp\_horm.  
 DR Pfam; PF00220; hormone4; 1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB45B04B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 PQ 6  
 DB 7 PQ 8

RESULT 39  
 YBFR\_AZOV STANDARD; PRT; 9 AA.  
 ID YBFR\_AZOV  
 AC P25825;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein in bfr 3'region (Fragment).  
 OS Azotobacter vinelandii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Azotobacter.  
 OC NCBI\_TaxID=354;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92196129; PubMed=1549605;  
 RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,  
 RA Stiefel E.I.;  
 RT "Unification of the ferritin family of proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; M83692; AAA22122.1; -.  
 DR PIR; B41983; B41983.  
 KW Hypothetical protein.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PP 3  
 DB 3 PP 4

RESULT 40  
 AMPN\_HELAM STANDARD; PRT; 10 AA.  
 ID AMPN\_HELAM  
 AC P81731;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Aminopeptidase N (EC 3.4.11.2) (CryIA(C) receptor) (Fragment).  
 OS Helicoverpa armigera (Cotton bollworm).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
 OC Noctuidae; Heliothinae; Helicoverpa.  
 OC NCBI\_TaxID=29058;  
 RN [1]  
 RP SEQUENCE.  
 RC Tissue=Midgut;  
 RA Ingle S.S., Trivedi N., Prasad R., Rao K.K., Chatpar H.S.;  
 RT "Aminopeptidase-N as a receptor for Bacillus thuringiensis CryIAC  
 RT toxin from Helicoverpa armigera.";  
 RL Submitted (MAR-1999) to the SWISS-PROT data bank.  
 CC -|- FUNCTION: ACTS AS A RECEPTOR FOR B.THURINGIENSIS TOXIN CRYIAC.  
 CC -|- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-  
 CC Xbb-from a peptide, amide or arylamide. Xaa is preferably Ala, but  
 CC may be most amino acids including Pro (slow action). When a  
 CC terminal hydrophobic residue is followed by a prolyl residue, the  
 CC two may be released as an intact Xaa-Pro dipeptide.  
 CC -|- COFACTOR: Binds 1 zinc ion (By similarity).  
 CC -|- SIMILARITY: Belongs to peptidase family M1.

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DR InterPro; IPR006025; Zn MTpeptidase.
KW PROSITE; PS00142; ZINC_PROTEASE; PARTIAL.
KW Hydrolase; Metalloprotease; Aminopeptidase; Zinc.
FT NON TER 10
SQ SEQUENCE 10 AA; 1093 MW; 05042EB87B11F1BB CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2
DB 9 DP 10

RESULT 41
BPP2_BOTJA STANDARD; PRT; 10 AA.
AC F30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC
CC PIR; B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 9 PP 10

RESULT 42
BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
DE inhibitor V-6-II).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;

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RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC
CC PIR; A01255; XAVI6B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C741773 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 9 PP 10

RESULT 43
BPP8_BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -|- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC
CC PIR; H37196; H37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
DB 9 PP 10

RESULT 44
BPP_VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Vipera aspis (Aspic viper).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Viperinae; Viper a.  
OX NCBI\_TaxID=8706;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom; PubMed=2169439;  
RX MEDLINE=90382616; PubMed=2169439;  
RA Komori Y., Sugihara H.;  
RT "Characterization of a new inhibitor for angiotensin converting  
enzyme from the venom of *Vipera aspis aspis*.";  
RL Int. J. Biochem. 22:767-771(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
angiotensin-converting enzyme and enhances the action of  
bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; A60377; XASNPC.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PP 3  
DB 9 PP 10  
RESULT 45  
BRK\_ONCMY  
ID BRK\_ONCMY STANDARD; PRT; 10 AA.  
AC Q9PRZ1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lysyl-bradykinin-like.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94039817; PubMed=8224232;  
RA Conlon J.M., Olson K.R.;  
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from  
trout plasma."  
RL FEBS Lett. 334:75-78(1993).  
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR  
THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Plasma.  
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
DR PIR; S39030; S39030.  
KW Bradykinin; Vasodilator.  
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PP 3  
DB 3 PP 4  
RESULT 46  
FAR6\_PANRE  
ID FAR6\_PANRE STANDARD; PRT; 10 AA.  
AC P82660;  
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE PMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE, FUNCTION, AND AMIDATION.  
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
Maule A.G.;  
RT "Isolation, characterization and pharmacology of RMRFamide-related  
peptides (FaRPs) from free-living nematode, *Panagrellus redivivus*."  
RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (PMRFAMIDE RELATED PEPTIDE)  
FAMILY.  
CC Neuropeptide; Amidation.  
KW MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D76C76D CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PQ 6  
DB 4 PQ 5  
RESULT 47  
LPK2\_LOCMY  
ID LPK2\_LOCMY STANDARD; PRT; 10 AA.  
AC P41488;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Brain;  
RC MEDLINE=94094539; PubMed=7903606;  
RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,  
de Loof A.;  
RT "Isolation, identification and synthesis of locustapyrokinin II from  
Locusta migratoria, another member of the FXPRL-amide peptide  
family."  
RL Comp. Biochem. Physiol. 106C:103-109(1993).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC  
ACTIVITY).  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 QS 7  
DB 1 QS 2  
RESULT 48

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LSK2 LEUMA
ID LSK2 LEUMA STANDARD; PRT; 10 AA.
AC P09039;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucosulfakinin-II (LSK-II).
OS Leucosphaera maderae (Madeira cockroach), and
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988, 6978;
RN [1]
RN [2]
RP SEQUENCE.
RC SPECIES=L.maderae; PubMed=3778455;
RX MEDLINE=87048769; PubMed=3778455;
RA Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
RT "Leucosulfakinin-II, a blocked sulfated insect neuropeptide with
RT homology to cholecystokinin and gastrin.";
RL Biochem. Biophys. Res. Commun. 140:357-364(1986).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana; TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
RT the American cockroach homologous to the leucosulfakinins.";
RL Neuropeptides 14:145-149(1989).
CC -!- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS OF
CC THE COCKROACH HINDGUT. STIMULATES MUSCLE CONTRACTION OF HINDGUT.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A26335; GMR02.
DR PIR; B60656; B60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 5 5 SULFATION (IN L.MADERAE, BUT NOT IN
FT P.AMERICANA).
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1285 MW; 984F5391E86B5AAA CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QS 7
DB 1 QS 2

RESULT 49
MALE_KLEPN
ID MALE_KLEPN STANDARD; PRT; 10 AA.
AC Q05564;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Maltose-binding periplasmic protein (Maltodextrin-binding protein)
DE (MWBp) (Fragment).
GN MALE.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1033-SP14 / KAY2026;
RX MEDLINE=93211295; PubMed=8459773;
RA Bachelier S., Perrin D., Hofnung M., Gilson E.;
RT "Bacterial interspersed mosaic elements (BIMES) are present in the
RT genome of Klebsiella.";

Mol. Microbiol. 7:537-544(1993).
-!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND
CHEMOTAXIS TOWARD MALTOLOGOSACCHARIDES.
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
PROTEIN FAMILY 1.
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EMBL; X68329; CAA48406.1;
InterPro; IPR006061; SBP_domi.
DR PROSITE; PS01037; SBP_BACTERIAL_1; PARTIAL.
KW Transport; Sugar transport; Periplasmic.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1159 MW; 8FD8DC4415A6DDDA CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QS 7
DB 5 QS 6

RESULT 50
NSI_MYCTU
ID NSI_MYCTU STANDARD; PRT; 10 AA.
AC P81135;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 1 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RC STRAIN=H37Rv;
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -!- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DP 2
DB 7 DP 8

RESULT 51
TKL3_LOCOMI
ID TKL3_LOCOMI STANDARD; PRT; 10 AA.
AC P30279;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin III (TK-III).
OS Locusta migratoria (Migratory locust).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=91219696; PubMed=2132575;  
 RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,  
 de Loof A.;  
 RT "Locustatachycin III and IV: two additional insect neuropeptides  
 RT with homology to peptides of the vertebrate tachykinin family.";  
 RL Regul. Pept. 31:199-212(1990).  
 CC -1- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE  
 CC OVIDUCT AND FOREGUT.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 DR PIR; A60073; ECUQ3M.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10 10  
 SQ SEQUENCE 10 AA; 1065 MW; C452CD6B59C87DC6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PQ 6  
 ||  
 Db 2 PQ 3

RESULT 52  
 TKUL\_UREUN  
 ID TKU1\_UREUN STANDARD; PRT; 10 AA.  
 AC P40751;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Urechistachycin I.  
 OS Urechis uncinatus.  
 OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.  
 OX NCBI\_TaxID=6432;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=ventral nerve cord;  
 RX MEDLINE=93236558; PubMed=8476410;  
 RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;  
 RT "Two novel tachykinin-related neuropeptides in the echiuroid worm,  
 RT Urechis uncinatus.";  
 RL Biochem. Biophys. Res. Commun. 192:1-6(1993).  
 CC -1- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL  
 CC MUSCLE OF THE ANIMAL.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10 10  
 SQ SEQUENCE 10 AA; 1177 MW; C6D1C462C9D6C5A6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QS 7  
 ||  
 Db 3 QS 4

RESULT 53  
 UPA2\_HUMAN  
 ID UPA2\_HUMAN STANDARD; PRT; 10 AA.  
 AC P30088;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier P., Pasquali C.,  
 Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing.";  
 RL Electrophoresis 13:707-714(1992).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.4, ITS MW IS: 49 kDa.  
 DR SWISS-2DPAGE; P30088; HUMAN.  
 FT NON\_TER 1 1  
 FT UNSURE 6 6  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PP 3  
 ||  
 Db 5 PP 6

RESULT 54  
 URE3\_MORMO  
 ID URE3\_MORMO STANDARD; PRT; 10 AA.  
 AC P17339;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea  
 DE amidohydrolase) (Fragment).  
 GN UREA.  
 OS Morganella morganii (Proteus morganii).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Morganella.  
 OX NCBI\_TaxID=582;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90264298; PubMed=2345135;  
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
 RT "Morganella morganii urease: purification, characterization, and  
 RT isolation of gene sequences.";  
 RL J. Bacteriol. 172:3073-3080(1990).  
 CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
 CC -1- SUBUNIT: (ALPHA, BETA, GAMMA) (3) [BY SIMILARITY].  
 CC -1- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.  
 DR PIR; C35389; C35389.  
 KW Hydrolase.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB07771A7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PP 3  
 ||  
 Db 5 PP 6

RESULT 55  
 BPP3\_BOTIN  
 ID BPP3\_BOTIN STANDARD; PRT; 11 AA.  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)

AC P30423;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Inland Jararaca) (Queimada Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; C37196; C37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 DB 4 PP 5

RESULT 56  
 BPP4 BOTIN STANDARD; PRT; 11 AA.  
 AC P30424;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Inland Jararaca) (Queimada Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; D37196; D37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1143 MW; 20B8BF13C7741777 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3

DB 4 PP 5

RESULT 57  
 BPPB AGKHA STANDARD; PRT; 11 AA.  
 ID BPPB AGKHA  
 AC P01021;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide B (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Agkistrodon.  
 OX NCBI\_TaxID=61300;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Kato H., Suzuki T.;  
 RT "Amino acid sequence of bradykinin-potentiating peptide isolated from  
 RT the venom of Agkistrodon halys blomhoffii.";  
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A01254; XASNBA.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PP 3  
 DB 4 PP 5

RESULT 58  
 BPP AGKHP STANDARD; PRT; 11 AA.  
 ID BPP AGKHP  
 AC F04562;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys  
 OS pallas).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Gloydius.  
 OX NCBI\_TaxID=8714;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=86177022; PubMed=3008123;  
 RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;  
 RT "Structure-function studies on the bradykinin potentiating peptide  
 RT from Chinese snake venom (Agkistrodon halys pallas).";  
 RL Peptides 6 Suppl. 3:339-342(1985).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; JC0002; XAVIBH.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

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SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PP 3
DB 4 PP 5

RESULT 59
BRK_MEGFL
ID BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
DE peptide ([Thr6]bradykinin)].
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Scolioidea;
OC Scoliididae; Megascolia.
OX NCBI_TaxID=7437;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87233024; PubMed=3617088;
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT "Two kinins isolated from an extract of the venom reservoirs of the
RT solitary wasp Megascolia flavifrons.";
RL Toxicon 25:527-535(1987).
RN [2]
RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yashuata T., Mantel P.;
RT "Two kinins isolated from the venom of Megascolia flavifrons.";
RL Toxicon 26:34-34(1988).
CC -1- FUNCTION: Both proteins have bradykinin-like, although lower
CC activities (e.g. smooth muscle contraction).
CC -1- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; B26744; B26744.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PP 3
DB 2 PP 3

RESULT 60
CEP1_ACHFV
ID CEP1_ACHFV STANDARD; PRT; 11 AA.
AC P22730;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC STRAIN=Perussac; TISSUE=Heart atrium;

SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 QS 7
DB 3 QS 4

RESULT 61
LADD_ONCMV
ID LADD_ONCMV STANDARD; PRT; 11 AA.
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ladderlectin (Fragment).
OS Oncochrychus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293418; PubMed=9149391;
RA Jensen L.E., Thiel S., Petersen T.E., Jensenius J.C.;
RT "A rainbow trout lectin with multimeric structure.";
Comp. Biochem. Physiol. 116B:385-390(1997).
RL Comp. Biochem. Physiol. 116B:385-390(1997).
CC -1- FUNCTION: LECTIN THAT BINDS SEPHAROSE.
CC -1- COPACTOR: CALCIUM IS ESSENTIAL FOR SEPHAROSE BINDING.
CC -1- SUBUNIT: MULTIMERIC.
KW Lectin; Calcium.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PP 3
DB 9 PP 10

RESULT 62
MORN_HUMAN
ID MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuroepitope (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Human, Rat, and Bovine;  
RX MEDLINE=82035850; PubMed=7290191;  
RA Bodenmuller H., Schaller H.C.;  
RT "Conserved amino acid sequence of a neuropeptide, the head activator,  
from coelenterates to humans.";  
RL Nature 293:579-580(1981).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=A.elegantissima, and H.attenuata;  
RA Schaller H.C., Bodenmuller H.;  
RT "Isolation and amino acid sequence of a morphogenetic peptide from  
hydra.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).  
RN [3]  
RP SYNTHESIS.  
RX MEDLINE=82050803; PubMed=7297679;  
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;  
RT "Synthesis of a new neuropeptide, the head activator from hydra.";  
RL FEBS Lett. 131:317-321(1981).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=90059923; PubMed=2583101;  
RA Schaller H.C., Druffel-Augustin S., Dubel S.;  
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells  
in the G2/mitosis transition.";  
RL EMBO J. 8:3311-3318(1989).  
RN [5]  
RP FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS  
IN THE G2/MITOSIS TRANSITION.  
CC -I- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA  
AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED  
HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS  
BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.  
DR PIR; A01427; YHRT.  
DR PIR; A93900; YHXA.  
DR PIR; B01427; YHHU.  
DR PIR; B93900; YHJFY.  
DR PIR; C01427; YHFO.  
DR GK; P01163; -.  
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1  
SQ SEQUENCE 11 AA; 1142 MW; 37927417C32258878 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred.No. 4.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 PP 3  
DB 2 PP 3  
  
RESULT 63  
RANC\_RANPI STANDARD; PRT; 11 AA.  
AC P08951;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ranatensin-C.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=84131098; PubMed=6141890;  
RA Nakajima T.;

Unpublished results, cited by:  
RL Erspamer V., Erspamer G.P., Mazzanti G., Endean R.;  
RL Comp. Biochem. Physiol. 77C:99-108(1984).  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- TISSUE SPECIFICITY: Skin.  
CC -I- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
FAMILY.  
DR InterPro; IPR000874; Bombesin.  
DR Pfam; PF02044; Bombesin; 1.  
DR PROSITE; PS00257; BOMBESIN; 1.  
KW Amphibian defense peptide; Bombesin family; Amidation.  
FT MOD RES 11 11  
SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred.No. 4.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 PQ 6  
DB 3 PQ 4  
  
RESULT 64  
TKN1\_UPEIN STANDARD; PRT; 11 AA.  
AC P82076;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Uperin 1.1.  
OS Uperoleia inundata (Floodplain toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
OC Myobatrachinae; Uperoleia.  
OX NCBI\_TaxID=104953;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,  
RA Adams G.W., Severini C.;  
RT "Novel uperin peptides from the dorsal glands of the Australian  
floodplain toadlet Uperoleia inundata.";  
RL Aust. J. Chem. 49:475-484(1996).  
CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
MUSCLES.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -I- MASS SPECTROMETRY: MW=1208; METHOD=FAE.  
CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR InterPro; IPR002040; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD RES 1 1  
FT MOD RES 11 11  
SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred.No. 4.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DP 2  
DB 3 DP 4  
  
RESULT 65  
TKN1\_UPERU STANDARD; PRT; 11 AA.  
ID TKN1\_UPERU

AC P08612;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Uperolein.  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=75131227; PubMed=1120493;  
 RA Anastasi A., Erspamer V., Edean R.;  
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring  
 RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";  
 RL Experientia 31:394-395(1975).  
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR InterPro; IPR003580; Protachykinin.  
 DR InterPro; IPR002040; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 11 11  
 FT MOD\_RES 11 11  
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DP 2  
 DB 3 DP 4

RESULT 66  
 TKN2 UPERU STANDARD; PRT; 11 AA.  
 AC P08616;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Rugosauperolein II ((Lys5,Thr6)physalaemin).  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=80223080; PubMed=7389029;  
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;  
 RT "Physalaemin- and bombesin-like peptides in the skin of the  
 RT Australian leptodactylid frog Uperoleia rugosa.";  
 RL Chem. Pharm. Bull. 28:689-695(1980).  
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR InterPro; IPR002040; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 11 11  
 FT MOD\_RES 11 11  
 SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DP 2  
 DB 3 DP 4

RESULT 67  
 TKNA CHICK STANDARD; PRT; 11 AA.  
 ID TKNA\_CHICK  
 AC P19850;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=88204263; PubMed=2452461;  
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;  
 RT "[Arg3]substance P and neurokinin A from chicken small intestine.";  
 RL Regul. Pept. 20:171-180(1988).  
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; JN0023; JN0023.  
 DR InterPro; IPR002040; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11  
 FT MOD\_RES 11 11  
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PQ 6  
 DB 4 PQ 5

RESULT 68  
 TKNA GADMO STANDARD; PRT; 11 AA.  
 ID TKNA\_GADMO  
 AC P28498;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Gadus morhua (Atlantic cod).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.

OX NCBI\_TaxID=8049;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=92298992; PubMed=1376687;  
RA Jensen J., Conlon J.M.;  
RT "Substance-P-related and neurokinin-A-related peptides from the brain  
of the cod and trout.";  
RL Eur. J. Biochem. 206:659-664(1992).  
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
MUSCLES.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR; S23306; S23306.  
DR InterPro: IPR003580; Protachykinin.  
DR InterPro: IPR002040; Tachykinin.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).  
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 PQ 6  
DB 4 PQ 5

RESULT 69  
ID TKNA\_HORSE STANDARD; PRT; 11 AA.  
AC P01290;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
GN TAC1 OR NKNA OR TAC2 OR NKA.  
OS Equus caballus (Horse), and  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796, 10141;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Horse;  
RA Studer R.O., Trzeciak A., Lergier W.;  
RT "Isolation and amino-acid sequence of substance P from horse  
intestine.";  
RL Helv. Chim. Acta 56:860-866(1973).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=C.porcellus;  
RX MEDLINE=90044685; PubMed=2478925;  
RA Murphy R.;  
RT "Primary amino acid sequence of guinea-pig substance P.";  
RL Neuropeptides 14:105-110(1989).  
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
MUSCLES.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR; A01558; SPHO.  
DR PIR; A60654; A60654.  
DR InterPro: IPR003580; Protachykinin.  
DR InterPro: IPR002040; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11 11 AMIDATION  
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 PQ 6  
DB 4 PQ 5

RESULT 70  
ID TKN\_PHYFU STANDARD; PRT; 11 AA.  
AC P08615;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Physalaemin.  
OS Physalaemus fuscumaculatus (Neotropical frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Leptodactylidae;  
OC Leptodactylinae; Physalaemus.  
OX NCBI\_TaxID=8378;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=66076612; PubMed=5857249;  
RA Bresnauer V., Anastasi A., Bertaccini G., Cei J.M.;  
RT "Structure and pharmacological actions of physalaemin, the main  
active polypeptide of the skin of Physalaemus fuscumaculatus.";  
RL Experientia 20:489-490(1964).  
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
MUSCLES.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR; S07201; S07201.  
DR InterPro: IPR002040; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION  
SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DP 2  
DB 3 DP 4

RESULT 71  
ID CXAL\_CONIM STANDARD; PRT; 12 AA.  
AC P50983;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Alpha-conotoxin ImI.  
OS Conus imperialis (Imperial cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

QC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=35631;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RX TISSUE=Venom;  
RC MEDLINE=94266889; PubMed=8206995;  
RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,  
RA Gray W.R., Olivera B.M.;  
RT "A nicotinic acetylcholine receptor ligand of unique specificity,  
RT alpha-conotoxin Imi";  
RL J. Biol. Chem. 269:16733-16739(1994).  
RN [2]  
RN CHARACTERIZATION.  
RP MEDLINE=9537976; PubMed=7651351;  
RX Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,  
RA McIntosh J.M.;  
RT "Alpha-conotoxin Imi exhibits subtype-specific nicotinic  
RT acetylcholine receptor blockade: preferential inhibition of homomeric  
RT alpha 7 and alpha 9 receptors";  
RL Mol. Pharmacol. 48:194-199(1995).  
RN [3]  
RN STRUCTURE BY NMR.  
RP MEDLINE=99212205; PubMed=10194298;  
RX Rogers J.P., Luginbuhl P., Shen G.S., McCabe R.T., Stevens R.C.,  
RA Wemmer D.E.;  
RT "NMR solution structure of alpha-conotoxin Imi and comparison to  
RT other conotoxins specific for neuronal nicotinic acetylcholine  
RT receptors";  
RL Biochemistry 38:3874-3882(1999).  
RN [4]  
RN STRUCTURE BY NMR.  
RP MEDLINE=99280313; PubMed=10350614;  
RX Gouda H., Hirono S.;  
RT "Solution structure of alpha-conotoxin Imi determined by  
RT two-dimensional NMR spectroscopy";  
RL Biochim. Biophys. Acta 1431:384-394(1999).  
RN [5]  
RN STRUCTURE BY NMR.  
RP MEDLINE=99158061; PubMed=10050774;  
RX Maslennikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,  
RA Methfessel C., Tsetlin V.I., Arseniev A.S.;  
RT "NMR spatial structure of alpha-conotoxin Imi reveals a common  
RT scaffold in snail and snake toxins recognizing neuronal nicotinic  
RT acetylcholine receptors";  
RL FEBS Lett. 444:275-280(1999).  
RN [6]  
RN STRUCTURE BY NMR.  
RP MEDLINE=99358772; PubMed=10431825;  
RX Lamthanh H., Jegou-Matheron C., Servent D., Menez A., Lancelin J.-M.;  
RA "Minimal conformation of the alpha-conotoxin Imi for the alpha7  
RT neuronal nicotinic acetylcholine receptor recognition: correlated CD,  
RT NMR and binding studies";  
RL FEBS Lett. 454:293-298(1999).  
RN [7]  
RN STRUCTURE BY NMR.  
RP MEDLINE=99324017; PubMed=10395477;  
RX Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;  
RT "Solution structure of alpha-conotoxin Imi by 1H nuclear magnetic  
RT resonance";  
RL J. Med. Chem. 42:2364-2372(1999).  
RN [8]  
RN MUTAGENESIS OF ASP-5; ARG-7 AND ARG-11; AND STRUCTURE BY NMR OF THESE  
RP THREE MUTANTS.  
RX MEDLINE=20574023; PubMed=11124036;  
RA Rogers J.P., Luginbuhl P., Pemberton K., Harty P., Wemmer D.E.,  
RA Stevens R.C.;  
RT "Structure-activity relationships in a peptidic alpha7 nicotinic  
RT acetylcholine receptor antagonist";  
RL J. Mol. Biol. 304:911-926(2000).  
CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
CC inhibit them. It is highly active against the neuromuscular  
CC receptor in frog but not in mice. In contrast, it induces seizures  
CC in rats.  
CC when injected centrally in mice and rats. It targets neuronal  
CC nAChRs in mammals. It blocks homomeric alpha-7 nicotinic receptors  
CC with the highest apparent affinity and homomeric alpha-9 receptors  
CC with 8-fold lower affinity. It has no effect on receptors composed  
CC of alpha-2/beta-2, alpha-3/beta-2, alpha-4/beta-2, alpha-2/beta-4,  
CC alpha-3/beta-4, or alpha-4/beta-4 subunit combinations.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
CC FAMILY.  
CC PIR; A53709; A53709.  
DR PDB; 1IM1; 15-JUN-99.  
DR PDB; 1IM1; 23-APR-99.  
DR PDB; 1CNL; 27-MAY-99.  
DR PDB; 1E74; 27-DEC-00.  
DR PDB; 1E75; 27-DEC-00.  
DR PDB; 1E76; 27-DEC-00.  
DR PDB; 1G2G; 08-NOV-00.  
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
FT DISULFID 2 8  
FT MOD RES 12 12  
FT MUTAGEN 5 5  
FT MUTAGEN 7 7  
FT MUTAGEN 11 11  
FT HELIX 2 4  
FT HELIX 6 8  
FT TURN 10 12  
SQ SEQUENCE 12 AA; 1357 MW; 9C29CBA545A176A CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;  
QY 1 DP 2  
DB 5 DP 6  
RESULT 72  
FARY PENMO STANDARD; PRT; 12 AA.  
AC P83322;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRamide-like neurotoxin FLP7 (GYRKPFGNSIF-amide).  
OS Penaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RN SEQUENCE, AND MASS SPECTROMETRY.  
RP TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sthangorungul P., Pupum J., Krungkarn C., Longyant S.,  
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;  
RT "Seven novel FMRamide-like neurotoxin peptide sequences from the eyestalk  
RT of the giant tiger prawn Penaeus monodon";  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -1- SUBCELLULAR LOCATION: Secreted  
CC -1- MASS SPECTROMETRY: MW=1381.4; METHOD=WALDI.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 12 12  
SQ SEQUENCE 12 AA; 1383 MW; 31209192EF49D777 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 PP 3
DB      5 PP 6

RESULT 73
HCY1_CARMA
ID      HCY1_CARMA      STANDARD;      PRT;      12 AA.
AC      P83176;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Hemocyanin subunit 1 (Fragment).
OS      Carcinus maenas (Common shore crab) (Green crab).
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC      Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX      NCBI_TaxID=6759;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Hemolymph; PubMed=2620501;
RX      MEDLINE=90151075; Sierdsma S.J., Beintema J.J.;
RA      Neuteboom B., Sierdsma S.J., Beintema J.J.;
RT      "The relationship between N-terminal sequences and immunological
RL      characterization of crustacean hemocyanins.";
RL      Comp. Biochem. Physiol. 94B:587-592(1989).
CC      -!- FUNCTION: Hemocyanins are copper-containing oxygen carriers
CC      occurring freely dissolved in the hemolymph of many mollusks and
CC      arthropods.
CC      -!- SUBCELLULAR LOCATION: Extracellular.
CC      -!- TISSUE SPECIFICITY: Hemolymph.
CC      -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
CC      SUBFAMILY.
DR      PIR; C60529; C60529.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0016970; F:hemocyanin; IDA.
DR      GO; GO:0015671; P:oxygen transport; TAS.
DR      GO; GO:0015671; P:oxygen transport; TAS.
KW      Transport; Oxygen transport; Copper; Hemolymph.
FT      NON_TER
FT      12
SQ      SEQUENCE 12 AA; 1237 MW; 8935EF6E2B5A2D5 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DP 2
DB      2 DP 3

RESULT 74
TA10_TREME
ID      TA10_TREME      STANDARD;      PRT;      12 AA.
AC      P01371;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      01-NOV-1991 (Rel. 20, Last annotation update)
DE      Tremorgen A-10.
OS      Tremella mesenterica (Jelly fungus).
OC      Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC      Tremellomycetidae; Tremellales; Tremellaceae; Tremella.
OX      NCBI_TaxID=5217;
RN      [1]
RP      SEQUENCE.
RA      Sakagami Y., Yoshida M., Isogai A., Suzuki A.;
RT      "Peptide sex hormones inducing conjugation tube formation in
RT      compatible mating-type cells of Tremella mesenterica.";
RL      Science 212:1525-1527(1981).
CC      -!- FUNCTION: TREMERGEN A-10 IS PRODUCED BY THE A MATING-TYPE CELLS
CC      AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.
CC      PIR; A01642; JTJGO.
KW      Lipoprotein; Prenylation; Pheromone.

FT      LIPID
SQ      SEQUENCE 12 AA; 1246 MW; 84EF574959676DCS CRC64;

Query Match      28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DP 2
DB      3 DP 4

RESULT 75
BOML_PSEGU
ID      BOML_PSEGU      STANDARD;      PRT;      13 AA.
AC      P42991;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Bombesin-like peptide L (PG-L).
OS      Pseudophryne guentheri (Guenther's toadlet).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC      Myobatrachinae; Pseudophryne.
OX      NCBI_TaxID=30349;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Skin secretion;
RX      MEDLINE=90287814; PubMed=2356157;
RA      Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA      Roberts J.D., Melchiorri P., Erspamer V.;
RT      "Six novel tachykinin- and bombesin-related peptides from the skin of
RT      the Australian frog Pseudophryne guentheri.";
RL      Peptides 11:299-304(1990).
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- TISSUE SPECIFICITY: Skin.
CC      -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC      FAMILY.
DR      PIR; A60409; A60409.
DR      InterPro; IPR000874; Bombesin.
DR      Pfam; PF02044; Bombesin; 1.
DR      PROSITE; PS00257; BOMBESIN; 1.
KW      Amphibian defense peptide; Bombesin family; Amidation;
KW      Pyrrolidone carboxylic acid.
FT      MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT      MOD_RES 13 13 AMIDATION.
SQ      SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PQ 6
DB      5 PQ 6

Search completed: November 25, 2003, 18:17:33
Job time : 3.3883 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 16.867 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-14

Perfect score: 7

Sequence: 1 DPPPQS 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL.23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	57.1	9	4 Q9UCS8	Q9UCS8 homo sapien
2	4	57.1	12	4 Q9B249	Q9B249 homo sapien
3	4	57.1	15	6 Q9TR14	Q9TR14 bos taurus
4	4	57.1	15	10 P82439	P82439 nicotiana t
5	4	57.1	17	6 Q9TR22	Q9TR22 bos taurus
6	4	57.1	17	10 O49225	O49225 glycine max
7	4	57.1	17	10 Q41400	Q41400 sebania ro
8	4	57.1	18	4 Q9UCT9	Q9UCT9 homo sapien
9	4	57.1	20	6 Q9TR87	Q9TR87 bos taurus
10	4	57.1	20	10 Q9S8R2	Q9S8R2 solanum tub
11	3	42.9	8	4 Q9HCQ0	Q9HCQ0 homo sapien
12	3	42.9	9	10 P82429	P82429 nicotiana t
13	3	42.9	10	12 Q9Q0W9	Q9Q0W9 polyomaviru
14	3	42.9	10	12 Q8JV70	Q8JV70 polyomaviru
15	3	42.9	10	12 Q9Q0W1	Q9Q0W1 polyomaviru
16	3	42.9	10	12 Q8JV68	Q8JV68 polyomaviru

Q9Q0V9	10	12	Q9Q0V9	42.9	3	17
Q9Q0W7	10	12	Q9Q0W7	42.9	3	18
Q8JV66	10	12	Q8JV66	42.9	3	19
Q9Q0V7	10	12	Q9Q0V7	42.9	3	20
Q8JV82	10	12	Q8JV82	42.9	3	21
Q8JV76	10	12	Q8JV76	42.9	3	22
Q8JV74	10	12	Q8JV74	42.9	3	23
Q9Q0W5	10	12	Q9Q0W5	42.9	3	24
Q9Q0X3	10	12	Q9Q0X3	42.9	3	25
Q9Q0X5	10	12	Q9Q0X5	42.9	3	26
Q9Q0W3	10	12	Q9Q0W3	42.9	3	27
Q8JV80	10	12	Q8JV80	42.9	3	28
Q9Q0X1	10	12	Q9Q0X1	42.9	3	29
Q9Q0X9	10	12	Q9Q0X9	42.9	3	30
Q8JV72	10	12	Q8JV72	42.9	3	31
P82436	11	10	P82436	42.9	3	32
Q93X21	12	10	Q93X21	42.9	3	33
Q9UDC6	13	4	Q9UDC6	42.9	3	34
Q9U5J2	13	5	Q9U5J2	42.9	3	35
P78359	14	4	P78359	42.9	3	36
Q9TR03	15	6	Q9TR03	42.9	3	37
Q9S8N8	15	10	Q9S8N8	42.9	3	38
Q9TWN7	16	5	Q9TWN7	42.9	3	39
Q9TG27	16	6	Q9TG27	42.9	3	40
Q88250	16	12	Q88250	42.9	3	41
Q88249	16	12	Q88249	42.9	3	42
Q9154	16	12	Q9154	42.9	3	43
Q9PRU6	16	13	Q9PRU6	42.9	3	44
Q9UDD6	17	4	Q9UDD6	42.9	3	45
Q9TWC6	17	5	Q9TWC6	42.9	3	46
Q9UCG7	18	4	Q9UCG7	42.9	3	47
Q8NFB4	18	4	Q8NFB4	42.9	3	48
Q97773	18	6	Q97773	42.9	3	49
Q8QFT3	18	13	Q8QFT3	42.9	3	50
Q9UCL3	19	4	Q9UCL3	42.9	3	51
P82941	19	10	P82941	42.9	3	52
Q90RF8	19	15	Q90RF8	42.9	3	53
Q905K8	19	15	Q905K8	42.9	3	54
Q905I4	19	15	Q905I4	42.9	3	55
Q905G8	19	15	Q905G8	42.9	3	56
Q90RG5	19	15	Q90RG5	42.9	3	57
Q9R4D7	20	2	Q9R4D7	42.9	3	58
Q9S7J0	20	3	Q9S7J0	42.9	3	59
Q9S965	20	10	Q9S965	42.9	3	60
Q9S8M1	20	10	Q9S8M1	42.9	3	61
Q9QVH2	20	11	Q9QVH2	42.9	3	62
Q912B4	20	12	Q912B4	42.9	3	63
Q912B2	20	12	Q912B2	42.9	3	64
P92214	7	8	P92214	28.6	2	65
amblyopyrum	7	8	amblyopyrum	28.6	2	66
hordeum vul	7	8	hordeum vul	28.6	2	67
lophopyrum	7	8	lophopyrum	28.6	2	68
peridictyon	7	8	peridictyon	28.6	2	69
agilops ta	7	8	agilops ta	28.6	2	70
bromus iner	7	8	bromus iner	28.6	2	71
pseudoroegn	7	8	pseudoroegn	28.6	2	72
hordeum bra	7	8	hordeum bra	28.6	2	73
henrardia p	7	8	henrardia p	28.6	2	74
agropyron c	7	8	agropyron c	28.6	2	75
thinopyrum	7	8	thinopyrum	28.6	2	76
austalophr	7	8	austalophr	28.6	2	77
heteranthe	7	8	heteranthe	28.6	2	78
haynaldia v	7	8	haynaldia v	28.6	2	79
taenitheru	7	8	taenitheru	28.6	2	80
crithopsis	7	8	crithopsis	28.6	2	81
hordeum mar	7	8	hordeum mar	28.6	2	82
psathyrosta	7	8	psathyrosta	28.6	2	83
human immun	7	15	human immun	28.6	2	84
Q8JE81	8	2	Q8JE81	28.6	2	85
Q45615	8	2	Q45615	28.6	2	86
Q9R7t2	8	2	Q9R7t2	28.6	2	87
escherichia	8	5	escherichia	28.6	2	88
periplaneta	8	5	periplaneta	28.6	2	89
Q9T2y3	8	8	Q9T2y3	28.6	2	90

90 Q94V82 varanus yuw 8 8 Q94V82  
 91 Q94V82 varanus yuw 8 8 Q94V82  
 92 Q94V82 varanus yuw 8 8 Q94V82  
 93 Q94V82 varanus yuw 8 8 Q94V82  
 94 Q94V82 varanus yuw 8 8 Q94V82  
 95 Q94V82 varanus yuw 8 8 Q94V82  
 96 Q94V82 varanus yuw 8 8 Q94V82  
 97 Q94V82 varanus yuw 8 8 Q94V82  
 98 Q94V82 varanus yuw 8 8 Q94V82  
 99 Q94V82 varanus yuw 8 8 Q94V82  
 100 Q94V82 varanus yuw 8 8 Q94V82

## ALIGNMENTS

## RESULT 1

Q9UCS8 ID Q9UCS8 PRELIMINARY; PRT; 9 AA.  
 AC Q9UCS8; 9 AA.  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 21, Last annotation update)  
 DE Apolipoprotein A-I (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92075698; PubMed=1742316;  
 RA Einholm C., Bozas S.E., Tenkanen H., Kirsbaum L., Metso J.,  
 RA Murphy B., Walker I.D.;  
 RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40  
 RT protein of human blood are different proteins which both bind to  
 RT apolipoprotein A-I";  
 RL Biochim. Biophys. Acta 1086:255-260(1991).  
 FT NON\_TER 1 1  
 FT NON\_TER 1 1  
 SQ SEQUENCE 9 AA; 981 MW; 7FE3775A6C776B CRC64;

Query Match 57.1%; Score 4; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPOS 7  
 DB 3 PPOS 6

## RESULT 2

Q9BZ49 ID Q9BZ49 PRELIMINARY; PRT; 12 AA.  
 AC Q9BZ49; 12 AA.  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE Glycophorin C (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,  
 RA Zimmerman P.A.;  
 RT "The association of the glycophorin C exon 3 deletion with  
 RT ovalocytosis and malaria susceptibility in the Wosera, Papua New  
 RT Guinea";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF342984; AAK01459.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 12 12

SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;  
 Query Match 57.1%; Score 4; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPOS 6  
 DB 9 PPOS 12

## RESULT 3

Q9TR14 ID Q9TR14 PRELIMINARY; PRT; 15 AA.  
 AC Q9TR14; 15 AA.  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide  
 DE (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96187584; PubMed=8611748;  
 RA Nakai Y., Nishimura T., Shimizu M., Arai S.;  
 RT "Effects of freezing on the proteolysis of beef during storage at 4  
 RT degrees C";  
 RL BioSci. Biotechnol. Biochem. 59:2255-2258(1995).  
 SQ SEQUENCE 15 AA; 1597 MW; C98A5B44A79E4777 CRC64;

Query Match 57.1%; Score 4; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPOS 5  
 DB 2 PPOS 5

## RESULT 4

P82439 ID P82439 PRELIMINARY; PRT; 15 AA.  
 AC P82439; 15 AA.  
 DT 01-JUN-2000 (TREMBlrel. 14, Created)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE 200 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture";  
 RL Planta 200:0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall; Hydroxylation.  
 FT MOD\_RES 6 6 HYDROXYLATION.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1870 MW; 3E1E05A20A3C5681 CRC64;

Query Match 57.1%; Score 4; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;



Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
|||||  
Db 6 PPPP 9

## RESULT 5

ID Q9TR22 PRELIMINARY; PRT; 17 AA.  
AC Q9TR22; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE NONAMELOGENIN glycoprotein (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96126798; PubMed=8564801;  
RA Funzi J.S.; DenBesten P.K.;  
RT "Purification of nonamelogenin proteins from bovine secretory  
RT enamel".  
RL Calif. Tissue Int. 57:379-384(1995).  
SQ SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;

Query Match 57.1%; Score 4; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
|||||  
Db 8 PPPP 11

## RESULT 6

ID Q49225 PRELIMINARY; PRT; 17 AA.  
AC Q49225;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hydroxyproline-rich glycoprotein (Fragment).  
GN HKGP.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosidia I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Essex; TISSUE=Root;  
RX MEDLINE=94211912; PubMed=8159793;  
RA Hong J.C.; Cheong Y.H.; Nagao R.T.; Bahk J.D.; Cho M.J.; Key J.L.;  
RT "Isolation and characterization of three soybean extensin cDNAs".  
RL Plant Physiol. 104:793-796(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Essex; TISSUE=Root;  
RA Mahalingam R.; Knapp H.T.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF047052; AAC03558.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;

Query Match 57.1%; Score 4; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5

Db 11 PPPP 14  
|||||

## RESULT 7

Q41400 PRELIMINARY; PRT; 17 AA.  
ID Q41400;  
AC Q41400;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Hydroxyproline-rich protein (Fragment).  
OS Sesbania rostrata.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosidia I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.  
OX NCBI\_TaxID=3895;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sesbania rostrata;  
RC TISSUE=Bacterial infected stem located root primordia;  
RX MEDLINE=96112737; PubMed=8664492;  
RA Goormachtig S.; Valerio-Lepiniec M.; Szczygłowski K.; Van Montagu M.;  
RA Holsters M.; De Bruijn F.;  
RT "Use of differential display to identify novel Sesbania rostrata genes  
RT enhanced by Azorhizobium caulinodans infection".  
RL Mol. Plant Microbe Interact. 8:816-824(1995).  
DR EMBL; Z48673; CAA88592.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match 57.1%; Score 4; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
|||||  
Db 10 PPPP 13

## RESULT 8

ID Q9UCT9 PRELIMINARY; PRT; 18 AA.  
AC Q9UCT9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE PRG=PROLINE-rich glycoprotein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91373355; PubMed=1894623;  
RA Gillette-Castro B.L.; Prakhophol A.; Burlingame A.L.; Leffler H.;  
RA Fisher S.J.;  
RT "Structure and bacterial receptor activity of a human salivary  
RT proline-rich glycoprotein".  
RL J. Biol. Chem. 266:17358-17368(1991).  
FT NON\_TER 1 1  
SQ SEQUENCE 18 AA; 1780 MW; 961F6FB0A83D2E40 CRC64;

Query Match 57.1%; Score 4; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPP 6  
|||||  
Db 14 PPPP 17

## RESULT 9

Q9TR87 PRELIMINARY; PRT; 20 AA.  
AC Q9TR87;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE PA28 protein (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP MEDLINE=95081084; PubMed=7989312;  
RA Mott J.D., Pramanik B.C., Moomaw C.R., Afendis S.J., DeMartino G.N.,  
RA Slaughter C.A.;  
RT "PA28, an activator of the 20 S proteasome, is composed of two  
RT nonidentical but homologous subunits";  
RL J. Biol. Chem. 269:31466-31471(1994).  
SQ SEQUENCE 20 AA; 2205 MW; 15DA3F0E8D20C2E9 CRC64;

Query Match 57.1%; Score 4; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 4  
Db ||||  
9 DPPP 12

## RESULT 10

Q9S8R2 PRELIMINARY; PRT; 20 AA.  
AC Q9S8R2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Starch branching enzyme (Fragment).  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94009663; PubMed=8405428;  
RA Khoshnoodi J., Ek B., Raak L., Larsson H.;  
RT "Characterization of the 97 and 103 kDa forms of starch branching  
RT enzyme from potato tubers";  
RL FEBS Lett. 332:132-138(1993).  
SQ SEQUENCE 20 AA; 2339 MW; 0C69903743FC686D CRC64;

Query Match 57.1%; Score 4; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 4  
Db ||||  
11 DPPP 14

## RESULT 11

Q9HCQ0 PRELIMINARY; PRT; 8 AA.  
AC Q9HCQ0;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Phosphodiesterase 10A7 (PDE10A7) (Fragment).  
GN HSPDE10A.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20453115; PubMed=10998054;  
RA Fujishige K., Kotera J., Yuasa K., Omori K.;  
RT "The human phosphodiesterase PDE10A gene. Genomic organization and  
RT evolutionary relatedness with other PDEs containing GAF domains";  
RL Eur. J. Biochem. 267:5943-5951(2000).  
DR EMBL; AB041779; BAB16368.1; -;  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 966 MW; FD4B19D5A6C76446 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
Db ||||  
3 PQS 5

## RESULT 12

P82429 PRELIMINARY; PRT; 9 AA.  
AC P82429;  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE 44 kDa cell wall protein (Fragment).  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE.  
RX STRAIN=cv. PETIT HAVANA;  
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
RA Wojtaszek P., Bolwell G.P.;  
RT "Proteomic study of secondary cell wall proteins from transformed  
RT tobacco culture";  
RL Planta 0:0-0(2000).  
CC -1- SUBCELLULAR LOCATION: CELL WALL.  
CC -1- TISSUE SPECIFICITY: XYLEM.  
KW Cell wall.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 986 MW; C22CCAADC6C77776 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
Db ||||  
3 PPQ 5

## RESULT 13

Q9Q0W9 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0W9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UMEA3;

```
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119350; AAF24106.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9

RESULT 14
Q8JV70 PRELIMINARY; PRT; 10 AA.
AC Q8JV70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 5;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304387; AAM97804.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9

RESULT 15
Q9Q0W1 PRELIMINARY; PRT; 10 AA.
AC Q9Q0W1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFB;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119354; AAF24114.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;
```

```
Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9

RESULT 16
Q8JV68 PRELIMINARY; PRT; 10 AA.
AC Q8JV68;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 6;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304388; AAM97806.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9

RESULT 17
Q9Q0V9 PRELIMINARY; PRT; 10 AA.
AC Q9Q0V9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFE;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119355; AAF24116.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9
```

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RESULT 18
Q9Q0W7 PRELIMINARY; PRT; 10 AA.
ID AC Q9Q0W7
AC Q9Q0W7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NANCY2;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119351; AAF24108.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB |||
7 PPP 9

RESULT 19
Q8JV66 PRELIMINARY; PRT; 10 AA.
ID AC Q8JV66
AC Q8JV66
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSF K;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304389; AAM97808.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB |||
7 PPP 9

RESULT 20
Q9Q0V7 PRELIMINARY; PRT; 10 AA.
ID AC Q9Q0V7
AC Q9Q0V7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFJ;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119356; AAF24118.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB |||
7 PPP 9

RESULT 21
Q8JV82 PRELIMINARY; PRT; 10 AA.
ID AC Q8JV82
AC Q8JV82
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EI;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303944; AAM97792.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB |||
7 PPP 9

RESULT 22
Q8JV76 PRELIMINARY; PRT; 10 AA.
ID AC Q8JV76
AC Q8JV76
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA2;
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RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303947; AAM97798.1; -.
FT NON TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9

RESULT 23
Q8JV74 PRELIMINARY; PRT; 10 AA.
AC Q8JV74;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA3;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303948; AAM97800.1; -.
FT NON TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9

RESULT 24
Q9Q0W5 PRELIMINARY; PRT; 10 AA.
AC Q9Q0W5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIA3;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119352; AAF24110.1; -.
FT NON TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9

RESULT 25
Q9Q0X3 PRELIMINARY; PRT; 10 AA.
AC Q9Q0X3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECN8;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119348; AAF24102.1; -.
FT NON TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9

RESULT 26
Q9Q0X5 PRELIMINARY; PRT; 10 AA.
AC Q9Q0X5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119347; AAF24100.1; -.
FT NON TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 7 PPP 9
```

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RESULT 27
Q900W3 ID Q900W3 PRELIMINARY; PRT; 10 AA.
AC Q900W3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIAL;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119353; AAF24112.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
Db |||
7 PPP 9

RESULT 28
Q8JV80 ID Q8JV80 PRELIMINARY; PRT; 10 AA.
AC Q8JV80;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303945; AAM97794.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
Db |||
7 PPP 9

RESULT 29
Q900X1 ID Q900X1 PRELIMINARY; PRT; 10 AA.
AC Q900X1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN15;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119349; AAF24104.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
Db |||
7 PPP 9

RESULT 30
Q900X9 ID Q900X9 PRELIMINARY; PRT; 10 AA.
AC Q900X9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCNU;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119345; AAF24096.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
Db |||
7 PPP 9

RESULT 31
Q8JV72 ID Q8JV72 PRELIMINARY; PRT; 10 AA.
AC Q8JV72;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 4;
RX MEDLINE=21465052; PubMed=11581397;

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RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL: AF304386; AM97802.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;  
 Query Match 42.9%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPP 4  
 Db |||  
 7 PPP 9

RESULT 32  
 P82436 PRELIMINARY; PRT; 11 AA.  
 ID P82436;  
 AC P82436;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 65 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.";  
 RL Planta 0:0-0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1068 MW; 34FD25CCB325B867 CRC64;  
 Query Match 42.9%; Score 3; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPP 4  
 Db |||  
 2 PPP 4

RESULT 33  
 Q93X21 PRELIMINARY; PRT; 12 AA.  
 ID Q93X21;  
 AC Q93X21;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Polyubiquitin homolog (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. INRA 258; TISSUE=Leaf;  
 RX MEDLINE=96236829; PubMed=8680303;  
 RA Didierjean L., Frendo P., Nasser W., Genot G., Marivet J., Burkard G.;  
 RT "Heavy-metal-responsive genes in maize: identification and comparison

RT of their expression upon various forms of abiotic stress.";  
 RL Planta 199:1-8(1996).  
 DR EMBL: S82313; AAB47175.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 12 AA; 1277 MW; 250D2D2F6F340DD8 CRC64;  
 Query Match 42.9%; Score 3; DB 10; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPP 4  
 Db |||  
 2 PPP 4

RESULT 34  
 Q9UDC6 PRELIMINARY; PRT; 13 AA.  
 ID Q9UDC6;  
 AC Q9UDC6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE ENDOTHELIUM-derived RELATING factor, nitric oxide synthase  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93054573; PubMed=1395404;  
 RA Janssens S.P., Simouchi A., Quertermous T., Bloch D.B., Bloch K.D.;  
 RT "Cloning and expression of a cDNA encoding human endothelium-derived  
 RT relating factor/nitric oxide synthase.";  
 RL J. Biol. Chem. 267:22694-22694(1992).  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1390 MW; 3231B6DFEC7EB867 CRC64;  
 Query Match 42.9%; Score 3; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DPP 3  
 Db |||  
 4 DPP 6

RESULT 35  
 Q9U5J2 PRELIMINARY; PRT; 13 AA.  
 ID Q9U5J2;  
 AC Q9U5J2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE GPI-phospholipase C (Fragment).  
 GN GPI-PLC  
 OS Trypanosoma brucei.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5691;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ILTar1;  
 RA Webb H.D., Gaud A.F., Carrington M.;  
 RT "The trypanosoma brucei GPI-PLC gene is not linked to functionally  
 RT related genes or to genes showing the same developmentally regulated  
 RT expression.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ250727; CAB60093.1; -.  
 DR InterPro: IPR003633; Varsurfglyc\_PPLC.  
 DR Pfam: PF03490; Varsurf\_PPLC; 1.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1541 MW; 535AA96B464CA373 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
 ||||  
 Db 9 PQS 11

## RESULT 36

P78359 ID P78359 PRELIMINARY; PRT; 14 AA.  
 AC P78359;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE NF-kappa-B transcription factor p65 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Umbilical vein;  
 RA Remacle J.E., Byrs R., Pype S., Nelles L., Huylebroeck D.;  
 RT "5' cDNA sequence RelA isolated from Human umbilical vein endothelial cells.";  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U88316; AAB48487.1; -.  
 FT NON TER 14 14  
 SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
 ||||  
 Db 10 PQS 12

## RESULT 37

Q9TR03 ID Q9TR03 PRELIMINARY; PRT; 15 AA.  
 AC Q9TR03;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Neuron-specific ASH/GRB-2 SH3 domain-binding protein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96257761; PubMed=8687411;  
 RA Miura K., Miki H., Shimazaki K., Kawai N., Takenawa T.;  
 RT "Interaction of Ash/Grb-2 via its SH3 domains with neuron-specific p150 and p65.";  
 RL Biochem. J. 316:639-645(1996).  
 SQ SEQUENCE 15 AA; 1635 MW; 25161E83C374F9CD CRC64;

Query Match 42.9%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPP 3  
 ||||  
 Db 3 DPP 5

## RESULT 38

Q9S8N8 ID Q9S8N8 PRELIMINARY; PRT; 15 AA.  
 AC Q9S8N8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Protein E-22 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=94170739; PubMed=8125056;  
 RA Flengsrud R.;  
 RT "Separation of acidic barley endosperm proteins by two-dimensional RT electrophoresis.";  
 RL Electrophoresis 14:1060-1066(1993).  
 SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
 ||||  
 Db 5 PPQ 7

## RESULT 39

Q9TWN7 ID Q9TWN7 PRELIMINARY; PRT; 16 AA.  
 AC Q9TWN7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Antigen P30-MAJOR surface immunodominant antigen (Fragment).  
 OS Toxoplasma gondii.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;  
 OC Toxoplasma.  
 OX NCBI\_TaxID=5811;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=94294203; PubMed=7517518;  
 RA Bonhomme A., Thirion C., Boulanger F., Charton F., Burtlet H.,  
 RA Pinon J.M., Alix A.J.;  
 RT "Toxoplasma gondii-structure variations of the antigen P30.";  
 RL Parasitology 108:281-287(1994).  
 FT NON TER 1 1  
 SQ SEQUENCE 16 AA; 1678 MW; FE4CF0A743A796CD CRC64;

Query Match 42.9%; Score 3; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPP 3  
 ||||  
 Db 2 DPP 4

## RESULT 40

Q9TQZ7 ID Q9TQZ7 PRELIMINARY; PRT; 16 AA.  
 AC Q9TQZ7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Factor H (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=96202005; PubMed=8615824;  
RA Soames C.J., Day A.J., Sim R.B.;  
RT "Prediction from sequence comparisons of residues of factor H involved  
in the interaction with complement component C3b.";  
RL Biochem. J. 315:523-531(1996).  
SQ SEQUENCE 16 AA; 1871 MW; 7052751E485EC825 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
Db |||  
6 PPP 8

RESULT 41  
Q88250 PRELIMINARY; PRT; 16 AA.  
ID Q88250  
AC Q88250  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE F protein (Fragment).  
OS Sendai virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.  
OX NCBI\_TaxID=11191;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91012818; PubMed=2170692;  
RA Itoh M., Ming T.D., Hayaashi T., Mochizuki Y., Homma M.;  
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,  
TcA, which is sensitive to trypsin and chymotrypsin.";  
RL J. Virol. 64:5660-5664(1990).  
DR ENBL; M60152; AAA47808.1; -.  
FT NON\_TER 1  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1648 MW; 049B529F01B29066 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
Db |||  
6 PQS 8

RESULT 42  
Q88249 PRELIMINARY; PRT; 16 AA.  
ID Q88249  
AC Q88249  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE F protein (Fragment).  
OS Sendai virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.  
OX NCBI\_TaxID=11191;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91012818; PubMed=2170692;  
RA Itoh M., Ming T.D., Hayaashi T., Mochizuki Y., Homma M.;  
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,  
TcA, which is sensitive to trypsin and chymotrypsin.";  
RL J. Virol. 64:5660-5664(1990).

DR EMBL; M60154; AAA47807.1; -.  
FT NON\_TER 1  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1649 MW; 049B529F01B298C4 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
Db |||  
6 PQS 8

RESULT 43  
Q99154 PRELIMINARY; PRT; 16 AA.  
ID Q99154  
AC Q99154  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE F protein (Fragment).  
OS Sendai virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.  
OX NCBI\_TaxID=11191;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91012818; PubMed=2170692;  
RA Itoh M., Ming T.D., Hayaashi T., Mochizuki Y., Homma M.;  
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,  
TcA, which is sensitive to trypsin and chymotrypsin.";  
RL J. Virol. 64:5660-5664(1990).  
DR EMBL; M60153; AAA47806.1; -.  
FT NON\_TER 1  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1606 MW; 739B529F01B298D0 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
Db |||  
6 PQS 8

RESULT 44  
Q9PRU6 PRELIMINARY; PRT; 16 AA.  
ID Q9PRU6  
AC Q9PRU6  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-CRK in VIVO  
(Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=95105151; PubMed=7806494;  
RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,  
RA Yazaki Y., Hirai H.;  
RT "Characterization, partial purification, and peptide sequencing of  
p130, the main phosphoprotein associated with v-Crk oncoprotein.";  
RL J. Biol. Chem. 269:32740-32746(1994).  
FT NON\_TER 1  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1480 MW; CAB880A931F8873F CRC64;

Query Match 42.9%; Score 3; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
|||  
Db 13 PPQ 15

## RESULT 45

Q9UDD6 PRELIMINARY; PRT; 17 AA.  
AC Q9UDD6  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Fatty acid ETHYL ester synthase-II, FAEE synthase-II (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=92317032; PubMed=1618826;  
RA Bora P.S., Wu X., Spilburg C.A., Lange L.G.;  
RT "Purification and characterization of fatty acid ethyl ester synthase-II from human myocardium.";  
RL J. Biol. Chem. 267:13217-13221(1992).  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1755 MW; 3456973BF1B39273 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPP 3  
|||  
Db 2 DPP 4

## RESULT 46

Q9TWC6 PRELIMINARY; PRT; 17 AA.  
AC Q9TWC6  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE 22L kDa excretory-secretory protein (Fragment).  
OS Dirofilaria immitis (Canine heartworm).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Dirofilaria.  
OX NCBI\_TaxID=6287;  
[1]  
RN SEQUENCE.  
RP MEDLINE=96258562; PubMed=899320;  
RA Frank G.R., Grieve R.B.;  
RT "Purification and characterization of three larval excretory-secretory proteins of Dirofilaria immitis.";  
RL Mol. Biochem. Parasitol. 75:221-229(1996).  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 2048 MW; 478557C5392B4AE7 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POS 7  
|||  
Db 2 POS 4

## RESULT 47

Q9PRU7 PRELIMINARY; PRT; 17 AA.  
AC Q9PRU7  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-CRK in VIVO (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
[1]  
RN SEQUENCE.  
RP MEDLINE=95105151; PubMed=7806494;  
RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,  
RA Yazaki Y., Hirai H.;  
RT "Characterization, partial purification, and peptide sequencing of RT p130, the main phosphoprotein associated with v-Crk oncoprotein.";  
RL J. Biol. Chem. 269:32740-32746(1994).  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1608 MW; 52EAB880A931F887 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
|||  
Db 13 PPQ 15

## RESULT 48

Q9UCG7 PRELIMINARY; PRT; 18 AA.  
AC Q9UCG7  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Urinary gonadotrophin peptide (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE.  
RP MEDLINE=93229246; PubMed=8471426;  
RA Kardana A., Bagshaw K.D., Coles B., Read D., Taylor M.;  
RT "Characterisation of UGP and its relationship with beta-core fragment.";  
RL Br. J. Cancer 67:686-692(1993).  
DR HSSP; P10153; 1H12.  
SQ SEQUENCE 18 AA; 2214 MW; BB0A2F0B8E933109 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
|||  
Db 2 PPQ 4

## RESULT 49

Q8NFB4 PRELIMINARY; PRT; 18 AA.  
AC Q8NFB4  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Mutant enamelin (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kida M., Ariga T.;  
 RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused  
 by an enamelin gene mutation at exon-intron boundary.";  
 RL J. Dent. Res. 0:0-0(2002).  
 DR EMBL; AF530444; AM97323.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1893 MW; 492D2B2E38B8E512 CRC64;  
 Query Match 42.9%; Score 3; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY / 2 PPP 4  
 Db ||| 3 PPP 5  
 RESULT 50  
 O97773 PRELIMINARY; PRT; 18 AA.  
 ID O97773  
 AC O97773  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
 DE Mibp protein (Fragment).  
 GN MIBP  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bliskovsky V., Zajac K.M.;  
 RT "Evolutionary conservation of a 2 kilobase intronic sequence flanking  
 a tissue specific alternative exon in the mibp gene.";  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U88970; RAD00667.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2069 MW; CA377C765AE8E28A CRC64;  
 Query Match 42.9%; Score 3; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PQS 7  
 Db ||| 11 PQS 13  
 RESULT 51  
 Q80FT3 PRELIMINARY; PRT; 18 AA.  
 ID Q80FT3  
 AC Q80FT3  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Sterol regulatory element binding protein 1 (Fragment).  
 GN SREBP-1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Assaf S., Pitel F., Morisson M., Alizadeh M., Gondret F., Diot C.,  
 RA Leclercq B., Vignal A., Douaire M., Lagarigue S.;  
 RT "Partial cloning, tissue expression, chromosomal localisation of  
 chicken SREBP genes and relationships to fatness variability in  
 RT genetically fat and lean chicken lines.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ441122; CAD29619.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1947 MW; 3206A67750EFD7EA CRC64;  
 Query Match 42.9%; Score 3; DB 13; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPP 4  
 Db ||| 15 PPP 17  
 RESULT 52  
 Q9UCL3 PRELIMINARY; PRT; 19 AA.  
 ID Q9UCL3  
 AC Q9UCL3  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Insulin-like growth factor binding protein 34 kDa form (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93091816; PubMed=1726837;  
 RA Roghani M., Segovia B., Whitechurch O., Binoux M.;  
 RT "Purification from human cerebrospinal fluid of insulin-like growth  
 factor binding proteins (IGFBPs). Isolation of IGFBP-2, an altered form  
 RT of IGFBP-3 and a new IGFBP species.";  
 RL Growth Regul. 1:125-130(1991).  
 SQ SEQUENCE 19 AA; 2032 MW; A73497C418219088 CRC64;  
 Query Match 42.9%; Score 3; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPP 4  
 Db ||| 16 PPP 18  
 RESULT 53  
 P82941 PRELIMINARY; PRT; 19 AA.  
 ID P82941  
 AC P82941  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Unknown endosperm protein V (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. BOMI; TISSUE=Starchy endosperm;  
 RX MEDLINE=21088911; PubMed=11271488;  
 RA Kristoffersen H.E., Flengsrud R.;  
 RT "Separation and characterization of basic barley seed proteins.";  
 RL Electrophoresis 21:3693-3700(2000).

CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 7.0, ITS MW IS: 19.9 KDA.

FT NON TER 19  
 SQ SEQUENCE 19 AA; 2026 MW; 053B874BADC602E0 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
 DB 2 PPP 4

## RESULT 54

Q90RFB PRELIMINARY; PRT; 19 AA.  
 AC Q90RFB  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 GN TAT.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97CG276;  
 RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,  
 RA Hayami M., Ichimura H., Parra J.H.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 RT Republic of Congo-Brazzaville."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF127550; AAK84913.1; -  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2304 MW; 2727D4B66AE69237 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PQS 7  
 DB 7 PQS 9

## RESULT 55

Q90SK8 PRELIMINARY; PRT; 19 AA.  
 AC Q90SK8  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=96CG14;  
 RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 RT Republic of Congo-Brazzaville."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF10437; AAL10214.1; -  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2208 MW; 77629CA42AE38630 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6  
 DB 6 PPQ 8

## RESULT 56

Q905I4 PRELIMINARY; PRT; 19 AA.  
 AC Q905I4  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=96CG30;  
 RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 RT Republic of Congo-Brazzaville."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF410443; AAL10238.1; -  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2151 MW; 2A91C2A4D1167636 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4  
 DB 6 PPP 8

## RESULT 57

Q905G8 PRELIMINARY; PRT; 19 AA.  
 AC Q905G8  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97CG281;  
 RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 RT Republic of Congo-Brazzaville."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF410447; AAL10254.1; -  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2366 MW; 367E64E194069237 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 POS 7
DB 7 POS 9

RESULT 58
ID Q90R5 PRELIMINARY; PRT; 19 AA.
AC Q90R5;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG34;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-V., Obengui, M'Pandi M., Harada Y.,
RA Hayani M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127548; AAK84907.1; -.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2211 MW; 2A81B42D64039636 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPQ 6
DB 6 PPQ 8

RESULT 59
ID Q9R4D7 PRELIMINARY; PRT; 20 AA.
AC Q9R4D7;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
DE 57 kDa outer membrane protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
RX MEDLINE=96355881; PubMed=8751919;
RA Yamanoto T., Wakisaka N., Nakae T., Kamano T., Serichantalergs O.,
RA Echeverria P.;
RT "Characterization of a novel hemagglutinin of diarrhea-associated
RT Escherichia coli that has characteristics of diffusely adhering E. coli
RT and enteroaggregative E. coli.";
RL Infect. Immun. 64:3694-3702(1996).
SQ SEQUENCE 20 AA; 1988 MW; A7AB6088E52F5458 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPP 4
DB 3 PPP 5

RESULT 60
ID Q9S965 PRELIMINARY; PRT; 20 AA.

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Q9UR76
ID Q9UR76 PRELIMINARY; PRT; 20 AA.
AC Q9UR76;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)
DE N-acetylglucosaminidase A (Fragment).
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE.
RX MEDLINE=943356217; PubMed=8075797;
RA Molloy C., Cannon R.D., Sullivan P.A., Shepherd M.G.;
RT "Purification and characterization of two forms of N-
RT acetylglucosaminidase from Candida albicans showing widely different
RT outer chain glycosylation.";
RL Microbiology 140:1543-1553(1994).
SQ SEQUENCE 20 AA; 2178 MW; DA602087EDB4D47 CRC64;

Query Match 42.9%; Score 3; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POS 7
DB 9 POS 11

RESULT 61
ID Q9S7J0 PRELIMINARY; PRT; 20 AA.
AC Q9S7J0;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Bromelain (Fragment).
OS Ananas comosus (Pineapple).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae incertae sedis;
OC Bromeliaceae; Ananas.
OX NCBI_TaxID=4615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95298192; PubMed=7779262;
RA Harrach T., Eckert K., Schulze-Forster K., Nuck R., Grunow D.,
RA Maurer H.R.;
RT "Isolation and partial characterization of basic proteinases from stem
RT bromelain.";
RL J. Protein Chem. 14:41-52(1995).
RN [2]
RP SEQUENCE.
RX MEDLINE=94330946; PubMed=8053898;
RA Napper A.D., Bennett S.P., Borowski M., Holdridge M.B., Leonard M.J.,
RA Rogers E.E., Duan Y., Laursen R.A., Reinhold B., Shames S.L.;
RL Biochem. J. 301:727-735(1994).
DR InterPro: IPR000668; Peptidase_C1.
DR Pfam: PF00112; Peptidase_C1; 1.
SQ SEQUENCE 20 AA; 2144 MW; 83A842BC812C3EBC CRC64;

Query Match 42.9%; Score 3; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 POS 7
DB 2 POS 4

RESULT 62
ID Q9S965 PRELIMINARY; PRT; 20 AA.

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AC Q9S965;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Bromelain (Fragment).  
 OS Ananas comosus (Pineapple).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae incertae sedis;  
 OC Bromeliaceae; Ananas.  
 OX NCBI\_TaxID=4615;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=95298192; PubMed=7779262;  
 RA Harrach T., Eckert K., Schulse-Forster K., Nuck R., Grunow D.,  
 RT "Isolation and partial characterization of basic proteinases from stem  
 RT bromelain."  
 RL J. Protein Chem. 14:41-52(1995).  
 DR InterPro; IPR000668; Peptidase\_C1.  
 DR Pfam; PF00112; Peptidase\_C1; 1\_C1.  
 SQ SEQUENCE 20 AA; 2277 MW; 8F984A1E812C3EBC CRC64;  
  
 Query Match 42.9%; Score 3; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 POS 7  
 DB 2 POS 4  
  
 RESULT 63  
 Q9S8M1 PRELIMINARY; PRT; 20 AA.  
 AC Q9S8M1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE COMOSAIN (Fragment).  
 OS Ananas comosus (Pineapple).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae incertae sedis;  
 OC Bromeliaceae; Ananas.  
 OX NCBI\_TaxID=4615;  
 RN [1]  
 RN SEQUENCE.  
 RP MEDLINE=94330946; PubMed=8053898;  
 RA Napper A.D., Bennett S.P., Borowski M., Holdridge M.B., Leonard M.J.,  
 RA Rogers E.E., Duan Y., Laursen R.A., Reinhold B., Shames S.L.;  
 RL Biochem. J. 301:727-735(1994).  
 DR InterPro; IPR000668; Peptidase\_C1.  
 DR Pfam; PF00112; Peptidase\_C1; 1\_C1.  
 SQ SEQUENCE 20 AA; 2219 MW; 83A84A16232C3EBC CRC64;  
  
 Query Match 42.9%; Score 3; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 POS 7  
 DB 2 POS 4  
  
 RESULT 64  
 Q9QVH2 PRELIMINARY; PRT; 20 AA.  
 AC Q9QVH2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Chromogranin-B, CGB=GLUCAGONOMA peptide (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RN SEQUENCE.  
 RX MEDLINE=92063871; PubMed=1954895;  
 RA Nielsen E., Weindler B.S., Madsen O.D.;  
 RT "Chromogranin-B, a putative precursor of eight novel rat glucagonoma  
 RT peptides through processing at mono-, di-, or tribasic residues."  
 RL Endocrinology 129:3147-3156(1991).  
 DR InterPro; IPR001990; Granin.  
 DR Pfam; PF01271; Granin; 1.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2549 MW; 9AA9A230D0F151A8 CRC64;  
  
 Query Match 42.9%; Score 3; DB 11; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 POS 7  
 DB 2 POS 4  
  
 RESULT 65  
 Q912B4 PRELIMINARY; PRT; 20 AA.  
 ID Q912B4;  
 AC Q912B4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 7.5-kDa nonstructural protein (Fragment).  
 GN 7.5-KDA.  
 OS Human erythrovirus V9.  
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.  
 OX NCBI\_TaxID=72197;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R234;  
 RA Nguyen Q.T.;  
 RT "Molecular cloning and sequencing of a novel human erythrovirus  
 RT genome: new species beside B19 in the genus Erythrovirus."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ249875; CAC80689.1;  
 KW Nonstructural protein.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 1977 MW; F00971E8578CE5490 CRC64;  
  
 Query Match 42.9%; Score 3; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 PPP 4  
 DB 4 PPP 6  
  
 RESULT 66  
 Q912B2 PRELIMINARY; PRT; 20 AA.  
 ID Q912B2;  
 AC Q912B2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 7.5-kDa nonstructural protein (Fragment).  
 GN 7.5-KDA.  
 OS Human parvovirus B19.  
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.  
 OX NCBI\_TaxID=10798;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R82;

RA Nguyen Q.T.;  
 RT "Molecular cloning and sequencing of a novel human erythrovirus  
 genome: new species beside B19 in the genus Erythrovirus."  
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ249876; CAB00691.1; -  
 KW Nonstructural protein.  
 FT NON\_TER 1 1  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2008 MW; F00971B8578CE5D5 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PPQ 6  
 ||||  
 Db 4 PPQ 6

## RESULT 67

P92214 PRELIMINARY; PRT; 7 AA.  
 ID P92214  
 AC P92214;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Amblyopryum muticum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Amblyopryum.  
 OX NCBI\_TaxID=4595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5572; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77756; CAB01346.1; -  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 AA; 894 MW; 6734140333277700 CRC64;  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PP 3  
 ||||  
 Db 1 PP 2

## RESULT 68

P92393 PRELIMINARY; PRT; 7 AA.  
 ID P92393  
 AC P92393;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Hordeum vulgare (Barley).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=H3139; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77764; CAB01370.1; -  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 AA; 894 MW; 6734140333277700 CRC64;  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PP 3  
 ||||  
 Db 1 PP 2

## RESULT 69

P92403 PRELIMINARY; PRT; 7 AA.  
 ID P92403  
 AC P92403;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Lophopyrum.  
 OX NCBI\_TaxID=4588;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6692; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77743; CAB01307.1; -  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 AA; 894 MW; 6734140333277700 CRC64;  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PP 3  
 ||||  
 Db 1 PP 2

## RESULT 70

P92427 PRELIMINARY; PRT; 7 AA.  
 ID P92427  
 AC P92427;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein (Fragment).  
 GN RPS11.  
 OS Peridictyon sanctum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Peridictyon.  
 OX NCBI\_TaxID=37683;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=H5575; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77749; CAB01325.1; --  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 ||  
 Db 1 PP 2

## RESULT 71

P92430  
 ID P92430 PRELIMINARY; PRT; 7 AA.  
 AC P92430;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Aegilops tauschii (Aegilops squarrosa).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Aegilops.  
 OX NCBI\_TaxID=37682;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6668; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77758; CAB01352.1; --  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 ||  
 Db 1 PP 2

## RESULT 72

P92221  
 ID P92221 PRELIMINARY; PRT; 7 AA.  
 AC P92221;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Bromus inermis (Smooth brome grass).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Bromae; Bromus.  
 OX NCBI\_TaxID=15371;

RN SEQUENCE FROM N.A.  
 RP STRAIN=OSA414; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77759; CAB01355.1; --  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 ||  
 Db 1 PP 2

## RESULT 73

P92425  
 ID P92425 PRELIMINARY; PRT; 7 AA.  
 AC P92425;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Pseudoroegneria.  
 OX NCBI\_TaxID=4604;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H9082; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77744; CAB01310.1; --  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 ||  
 Db 1 PP 2

## RESULT 74

P92381  
 ID P92381 PRELIMINARY; PRT; 7 AA.  
 AC P92381;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Hordeum brachyantherum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.



OX NCBI\_TaxID=52712;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; 277761; CAB01361.1; --  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 1 1  
 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 ||  
 Db 1 PP 2

## RESULT 75

P92387  
 ID P92387 PRELIMINARY; PRT; 7 AA.  
 AC P92387;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein l1 (fragment).  
 GN RPS11.  
 OS Henrardia persica.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Henrardia.  
 OX NCBI\_TaxID=37678;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5556; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; 277748; CAB01322.1; --  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 1 1  
 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3  
 ||  
 Db 1 PP 2

Search completed: November 25, 2003, 18:25:37  
 Job time : 17.917 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 22.6755 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-14

Perfect score: 7

Sequence: 1 DPPPPQS 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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- 21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	22	Colostrinin derive
2	7	100.0	7	22	Colostrinin peptid
3	7	100.0	7	22	Colostrinin peptid
4	7	100.0	7	22	Ewe colostrinin pe
5	7	100.0	7	23	Colostrinin consti
6	7	100.0	7	23	Colostrinin consti
7	7	100.0	7	23	Colostrinin consti
8	5	71.4	9	24	Neural cell regula
9	5	71.4	9	24	Human cancer-relat

10	5	71.4	9	24	ABR27387	Human cancer-relat
11	5	71.4	9	24	ABR27389	Human cancer-relat
12	5	71.4	9	24	ABR27601	Human cancer-relat
13	5	71.4	9	24	ABR27604	Human cancer-relat
14	5	71.4	9	24	ABR27635	Human cancer-relat
15	5	71.4	9	24	ABR27801	Human cancer-relat
16	5	71.4	9	24	ABR27824	Human cancer-relat
17	5	71.4	9	24	ABR27844	Human cancer-relat
18	5	71.4	9	24	ABR27971	Human cancer-relat
19	5	71.4	9	24	ABR27975	Human cancer-relat
20	5	71.4	9	24	ABR28044	Human cancer-relat
21	5	71.4	9	24	ABR28179	Human cancer-relat
22	5	71.4	9	24	ABR28181	Human cancer-relat
23	5	71.4	9	24	ABR28244	Human cancer-relat
24	5	71.4	9	24	ABR28248	Human cancer-relat
25	5	71.4	9	24	ABR28254	Human cancer-relat
26	5	71.4	9	24	ABR28357	Human cancer-relat
27	5	71.4	9	24	ABR28411	Human cancer-relat
28	5	71.4	9	24	ABR28417	Human cancer-relat
29	5	71.4	9	24	ABR28437	Human cancer-relat
30	5	71.4	10	24	ABR27368	Human cancer-relat
31	5	71.4	10	24	ABR27308	Human cancer-relat
32	5	71.4	10	24	ABR27336	Human cancer-relat
33	5	71.4	10	24	ABR27487	Human cancer-relat
34	5	71.4	10	24	ABR27537	Human cancer-relat
35	5	71.4	10	24	ABR27692	Human cancer-relat
36	5	71.4	10	24	ABR27707	Human cancer-relat
37	5	71.4	10	24	ABR27737	Human cancer-relat
38	5	71.4	10	24	ABR27891	Human cancer-relat
39	5	71.4	10	24	ABR27904	Human cancer-relat
40	5	71.4	10	24	ABR27913	Human cancer-relat
41	5	71.4	10	24	ABR28074	Human cancer-relat
42	5	71.4	10	24	ABR28076	Human cancer-relat
43	5	71.4	10	24	ABR28145	Human cancer-relat
44	5	71.4	10	24	ABR28150	Human cancer-relat
45	5	71.4	10	24	ABR28280	Human cancer-relat
46	5	71.4	10	24	ABR28281	Human cancer-relat
47	5	71.4	10	24	ABR28332	Human cancer-relat
48	5	71.4	10	24	ABR28335	Human cancer-relat
49	5	71.4	10	24	ABR28354	Human cancer-relat
50	5	71.4	10	24	ABR28479	Human cancer-relat
51	5	71.4	10	24	ABR28486	Human cancer-relat
52	5	71.4	10	24	ABR28502	Human cancer-relat
53	5	71.4	10	24	ABR28513	Human cancer-relat
54	5	71.4	10	24	ABR28537	Human cancer-relat
55	5	71.4	13	22	ABR30652	Trypsin modulating
56	5	71.4	15	14	AA426641	N-terminal sequenc
57	5	71.4	15	18	AAW39038	Peptide resembling
58	5	71.4	15	18	AAW39006	Peptide resembling
59	5	71.4	15	18	AAW38970	Peptide resembling
60	5	71.4	15	18	AAW38976	Peptide resembling
61	5	71.4	15	18	AAW38942	Peptide resembling
62	5	71.4	15	18	AAW38952	Peptide resembling
63	5	71.4	15	19	AAW45819	Peptide recognised
64	5	71.4	15	19	AAW45614	Peptide recognised
65	5	71.4	15	20	AAW95144	Phage peptide K5 b
66	5	71.4	15	20	AAW95125	Peptide K5 express
67	5	71.4	15	21	AAW93014	Transforming growt
68	5	71.4	15	21	AAW93015	Colostrinin derive
69	5	71.4	15	22	AAW72252	Colostrinin derive
70	5	71.4	15	22	AAW72506	Colostrinin peptid
71	5	71.4	15	22	AAW72538	Colostrinin peptid
72	5	71.4	15	22	AAW59312	Ewe colostrinin pe
73	5	71.4	15	23	AAE20234	Colostrinin consti
74	5	71.4	15	23	AAW51042	Colostrinin consti
75	5	71.4	15	23	AAO14583	Neural cell regula
76	5	71.4	15	24	ABR38294	Human cancer-relat
77	5	71.4	15	24	ABR38296	Human cancer-relat
78	5	71.4	15	24	ABR38351	Human cancer-relat
79	5	71.4	15	24	ABR38352	Human cancer-relat
80	5	71.4	15	24	ABR38369	Human cancer-relat
81	5	71.4	15	24	ABR38370	Human cancer-relat
82	5	71.4	15	24	ABR38380	Human cancer-relat

83 Human cancer-relat  
84 Human cancer-relat  
85 Human cancer-relat  
86 Human cancer-relat  
87 Human cancer-relat  
88 Human cancer-relat  
89 Human cancer-relat  
90 Human cancer-relat  
91 Human cancer-relat  
92 B-cell epitopic pe  
93 WW domain binding  
94 Crk N-terminal SH3  
95 Two tandem copies  
96 Ewe colostrinin pe  
97 P. berghi CS B cel  
98 Malarial B cell ep  
99 Peptide resembling  
100 Peptide resembling

ALIGNMENTS

RESULT 1  
AAB72259  
ID AAB72259 standard; peptide; 7 AA.  
XX  
AC AAB72259;  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Colostrinin derived cytokine inducing peptide SEQ ID 14.  
XX  
KW Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.  
XX  
OS Synthetic.  
XX  
XX WO200111937-A2.  
PN  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US22818.  
XX  
XX 17-AUG-1999; 99US-0149311.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX (REG-) REGEN THERAPEUTICS PLC.  
PA  
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX  
XX MPI; 2001-202804/20.  
DR  
XX  
XX Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator -  
XX  
XX Claim 1; Page 34; 50pp; English.  
PS  
XX  
XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The  
CC peptides have immune response modulatory activity, and are capable of  
CC inducing cytokines. Colostrinin and its derived peptides are useful for  
CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.

XX SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DPPPQPS 7  
Db 1 DPPPQPS 7  
RESULT 2  
AAB72512  
ID AAB72512 standard; Peptide; 7 AA.  
XX  
AC AAB72512;  
XX  
DT 09-MAY-2001 (first entry)  
XX  
DE Colostrinin peptide #13.  
XX  
KW Dermatological; oxidative stress regulator; colostrinin.  
XX  
OS Unidentified.  
XX  
XX WO200112650-A2.  
PN  
XX 22-FEB-2001.  
PD  
XX 17-AUG-2000; 2000WO-US22665.  
PF  
XX 17-AUG-1999; 99US-0149310.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX Stanton GJ, Hughes TK, Boldogh I;  
PI  
XX MPI; 2001-218342/22.  
DR  
XX  
XX Modulating oxidative stress level in a cell, involves contacting the  
PT cell with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations -  
PT  
XX  
XX Claim 6; Page 25; 48pp; English.  
PS  
XX  
XX The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidizing species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient.  
XX  
XX SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DPPPQPS 7  
Db 1 DPPPQPS 7  
RESULT 3  
AAB72544  
ID AAB72544 standard; Peptide; 7 AA.  
XX  
AC AAB72544;  
XX  
XX 09-MAY-2001 (first entry)  
DT  
XX

```

DE Colostrinin peptide #13.
XX
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
XX colostrum.
XX
XX Unidentified.
XX
XX W0200112651-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22774.
XX
XX 17-AUG-1999; 99US-0149633.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Boldogh I;
XX
XX WPI; 2001-226545/23.
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient -
XX
XX Claim 6; Page 21; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
XX differentiation and treating damaged neural cells, using colostrinin and
XX colostrinin constituent peptides (e.g. the present peptide) as a neural
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX Sequence 7 AA;
XX
XX Query Match 100.0%; Score 7; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DPPPQQS 7
XX |||||
XX Db 1 DPPPQQS 7
XX
XX RESULT 5
XX AAE20241
XX ID AAE20241 standard; peptide; 7 AA.
XX
XX AC AAE20241;
XX
XX 18-JUN-2002 (first entry)
XX
XX Colostrinin constituent peptide #13.
XX
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX transplantation; implantation; dermatological; vulnery.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Modified-site 7
XX /note= "Optionally C-terminal amide"
XX
XX W0200213850-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
XX patient comprises a blood cell regulator selected from colostrinin, its
XX constituent peptide and/or analog -
XX
XX Claim 6; Page 25; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
XX regulator selected from colostrinin, its constituent peptide and/or
XX analogue. The invention is used for modulating the oxidative stress
XX level in a cell e.g. mammalian or human cell present in a cell culture,
XX tissue, organ, or organism; or for treating oxidative damage to the skin
XX of a patient e.g. animal or human; to modulate oxidative stress during/
XX

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---

```

DE Colostrinin peptide #13.
XX
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
XX colostrum.
XX
XX Unidentified.
XX
XX W0200112651-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22774.
XX
XX 17-AUG-1999; 99US-0149633.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Boldogh I;
XX
XX WPI; 2001-226545/23.
XX
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient -
XX
XX Claim 6; Page 21; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
XX differentiation and treating damaged neural cells, using colostrinin and
XX colostrinin constituent peptides (e.g. the present peptide) as a neural
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX Sequence 7 AA;
XX
XX Query Match 100.0%; Score 7; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DPPPQQS 7
XX |||||
XX Db 1 DPPPQQS 7
XX
XX RESULT 4
XX AAB59315
XX ID AAB59315 standard; Peptide; 7 AA.
XX
XX AC AAB59315;
XX
XX 21-MAR-2001 (first entry)
XX
XX Ewe colostrinin peptide fragment A-7.
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX Ovis sp.
XX
XX W0200075173-A2.
XX
XX 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-GB02128.
XX
XX 02-JUN-1999; 99GB-0012852.
XX
XX (REGE-) REGEN THERAPEUTICS PLC.
XX
XX Georgiades JA;
XX
XX WPI; 2001-071058/08.
XX
XX Peptides having an N-terminal amino acid sequence isolated from
XX

```

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidizing species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 7 AA;  
 SQ Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPPQSQ 7  
 |||||  
 DB 1 DPPPQSQ 7

RESULT 6  
 AAM51048  
 ID AAM51048 standard; Peptide; 7 AA.

XX  
 AC AAM51048;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide.

XX Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "optional C-terminal amidation"

FT WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA (REGG-) REGEN THERAPEUTICS, PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue

PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. Methods are  
 CC claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions  
 CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide.

XX Sequence 7 AA;

QY 1 DPPPQSQ 7  
 |||||  
 DB 1 DPPPQSQ 7

RESULT 7

AAO14590

ID AAO14590 standard; peptide; 7 AA.

XX  
 AC AAO14590;

DT 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 13.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "Optional C-terminal amide"

FT WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.

```

XX SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPPQS 7
Db 1 DPPPQS 7

RESULT 8
ABR27168
ID ABR27168 standard; Peptide; 9 AA.
XX AC ABR27168;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 187P3F2 HLA peptide #3.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients
XX PS Claim 13; Page 400; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 9 AA;
Query Match 71.4%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPQS 7
Db 2 PPPQS 6

RESULT 9
ABR27236
ID ABR27236 standard; Peptide; 9 AA.
XX AC ABR27236;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 187P3F2 HLA peptide #71.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients
XX PS Claim 13; Page 401; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 9 AA;
Query Match 71.4%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPQ 6
Db 4 PPPQ 8

RESULT 10
ABR27387
ID ABR27387 standard; Peptide; 9 AA.
XX AC ABR27387;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 187P3F2 HLA peptide #71.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients
XX PS Claim 13; Page 400; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 9 AA;
Query Match 71.4%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPQS 7
Db 2 PPPQS 6

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Wed Nov 26 09:06:42 2003

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DE Human cancer-related protein 187P3F2 HLA peptide #222.
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
XX WO200283921-A2.
XX 24-OCT-2002.
XX 10-APR-2002; 2002WO-US11654.
XX 10-APR-2001; 2001US-282739P.
XX 10-APR-2001; 2001US-283112P.
XX 25-APR-2001; 2001US-286630P.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients
XX Claim 13; Page 403; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX Sequence 9 AA;
SQ Query Match 71.4%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 PPPQS 7
DB 4 PPPQS 8
RESULT 11
ABR27389
ID ABR27389 standard; Peptide; 9 AA.
XX AC ABR27389;
XX 19-MAY-2003 (first entry)
XX Human cancer-related protein 187P3F2 HLA peptide #224.
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
XX WO200283921-A2.
XX 24-OCT-2002.
DE Human cancer-related protein 187P3F2 HLA peptide #436.
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
XX WO200283921-A2.
XX 24-OCT-2002.
XX 10-APR-2001; 2001US-282739P.
XX 10-APR-2001; 2001US-283112P.
XX 25-APR-2001; 2001US-286630P.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients
XX Claim 13; Page 403; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX Sequence 9 AA;
SQ Query Match 71.4%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 PPPQS 7
DB 3 PPPQS 7
RESULT 12
ABR27601
ID ABR27601 standard; Peptide; 9 AA.
XX AC ABR27601;
XX 19-MAY-2003 (first entry)
XX Human cancer-related protein 187P3F2 HLA peptide #436.
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
XX WO200283921-A2.
XX 24-OCT-2002.
XX 10-APR-2002; 2002WO-US11654.
XX 10-APR-2001; 2001US-282739P.
XX 10-APR-2001; 2001US-283112P.
XX 25-APR-2001; 2001US-286630P.
XX (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients
XX Claim 13; Page 403; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX Sequence 9 AA;
SQ Query Match 71.4%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 PPPQS 7
DB 3 PPPQS 7
```



PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 XX Claim 13; Page 405; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic agents. The proteins and peptides are useful as  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 XX Sequence 9 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPPQS 7  
 DB 4 PPPQS 8  
 |||||  
 |||||

RESULT 13  
 ABR27604  
 ID ABR27604 standard; Peptide; 9 AA.  
 AC ABR27604;  
 DT 19-MAY-2003 (first entry)  
 DE Human cancer-related protein 187P3F2 HLA peptide #439.  
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW Human leukocyte antigen.  
 KW Homo sapiens.  
 OS WO200283921-A2.  
 PN 24-OCT-2002.  
 PD 10-APR-2002; 2002WO-US11654.  
 PF 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX  
 CC New composition comprising a substance that modulates the structure of  
 CC proteins and polynucleotides, useful for therapeutic, prognostic and  
 CC diagnostic reagents for eliciting cellular or humoral immune response  
 CC in cancer patients -  
 XX  
 XX Claim 13; Page 405; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic agents. The proteins and peptides are useful as  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 XX Sequence 9 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPPQS 7  
 DB 2 PPPQS 6  
 |||||  
 |||||

RESULT 14  
 ABR27635  
 ID ABR27635 standard; Peptide; 9 AA.  
 AC ABR27635;  
 DT 19-MAY-2003 (first entry)  
 DE Human cancer-related protein 187P3F2 HLA peptide #470.  
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW Human leukocyte antigen.  
 KW Homo sapiens.  
 OS WO200283921-A2.  
 PN 24-OCT-2002.  
 PD 10-APR-2002; 2002WO-US11654.  
 PF 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX  
 CC New composition comprising a substance that modulates the structure of  
 CC proteins and polynucleotides, useful for therapeutic, prognostic and  
 CC diagnostic reagents for eliciting cellular or humoral immune response  
 CC in cancer patients -  
 XX  
 XX Claim 13; Page 406; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as

CC	therapeutic, prognostic and diagnostic reagents for cancer. The present
CC	sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC	from the invention.
XX	
XX	
SQ	Sequence 9 AA;
	Query Match 71.4%; Score 5; DB 24; Length 9;
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 PPGQS 7
Db	3 PPGQS 7
RESULT 15	
ABR27801	
ID	ABR27801 standard; Peptide; 9 AA.
XX	
AC	ABR27801;
XX	
DT	19-MAY-2003 (first entry)
XX	
DE	Human cancer-related protein 187P3F2 HLA peptide #636.
XX	
KW	Human; cytostatic; vaccine; cancer; immune response; HLA;
KW	human leukocyte antigen.
XX	
OS	Homo sapiens.
XX	
PN	WO200283921-A2.
XX	
PD	24-OCT-2002.
XX	
PF	10-APR-2002; 2002WO-US11654.
XX	
PR	10-APR-2001; 2001US-282739P.
PR	10-APR-2001; 2001US-283112P.
PR	25-APR-2001; 2001US-286630P.
XX	
XX	(AGEN-) AGENSYS INC.
PA	
XX	
PI	Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI	Morrison K, Morrison RK, Raitano AB;
XX	
XX	WPI; 2003-075555/07.
XX	
PT	New composition comprising a substance that modulates the structure of
PT	proteins and polynucleotides, useful for therapeutic, prognostic and
PT	diagnostic reagents for eliciting cellular or humoral immune response
PT	in cancer patients
XX	
PS	Claim 13; Page 408; 102lpp; English.
XX	
CC	The present invention relates to novel human cancer-related genes and
CC	proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC	proteins are useful for eliciting a humoral or cellular immune response.
CC	The genes are useful as probes and primers for the amplification and/or
CC	detection of genes, mRNAs or their fragments, as reagents for the
CC	diagnosis and/or prognosis of cancer, as coding sequences capable of
CC	directing the expression of the protein, as tools for modulating or
CC	inhibiting the expression of genes and/or translation of transcripts, and
CC	as therapeutic agents. The proteins and peptides are useful as
CC	therapeutic, prognostic and diagnostic reagents for cancer. The present
CC	sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC	from the invention.
XX	
SQ	Sequence 9 AA;
	Query Match 71.4%; Score 5; DB 24; Length 9;
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 PPGQS 7
Db	3 PPGQS 7
RESULT 17	
ABR27844	
ID	ABR27844 standard; Peptide; 9 AA.
XX	
AC	ABR27844;

XX DT 19-MAY-2003 (first entry)  
 XX DE Human cancer-related protein 187P3F2 HLA peptide #679.  
 XX DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX DR New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 408; 1021pp; English.  
 XX PS The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPPQS 7  
 Db 2 PPPQS 6  
 RESULT 18  
 ABR27971  
 ID ABR27971 standard; Peptide; 9 AA.  
 AC ABR27971;  
 XX 19-MAY-2003 (first entry)  
 XX DT Human cancer-related protein 187P3F2 HLA peptide #806.  
 XX DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX DR New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 408; 1021pp; English.  
 XX PS The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPPQS 7  
 Db 2 PPPQS 6  
 RESULT 19  
 ABR27975  
 ID ABR27975 standard; Peptide; 9 AA.  
 AC ABR27975;  
 XX 19-MAY-2003 (first entry)  
 XX DT Human cancer-related protein 187P3F2 HLA peptide #810.  
 XX DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.

PN WO200283921-A2.  
 XX 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX DR New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 410; 1021pp; English.  
 XX PS The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPPQS 7  
 Db 4 PPPQS 8  
 RESULT 19  
 ABR27975  
 ID ABR27975 standard; Peptide; 9 AA.  
 AC ABR27975;  
 XX 19-MAY-2003 (first entry)  
 XX DT Human cancer-related protein 187P3F2 HLA peptide #810.  
 XX DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.

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PA (AGEN-) AGENSYS INC.
XX Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX Claim 13; Page 410; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX SQ Sequence 9 AA;
XX Query Match 71.4%; Score 5; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 PPPQS 7
XX Db 3 PPPQS 7
XX
XX RESULT 20
XX ABR28044
XX ID ABR28044 standard; Peptide; 9 AA.
XX AC ABR28044;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 187P3F2 HLA peptide #879.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX XX
XX (AGEN-) AGENSYS INC.
XX PA Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX XX
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX Claim 13; Page 412; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX SQ Sequence 9 AA;
XX Query Match 71.4%; Score 5; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 PPPQS 7
XX Db 3 PPPQS 7
XX
XX RESULT 21
XX ABR28179
XX ID ABR28179 standard; Peptide; 9 AA.
XX AC ABR28179;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 187P3F2 HLA peptide #1014.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX XX
XX (AGEN-) AGENSYS INC.
XX PA Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX XX
XX WPI; 2003-075555/07.
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX Claim 13; Page 412; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX SQ Sequence 9 AA;
XX Query Match 71.4%; Score 5; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 PPPQS 7
XX Db 2 PPPQS 6
XX

```

CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention.

XX SQ Sequence 9 AA;

Query Match 71.4%; Score 5; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 3 PPFQS 7  
|||  
DB 3 PPFQS 7

RESULT 22

ABR28181  
ID ABR28181 standard; Peptide; 9 AA.

XX AC ABR28181;

DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 187P3F2 HLA peptide #1016.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 25-APR-2001; 2001US-283112P.

XX XX (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response  
PT in cancer patients

PS Claim 13; Page 412; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention.

XX SQ Sequence 9 AA;

Query Match 71.4%; Score 5; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPFQS 7  
|||  
DB 4 PPFQS 8

RESULT 23

ABR28244  
ID ABR28244 standard; Peptide; 9 AA.

XX AC ABR28244;

DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 187P3F2 HLA peptide #1079.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 25-APR-2001; 2001US-283112P.

XX XX (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response  
PT in cancer patients

PS Claim 13; Page 413; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention.

SQ Sequence 9 AA;

Query Match 71.4%; Score 5; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPFQS 7  
|||  
DB 2 PPFQS 6

RESULT 24

ABR28248

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ID  ABR28248 standard; Peptide; 9 AA.
XX
AC  ABR28248;
XX
DT  19-MAY-2003 (first entry)
XX
DE  Human cancer-related protein 187P3F2 HLA peptide #1083.
XX
KW  Human; cytostatic; vaccine; cancer; immune response; HLA;
XX  human leukocyte antigen.
OS  Homo sapiens.
XX
PN  WO200283921-A2.
XX
PD  24-OCT-2002.
XX
PF  10-APR-2002; 2002WO-US11654.
XX
PR  10-APR-2001; 2001US-282739P.
XX  10-APR-2001; 2001US-283112P.
PR  25-APR-2001; 2001US-286630P.
XX
PA  (AGEN-) AGENSYS INC.
XX
PI  Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX  Morrison K, Morrison RK, Raitano AB;
XX
XX  WPI; 2003-075555/07.
XX
XX  New composition comprising a substance that modulates the structure of
XX  proteins and polynucleotides, useful for therapeutic, prognostic and
XX  diagnostic reagents for eliciting cellular or humoral immune response
XX  in cancer patients.
XX
PS  Claim 13; Page 413; 1021pp; English.
XX
XX  The present invention relates to novel human cancer-related genes and
XX  proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX  proteins are useful for eliciting a humoral or cellular immune response.
XX  The genes are useful as probes and primers for the amplification and/or
XX  detection of genes, mRNAs or their fragments, as reagents for the
XX  diagnosis and/or prognosis of cancer, as coding sequences capable of
XX  directing the expression of the protein, as tools for modulating or
XX  inhibiting the expression of genes and/or translation of transcripts, and
XX  as therapeutic agents. The proteins and peptides are useful as
XX  therapeutic, prognostic and diagnostic reagents for cancer. The present
XX  sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX  from the invention.
XX
PS  Sequence 9 AA;
XX
XX  Query Match 71.4%; Score 5; DB 24; Length 9;
XX  Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  2 PPPPQ 6
DB  1 PPPPQ 5

RESULT 25
ABR28254
ID  ABR28254 standard; Peptide; 9 AA.
XX
AC  ABR28254;
XX
DT  19-MAY-2003 (first entry)
XX
DE  Human cancer-related protein 187P3F2 HLA peptide #1089.
XX
KW  Human; cytostatic; vaccine; cancer; immune response; HLA;
XX  human leukocyte antigen.
XX

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XX
OS  Homo sapiens.
XX
PN  WO200283921-A2.
XX
PD  24-OCT-2002.
XX
PF  10-APR-2002; 2002WO-US11654.
XX
PR  10-APR-2001; 2001US-282739P.
XX  10-APR-2001; 2001US-283112P.
PR  25-APR-2001; 2001US-286630P.
XX
PA  (AGEN-) AGENSYS INC.
XX
PI  Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX  Morrison K, Morrison RK, Raitano AB;
XX
XX  WPI; 2003-075555/07.
XX
XX  New composition comprising a substance that modulates the structure of
XX  proteins and polynucleotides, useful for therapeutic, prognostic and
XX  diagnostic reagents for eliciting cellular or humoral immune response
XX  in cancer patients.
XX
PS  Claim 13; Page 413; 1021pp; English.
XX
XX  The present invention relates to novel human cancer-related genes and
XX  proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX  proteins are useful for eliciting a humoral or cellular immune response.
XX  The genes are useful as probes and primers for the amplification and/or
XX  detection of genes, mRNAs or their fragments, as reagents for the
XX  diagnosis and/or prognosis of cancer, as coding sequences capable of
XX  directing the expression of the protein, as tools for modulating or
XX  inhibiting the expression of genes and/or translation of transcripts, and
XX  as therapeutic agents. The proteins and peptides are useful as
XX  therapeutic, prognostic and diagnostic reagents for cancer. The present
XX  sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX  from the invention.
XX
PS  Sequence 9 AA;
XX
XX  Query Match 71.4%; Score 5; DB 24; Length 9;
XX  Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  2 PPPPQ 6
DB  4 PPPPQ 8

RESULT 26
ABR28357
ID  ABR28357 standard; Peptide; 9 AA.
XX
AC  ABR28357;
XX
DT  19-MAY-2003 (first entry)
XX
DE  Human cancer-related protein 187P3F2 HLA peptide #1192.
XX
KW  Human; cytostatic; vaccine; cancer; immune response; HLA;
XX  human leukocyte antigen.
XX
OS  Homo sapiens.
XX
PN  WO200283921-A2.
XX
PD  24-OCT-2002.
XX
PR  10-APR-2002; 2002WO-US11654.
XX
PR  10-APR-2001; 2001US-282739P.
XX

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CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC diagnostic and prognostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention.

SQ Sequence 9 AA;  
Query Match 71.4%; Score 5; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPQS 7  
Db 3 PPPQS 7

RESULT 29  
ABR28437  
ID ABR28437 standard; Peptide; 9 AA.

AC ABR28437;  
XX  
DT 19-MAY-2003 (first entry)  
DE Human cancer-related protein 187P3F2 HLA peptide #1272.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX Homo sapiens.  
XX WO200283921-A2.

XX 24-OCT-2002.  
XX 10-APR-2002; 2002WO-US11654.  
XX 10-APR-2001; 2001US-282739P.  
XX 10-APR-2001; 2001US-283112P.  
XX 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.  
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response  
XX in cancer patients

XX Claim 13; Page 415; 1021pp; English.  
XX The present invention relates to novel human cancer-related genes and  
XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
XX proteins are useful for eliciting a humoral or cellular immune response.

XX The genes are useful as probes and primers for the amplification and/or  
XX detection of genes, mRNAs or their fragments, as reagents for the  
XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
XX directing the expression of the protein, as tools for modulating or  
XX inhibiting the expression of genes and/or translation of transcripts, and  
XX as therapeutic agents. The proteins and peptides are useful as  
XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.

SQ Sequence 9 AA;  
Query Match 71.4%; Score 5; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPQ 6  
Db 1 PPPQ 5

RESULT 30  
ABR27268  
ID ABR27268 standard; Peptide; 10 AA.

XX ABR27268;  
XX 19-MAY-2003 (first entry)  
XX Human cancer-related protein 187P3F2 HLA peptide #103.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX Homo sapiens.  
XX WO200283921-A2.

XX 24-OCT-2002.  
XX 10-APR-2002; 2002WO-US11654.  
XX 10-APR-2001; 2001US-282739P.  
XX 10-APR-2001; 2001US-283112P.  
XX 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.  
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response  
XX in cancer patients

XX Claim 13; Page 402; 1021pp; English.  
XX The present invention relates to novel human cancer-related genes and  
XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
XX proteins are useful for eliciting a humoral or cellular immune response.

XX The genes are useful as probes and primers for the amplification and/or  
XX detection of genes, mRNAs or their fragments, as reagents for the  
XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
XX directing the expression of the protein, as tools for modulating or  
XX inhibiting the expression of genes and/or translation of transcripts, and  
XX as therapeutic agents. The proteins and peptides are useful as  
XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.

SQ Sequence 10 AA;  
Query Match 71.4%; Score 5; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPQS 7  
Db 3 PPPQS 7



RESULT 31  
 ABR27308  
 ID ABR27308 standard; Peptide; 10 AA.  
 XX AC ABR27308;  
 XX DT 19-MAY-2003 (first entry)  
 XX DE Human cancer-related protein 187P3F2 HLA peptide #143.  
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 10-APR-2001; 2001US-283112P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 XX PI Morrison K, Morrison RK, Raitano AB;  
 XX DR WPI; 2003-075555/07.  
 XX PT New composition comprising a substance that modulates the structure of  
 XX PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 XX PT diagnostic reagents for eliciting cellular or humoral immune response  
 XX PT in cancer patients -  
 XX PS Claim 13; Page 402; 1021pp; English.  
 XX CC The present invention relates to novel human cancer-related genes and  
 XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 XX CC proteins are useful for eliciting a humoral or cellular immune response.  
 XX CC The genes are useful as probes and primers for the amplification and/or  
 XX CC detection of genes, mRNAs or their fragments, as reagents for the  
 XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 XX CC directing the expression of the protein, as tools for modulating or  
 XX CC inhibiting the expression of cancer, as coding sequences capable of  
 XX CC as therapeutic agents. The proteins and peptides are useful as  
 XX CC diagnostic, prognostic and diagnostic reagents for cancer. The present  
 XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 XX CC from the invention.  
 XX SQ Sequence 10 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPPQS 7  
 DB 2 PPPQS 6  
 RESULT 32  
 ABR27336  
 ID ABR27336 standard; Peptide; 10 AA.  
 XX AC ABR27336;  
 XX DT 19-MAY-2003 (first entry)  
 XX DE Human cancer-related protein 187P3F2 HLA peptide #171.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX Homo sapiens.  
 XX WO200283921-A2.  
 XX 24-OCT-2002.  
 XX 10-APR-2002; 2002WO-US11654.  
 XX 10-APR-2001; 2001US-282739P.  
 XX 10-APR-2001; 2001US-283112P.  
 XX 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 XX PI Morrison K, Morrison RK, Raitano AB;  
 XX DR WPI; 2003-075555/07.  
 XX PT New composition comprising a substance that modulates the structure of  
 XX PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 XX PT diagnostic reagents for eliciting cellular or humoral immune response  
 XX PT in cancer patients -  
 XX PS Claim 13; Page 402; 1021pp; English.  
 XX CC The present invention relates to novel human cancer-related genes and  
 XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 XX CC proteins are useful for eliciting a humoral or cellular immune response.  
 XX CC The genes are useful as probes and primers for the amplification and/or  
 XX CC detection of genes, mRNAs or their fragments, as reagents for the  
 XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 XX CC directing the expression of the protein, as tools for modulating or  
 XX CC inhibiting the expression of cancer, as coding sequences capable of  
 XX CC as therapeutic agents. The proteins and peptides are useful as  
 XX CC diagnostic, prognostic and diagnostic reagents for cancer. The present  
 XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 XX CC from the invention.  
 XX SQ Sequence 10 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPPPQ 6  
 DB 1 PPPPQ 5  
 RESULT 33  
 ABR27487  
 ID ABR27487 standard; Peptide; 10 AA.  
 XX AC ABR27487;  
 XX DT 19-MAY-2003 (first entry)  
 XX DE Human cancer-related protein 187P3F2 HLA peptide #322.  
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.

PF 10-APR-2002; 2002WO-US11654.  
XX 10-APR-2001; 2001US-282739P.  
PR 10-APR-2001; 2001US-283112P.  
PR 25-APR-2001; 2001US-286630P.  
XX (AGEN-) AGENSYS INC.  
PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX WPI; 2003-075555/07.  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response  
XX in cancer patients -  
XX Claim 13; Page 404; 1021pp; English.  
XX The present invention relates to novel human cancer-related genes and  
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
XX proteins are useful for eliciting a humoral or cellular immune response.  
XX The genes are useful as probes and primers for the amplification and/or  
XX detection of genes, mRNAs or their fragments, as reagents for the  
XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
XX directing the expression of the protein, as tools for modulating or  
XX inhibiting the expression of genes and/or translation of transcripts, and  
XX as therapeutic agents. The proteins and peptides are useful as  
XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.  
XX Sequence 10 AA;  
XX Query Match 71.4%; Score 5; DB 24; Length 10;  
XX Best Local Similarity 100.0%; Pred. No. 35;  
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 PPSQS 7  
Db 4 PPSQS 8  
RESULT 34  
ABR27537  
ID ABR27537 standard; Peptide; 10 AA.  
XX ABR27537;  
AC 19-MAY-2003 (first entry)  
XX Human cancer-related protein 187P3F2 HLA peptide #372.  
DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX human leukocyte antigen.  
KW Homo sapiens.  
XX WO200283921-A2.  
PN 24-OCT-2002.  
XX 10-APR-2002; 2002WO-US11654.  
PF 10-APR-2001; 2001US-282739P.  
PR 10-APR-2001; 2001US-283112P.  
PR 25-APR-2001; 2001US-286630P.  
XX (AGEN-) AGENSYS INC.  
PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX WPI; 2003-075555/07.  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response  
XX in cancer patients -  
XX Claim 13; Page 406; 1021pp; English.

XX WPI; 2003-075555/07.  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response  
XX in cancer patients -  
XX Claim 13; Page 405; 1021pp; English.  
XX The present invention relates to novel human cancer-related genes and  
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
XX proteins are useful for eliciting a humoral or cellular immune response.  
XX The genes are useful as probes and primers for the amplification and/or  
XX detection of genes, mRNAs or their fragments, as reagents for the  
XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
XX directing the expression of the protein, as tools for modulating or  
XX inhibiting the expression of genes and/or translation of transcripts, and  
XX as therapeutic agents. The proteins and peptides are useful as  
XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.  
XX Sequence 10 AA;  
XX Query Match 71.4%; Score 5; DB 24; Length 10;  
XX Best Local Similarity 100.0%; Pred. No. 35;  
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 PPSQS 7  
Db 5 PPSQS 9  
RESULT 35  
ABR27692  
ID ABR27692 standard; Peptide; 10 AA.  
XX ABR27692;  
AC 19-MAY-2003 (first entry)  
XX Human cancer-related protein 187P3F2 HLA peptide #527.  
DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX human leukocyte antigen.  
KW Homo sapiens.  
XX WO200283921-A2.  
PN 24-OCT-2002.  
XX 10-APR-2002; 2002WO-US11654.  
PF 10-APR-2001; 2001US-282739P.  
PR 10-APR-2001; 2001US-283112P.  
PR 25-APR-2001; 2001US-286630P.  
XX (AGEN-) AGENSYS INC.  
PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX WPI; 2003-075555/07.  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response  
XX in cancer patients -  
XX Claim 13; Page 406; 1021pp; English.

The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ79168 and ABZ01789-ABZ01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

SQ Sequence 10 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 36	
ABR27707	
ID	ABR27707 standard; Peptide; 10 AA.
XX	
XX	ABR27707;
XX	
XX	
XX	19-MAY-2003 (first entry)
XX	
DE	Human cancer-related protein 187pF2 HLA peptide #542.
XX	
XX	Human; cytostatic; vaccine; cancer; immune response; HLA;
KW	human leukocyte antigen.
KW	

PI Jakobovits A, Chāllita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;

WPI: 2003-075555/07

New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients -

PS Claim 13: Page 407: 1021pp: English.

The present invention relates to novel human cancer-related genes and proteins (AB278120-AB278168 and AB2801789-AB2801861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention.

SQ Sequence 10 AA; Query Match 71.4%; Score 5; DB 24; Length 10; Best Local Similarity 100.0%; Pred. No. 35; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 37  
ABR27737  
ID ABR27737 standard; Peptide; 10 AA.

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;

XX  
DR WPI: 2003-075555/07.

AA New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response  
PT in cancer patients -

PS Claim 13; Page 407; 1021pp; English.

The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, or as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

XX	Sequence	10 AA;
SQ		

Wed Nov 26 09:06:42 2003

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Db      1 PPPPQ 5
      |||||
RESULT 38
ABR27891
ID ABR27891 standard; Peptide; 10 AA.
XX
AC ABR27891;
XX
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 187P3F2 HLA peptide #726.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
OS Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
XX
XX 10-APR-2001; 2001US-283112P.
XX
XX 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients -
XX
XX Claim 13; Page 409; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
XX Sequence 10 AA;
XX
XX Query Match 71.4%; Score 5; DB 24; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 35;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 3 PPPPQ 7
XX |||||
XX Db 4 PPPPQ 8
XX
XX RESULT 40
XX ABR27913
XX ID ABR27913 standard; Peptide; 10 AA.
XX
XX AC ABR27913;
XX
XX DT 19-MAY-2003 (first entry)
XX
XX DE Human cancer-related protein 187P3F2 HLA peptide #748.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX OS Homo sapiens.
XX
XX WO200283921-A2.
XX
XX PN

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XX PD 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 10-APR-2001; 2001US-283112P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX PS Claim 13; Page 409; 1021pp; English.  
 XX CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX SQ Sequence 10 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPPQS 7  
 Db |||||  
 3 PPPQS 7  
 RESULT 41  
 ABR28074  
 ID ABR28074 standard; Peptide; 10 AA.  
 XX AC ABR28074;  
 XX DT 19-MAY-2003 (first entry)  
 XX DE Human cancer-related protein 187P3F2 HLA peptide #909.  
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 10-APR-2001; 2001US-283112P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX PS Claim 13; Page 411; 1021pp; English.  
 XX CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX SQ Sequence 10 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPPQS 7  
 Db |||||  
 4 PPPQS 8  
 RESULT 42  
 ABR28076  
 ID ABR28076 standard; Peptide; 10 AA.  
 XX AC ABR28076;  
 XX DT 19-MAY-2003 (first entry)  
 XX DE Human cancer-related protein 187P3F2 HLA peptide #911.  
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 10-APR-2001; 2001US-283112P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 PT

XX Claim 13; Page 411; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

XX Sequence 10 AA;

Query Match 71.4%; Score 5; DB 24; Length 10;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPQS 7

DB 5 PPPQS 9

RESULT 43

ABR28145

ID ABR28145 standard; Peptide; 10 AA.

XX ABR28145;

AC ABR28145;

XX 19-MAY-2003 (first entry)

DT Human cancer-related protein 187P3F2 HLA peptide #980.

DE Human; cytostatic; vaccine; cancer; immune response; HLA;

XX Human leukocyte antigen.

KW Homo sapiens.

OS WO200283921-A2.

XX 24-OCT-2002.

PD 10-APR-2001; 2001US-282739P.

PF 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

PA Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

XX Claim 13; Page 412; 1021pp; English.

PS The present invention relates to novel human cancer-related genes and proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

XX Sequence 10 AA;

Query Match 71.4%; Score 5; DB 24; Length 10;

Best Local Similarity 100.0%; Pred. No. 35;

CC inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

CC Sequence 10 AA;

Query Match 71.4%; Score 5; DB 24; Length 10;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPQS 7

DB 2 PPPQS 6

RESULT 44

ABR28150

ID ABR28150 standard; Peptide; 10 AA.

XX ABR28150;

AC ABR28150;

XX 19-MAY-2003 (first entry)

DT Human cancer-related protein 187P3F2 HLA peptide #985.

DE Human; cytostatic; vaccine; cancer; immune response; HLA;

XX Human leukocyte antigen.

KW Homo sapiens.

OS WO200283921-A2.

XX 24-OCT-2002.

PD 10-APR-2001; 2001US-282739P.

PF 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

PA Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

XX Claim 13; Page 412; 1021pp; English.

PS The present invention relates to novel human cancer-related genes and proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

XX Sequence 10 AA;

Query Match 71.4%; Score 5; DB 24; Length 10;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPQS 7  
|||||  
Db 3 PPPQS 7

## RESULT 45

ABR28280  
ID ABR28280 standard; Peptide; 10 AA.

XX ABR28280;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 187P3F2 HLA peptide #1115.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX Homo sapiens.

OS WO200283921-A2.

PN 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

PR 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

DR New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prognostic and

PT diagnostic reagents for eliciting cellular or humoral immune response

PT in cancer patients

XX Claim 13; Page 413; 1021pp; English.

PS The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.

XX Sequence 10 AA;

Query Match 71.4%; Score 5; DB 24; Length 10;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPQS 7

|||||

Db 4 PPPQS 8

## RESULT 46

ABR28281  
ID ABR28281 standard; Peptide; 10 AA.

XX

AC ABR28281;

XX 19-MAY-2003 (first entry)

DT Human cancer-related protein 187P3F2 HLA peptide #1116.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX Homo sapiens.

OS WO200283921-A2.

PN 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

DR New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prognostic and

PT diagnostic reagents for eliciting cellular or humoral immune response

PT in cancer patients

XX Claim 13; Page 413; 1021pp; English.

PS The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention.

XX Sequence 10 AA;

Query Match 71.4%; Score 5; DB 24; Length 10;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPQS 7

|||||

Db 5 PPPQS 9

## RESULT 47

ABR28332  
ID ABR28332 standard; Peptide; 10 AA.

XX ABR28332;

XX 19-MAY-2003 (first entry)

DT Human cancer-related protein 187P3F2 HLA peptide #1167.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX





PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response  
PS in cancer patients  
PS Claim 13; Page 414; 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and  
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.  
XX  
SQ Sequence 10 AA;  
Query Match 71.4%; Score 5; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PPPPQ 6  
DB 4 PPPPQ 8  
RESULT 50  
ABR28479  
ID ABR28479 standard; Peptide; 10 AA.  
XX  
AC ABR28479;  
XX  
DT 19-MAY-2003 (first entry)  
DE Human cancer-related protein 187P3P2 HLA peptide #1314.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
PR 10-APR-2001; 2001US-283112P.  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response  
PT in cancer patients  
XX  
XX Claim 13; Page 416; 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and  
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.  
XX  
SQ Sequence 10 AA;  
Query Match 71.4%; Score 5; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PPPQS 7  
DB 3 PPPQS 7  
RESULT 51  
ABR28486  
ID ABR28486 standard; Peptide; 10 AA.  
XX  
AC ABR28486;  
XX  
DT 19-MAY-2003 (first entry)  
DE Human cancer-related protein 187P3P2 HLA peptide #1321.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
PR 10-APR-2001; 2001US-283112P.  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response  
PT in cancer patients  
XX  
XX Claim 13; Page 416; 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and  
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.  
XX  
SQ Sequence 10 AA;

Wed Nov 26 09:06:42 2003

RESULT 53

ABR28513  
ID ABR28513 standard; Peptide; 10 AA.  
XX  
AC ABR28513;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1348.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX  
OS human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
XX  
PR 10-APR-2001; 2001US-283112P.  
XX  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS New composition comprising a substance that modulates the structure of  
XX  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
XX  
PT diagnostic reagents for eliciting cellular or humoral immune response  
XX  
PT in cancer patients  
XX  
PS Claim 13; Page 416; 1021pp; English.

RESULT 54

ABR28537  
ID ABR28537 standard; Peptide; 10 AA.  
XX  
AC ABR28537;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1372.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX  
OS human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
XX  
PR 10-APR-2001; 2001US-283112P.  
XX  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS New composition comprising a substance that modulates the structure of  
XX  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
XX  
PT diagnostic reagents for eliciting cellular or humoral immune response  
XX  
PT in cancer patients  
XX  
PS Claim 13; Page 416; 1021pp; English.

RESULT 55

ABR28513  
ID ABR28513 standard; Peptide; 10 AA.  
XX  
AC ABR28513;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1348.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX  
OS human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
XX  
PR 10-APR-2001; 2001US-283112P.  
XX  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS New composition comprising a substance that modulates the structure of  
XX  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
XX  
PT diagnostic reagents for eliciting cellular or humoral immune response  
XX  
PT in cancer patients  
XX  
PS Claim 13; Page 416; 1021pp; English.

RESULT 56

ABR28537  
ID ABR28537 standard; Peptide; 10 AA.  
XX  
AC ABR28537;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1372.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX  
OS human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
XX  
PR 10-APR-2001; 2001US-283112P.  
XX  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS New composition comprising a substance that modulates the structure of  
XX  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
XX  
PT diagnostic reagents for eliciting cellular or humoral immune response  
XX  
PT in cancer patients  
XX  
PS Claim 13; Page 416; 1021pp; English.

RESULT 57

ABR28513  
ID ABR28513 standard; Peptide; 10 AA.  
XX  
AC ABR28513;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1348.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX  
OS human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
XX  
PR 10-APR-2001; 2001US-283112P.  
XX  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS New composition comprising a substance that modulates the structure of  
XX  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
XX  
PT diagnostic reagents for eliciting cellular or humoral immune response  
XX  
PT in cancer patients  
XX  
PS Claim 13; Page 416; 1021pp; English.

RESULT 58

ABR28537  
ID ABR28537 standard; Peptide; 10 AA.  
XX  
AC ABR28537;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1372.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX  
OS human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
XX  
PR 10-APR-2001; 2001US-283112P.  
XX  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS New composition comprising a substance that modulates the structure of  
XX  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
XX  
PT diagnostic reagents for eliciting cellular or humoral immune response  
XX  
PT in cancer patients  
XX  
PS Claim 13; Page 416; 1021pp; English.

Query Match 71.4%; Score 5; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPSQS 7  
Db 2 PPSQS 6

RESULT 52

ABR28502  
ID ABR28502 standard; Peptide; 10 AA.  
XX  
AC ABR28502;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1337.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX  
OS human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
XX  
PR 10-APR-2001; 2001US-283112P.  
XX  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS New composition comprising a substance that modulates the structure of  
XX  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
XX  
PT diagnostic reagents for eliciting cellular or humoral immune response  
XX  
PT in cancer patients  
XX  
PS Claim 13; Page 416; 1021pp; English.

RESULT 51

ABR28513  
ID ABR28513 standard; Peptide; 10 AA.  
XX  
AC ABR28513;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1348.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX  
OS human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
XX  
PR 10-APR-2001; 2001US-283112P.  
XX  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS New composition comprising a substance that modulates the structure of  
XX  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
XX  
PT diagnostic reagents for eliciting cellular or humoral immune response  
XX  
PT in cancer patients  
XX  
PS Claim 13; Page 416; 1021pp; English.

The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

Query Match

Best Local Similarity 71.4%; Score 5; DB 24; Length 10;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPSQS 7  
Db 4 PPSQS 8

RESULT 53

ABR28537  
ID ABR28537 standard; Peptide; 10 AA.  
XX  
AC ABR28537;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1372.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX  
OS human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
XX  
PR 10-APR-2001; 2001US-283112P.  
XX  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS New composition comprising a substance that modulates the structure of  
XX  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
XX  
PT diagnostic reagents for eliciting cellular or humoral immune response  
XX  
PT in cancer patients  
XX  
PS Claim 13; Page 416; 1021pp; English.

Query Match

Best Local Similarity 71.4%; Score 5; DB 24; Length 10;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPSQS 7  
Db 5 PPSQS 9

RESULT 54

ABR28537  
ID ABR28537 standard; Peptide; 10 AA.  
XX  
AC ABR28537;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 187P3F2 HLA peptide #1372.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX  
OS human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
XX  
PR 10-APR-2001; 2001US-283112P.  
XX  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS New composition comprising a substance that modulates the structure of  
XX  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
XX  
PT diagnostic reagents for eliciting cellular or humoral immune response  
XX  
PT in cancer patients  
XX  
PS Claim 13; Page 416; 1021pp; English.

Query Match

Best Local Similarity 71.4%; Score 5; DB 24; Length 10;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPSQS 7  
Db 5 PPSQS 9

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX Homo sapiens.  
 OS  
 XX WO200283921-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX  
 PF 10-APR-2002; 2002WO-US11654.  
 XX  
 XX 10-APR-2001; 2001US-282739P.  
 PR  
 XX 10-APR-2001; 2001US-283112P.  
 PR  
 XX 25-APR-2001; 2001US-286630P.  
 XX  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 XX WPI; 2003-075555/07.  
 DR  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 XX Claim 13; Page 416; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of the protein, as tools for translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 XX Sequence 10 AA;  
 SQ  
 Query Match 71.4%; Score 5; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPPPQ 6  
 DB |||||  
 2 PPPPQ 6  
 RESULT 55  
 AAB30652  
 ID AAB30652 standard; peptide; 13 AA.  
 XX  
 AC AAB30652;  
 XX  
 DT 19-MAR-2001 (first entry)  
 XX  
 DE Trypsin modulating oostatic factor (TMOF) pesticidal analogue.  
 XX  
 KW Hormone; trypsin modulating oostatic factor; TMOF; analogue; mosquito;  
 KW trypsin; trypsin-like enzyme; metabolic energy; insect pest; pesticide;  
 KW digestion; digestive enzyme; flesh fly; flea; sand fly; house fly;  
 KW dog fly; coleopteran; lepidopteran; dipteran; blood-sucking insect;  
 KW Diptera.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200062792-A2.  
 XX

PD 26-OCT-2000.  
 XX  
 PF 04-APR-2000; 2000WO-US08879.  
 XX  
 PR 21-APR-1999; 99US-0295924.  
 XX  
 XX (INSE-) INSECT BIOTECHNOLOGY INC.  
 PA (UYFL ) UNIV FLORIDA.  
 XX  
 XX Bennett J, Brandt A, Borovsky D;  
 PI  
 XX WPI; 2001-006951/01.  
 DR  
 XX New polypeptide is useful for preventing, reducing and eliminating  
 PT infestation of area by pests e.g. flesh flies or mosquito larvae.  
 PT optionally in combination with e.g. repellent, attractant, acaricide,  
 PT fungicide or herbicide -  
 XX  
 XX Example; Page 49; 87pp; English.  
 PS  
 XX The present sequence represents an analogue of a peptide hormone named  
 CC trypsin modulating oostatic factor (TMOF). Mosquitoes regulate trypsin  
 CC and trypsin-like enzymes with this hormone to conserve metabolic  
 CC energy. Other insect pests use it for the same purpose. The peptide  
 CC functions as a pesticidal compound, which inhibits digestion in pests by  
 CC inhibiting synthesis of pests digestive enzymes. The pesticidal  
 CC compound is useful for preventing, reducing or eliminating infestation  
 CC of geographical areas by an insect population such as flesh flies, fleas,  
 CC sand flies, house flies and dog flies. The pesticidal compound is applied  
 CC to pest inhabited loci of the geographical area such as the body of  
 CC water inhabited by mosquito larvae, or insects such as coleopterans,  
 CC lepidopterans, dipterans or blood-sucking insects of order Diptera,  
 CC suborder Nematocera, family Colicidae or subfamily Culicinae,  
 CC Corethrinae, Ceratopogonidae and Simuliidae.  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 71.4%; Score 5; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 D PPPP 5  
 DB |||||  
 2 D PPPP 6  
 RESULT 56  
 AAR42641  
 ID AAR42641 standard; peptide; 15 AA.  
 XX  
 AC AAR42641;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 22-APR-1994 (first entry)  
 XX  
 DE N-terminal sequence of protein from BCG culture supernatant.  
 XX  
 KW Tuberculosis; delayed hypersensitivity; antigen; immunogen; vaccine;  
 KW T lymphocyte stimulation; BCG.  
 XX  
 OS Mycobacterium tuberculosis BCG.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 4  
 FT /label= OTHER  
 FT /note= "defined only as modified amino acid"  
 FT Modified-site 6  
 FT /label= OTHER  
 FT /note= "defined only as modified amino acid"  
 FT Modified-site 12  
 FT /label= OTHER  
 FT /note= "defined only as modified amino acid"  
 FT Modified-site 14

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PT Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX  
 XX  
 PS Claim 22; Page 94; 131pp; English.  
 XX  
 CC The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
 CC domain of Crk; (h) peptides which bind the SH3 domain of Grb2. The purified  
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.  
 XX  
 XX Sequence 15 AA;  
 SQ Query Match 71.4%; Score 5; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPPPQ 6  
 DB |||||  
 6 PPPPQ 10  
 RESULT 58  
 AAW39006  
 ID AAW39006 standard; peptide; 15 AA.  
 XX  
 XX AAW39006;  
 AC  
 XX 27-MAR-1998 (first entry)  
 DT Peptide resembling an SH3 domain binding peptide SEQ ID NO:405.  
 DE  
 DE  
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9730074-A1.  
 PN  
 XX 21-AUG-1997.  
 PD  
 XX 14-FEB-1997; 97WO-US02298.  
 PF  
 XX 16-FEB-1996; 96US-0602999.  
 PR  
 XX (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 XX Sparks AB, Thorn JM;  
 PI  
 XX WPI; 1997-424972/39.  
 DR  
 XX Src homology region 3 binding peptide - used to activate Src  
 XX tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 PT  
 XX Claim 22; Page 93; 131pp; English.  
 PS

PT /label= OTHER  
 PT /notes "defined only as modified amino acid"  
 XX  
 XX WO9319093-A1.  
 PN  
 XX 30-SEP-1993.  
 PD  
 XX 17-MAR-1993; 93WO-FR00268.  
 PF  
 XX 19-MAR-1992; 92FR-0003286.  
 PR  
 XX (INSP ) INST PASTEUR.  
 PA  
 XX Marchal G, Romain F;  
 PI  
 XX WPI; 1993-320686/40.  
 DR  
 XX New peptide inducing intense delayed hypersensitivity reactions -  
 XX in presence of live, but not dead, Mycobacterium tuberculosis,  
 PT useful diagnostically and in therapeutic immunogens  
 PT  
 XX Claim 2; Page 17; 31pp; French.  
 PS  
 XX A peptide which can initiate delayed hypersensitivity reactions of  
 CC different intensity in the presence of live or dead Mycobacterium  
 CC tuberculosis complex bacteria is isolated from supernatant of BCG  
 CC cell culture. The N-terminal sequence of the peptide has been  
 CC determined.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX Sequence 15 AA;  
 SQ Query Match 71.4%; Score 5; DB 14; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PPPPQ 6  
 DB |||||  
 7 PPPPQ 11  
 RESULT 57  
 AAW39038  
 ID AAW39038 standard; peptide; 15 AA.  
 XX  
 XX AAW39038;  
 AC  
 XX 27-MAR-1998 (first entry)  
 DT Peptide resembling an SH3 domain binding peptide SEQ ID NO:439.  
 DE  
 DE  
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9730074-A1.  
 PN  
 XX 21-AUG-1997.  
 PD  
 XX 14-FEB-1997; 97WO-US02298.  
 PF  
 XX 16-FEB-1996; 96US-0602999.  
 PR  
 XX (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 XX Sparks AB, Thorn JM;  
 PI  
 XX WPI; 1997-424972/39.  
 DR  
 XX

XX The present sequence represents a peptide which resembles a Src homology region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i) peptides which bind the amino-terminal SH3 domain of Grb2. The purified binding peptides can be used in the method to identify inhibitors of Src or Src-related protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. tumour necrosis factor-alpha and interleukin-1, or to deliver a conjugated molecule to certain cellular compartments containing Src or Src related proteins.

XX Sequence 15 AA;  
 Query Match 71.4%; Score 5; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
 DB 6 PPPPQ 10  
 |||||

RESULT 59  
 AAW38970  
 ID AAW38970 standard; peptide; 15 AA.  
 XX AC AAW38970;  
 XX DT 27-MAR-1998 (first entry)  
 XX DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:367.  
 XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX OS Synthetic.  
 XX PN WO9730074-A1.  
 XX PD 21-AUG-1997.  
 XX PF 14-FEB-1997; 97WO-US02298.  
 XX PR 16-FEB-1996; 96US-0602999.  
 XX PA (CYTO-) CYTOGEN CORP.  
 XX PA (UYNC-) UNIV NORTH CAROLINA.  
 XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JM;  
 XX WPI; 1997-424972/39.  
 XX Src homology region 3 binding peptide - used to activate Src tyrosine kinase(s) and to stimulate immune response by increasing production of certain lymphokine(s), e.g. interleukin-1  
 XX Claim 22; Page 92; 131pp; English.  
 XX The present sequence represents a peptide which resembles a Src homology region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i) peptides which bind the amino-terminal SH3 domain of Grb2. The purified binding peptides can be used in the method to identify inhibitors of Src or Src-related protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. tumour necrosis factor-alpha and interleukin-1, or to deliver a conjugated molecule to certain cellular compartments containing Src or Src related proteins.

CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i) peptides which bind the amino-terminal SH3 domain of Grb2. The purified binding peptides can be used in the method to identify inhibitors of Src or Src-related protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. tumour necrosis factor-alpha and interleukin-1, or to deliver a conjugated molecule to certain cellular compartments containing Src or Src related proteins.

XX Sequence 15 AA;  
 Query Match 71.4%; Score 5; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
 DB 9 PPPPQ 13  
 |||||

RESULT 60  
 AAW38976  
 ID AAW38976 standard; peptide; 15 AA.  
 XX AC AAW38976;  
 XX DT 27-MAR-1998 (first entry)  
 XX DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:373.  
 XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX OS Synthetic.  
 XX PN WO9730074-A1.  
 XX PD 21-AUG-1997.  
 XX PF 14-FEB-1997; 97WO-US02298.  
 XX PR 16-FEB-1996; 96US-0602999.  
 XX PA (CYTO-) CYTOGEN CORP.  
 XX PA (UYNC-) UNIV NORTH CAROLINA.  
 XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JM;  
 XX WPI; 1997-424972/39.  
 XX Src homology region 3 binding peptide - used to activate Src tyrosine kinase(s) and to stimulate immune response by increasing production of certain lymphokine(s), e.g. interleukin-1  
 XX Claim 22; Page 92; 131pp; English.  
 XX The present sequence represents a peptide which resembles a Src homology region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i) peptides which bind the amino-terminal SH3 domain of Grb2. The purified binding peptides can be used in the method to identify inhibitors of Src or Src-related protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. tumour necrosis factor-alpha and interleukin-1, or to deliver a conjugated molecule to certain cellular compartments containing Src or Src related proteins.

CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

XX Sequence 15 AA;  
 SQ Query Match 71.4%; Score 5; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
 DB 6 PPPPQ 10  
 |||||

RESULT 61  
 AAW38942  
 ID AAW38942 standard; peptide; 15 AA.  
 XX  
 AC AAW38942;  
 XX  
 DT 27-MAR-1998 (first entry)  
 XX  
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:339.  
 XX  
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9730074-A1.  
 XX  
 PD 21-AUG-1997.  
 XX  
 PF 14-FEB-1997; 97WO-US02298.  
 XX  
 PR 16-FEB-1996; 96US-0602999.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JB;  
 PI Sparks AB, Thorn JM;  
 XX  
 WPI; 1997-424972/39.  
 XX  
 SR Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX  
 PS Claim 22; Page 91; 131pp; English.  
 XX  
 XX The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the SH3 domain of Grb2. The purified  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune

CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

XX Sequence 15 AA;  
 SQ Query Match 71.4%; Score 5; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
 DB 6 PPPPQ 10  
 |||||

RESULT 62  
 AAW38952  
 ID AAW38952 standard; peptide; 15 AA.  
 XX  
 AC AAW38952;  
 XX  
 DT 27-MAR-1998 (first entry)  
 XX  
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:349.  
 XX  
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9730074-A1.  
 XX  
 PD 21-AUG-1997.  
 XX  
 PF 14-FEB-1997; 97WO-US02298.  
 XX  
 PR 16-FEB-1996; 96US-0602999.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JB;  
 PI Sparks AB, Thorn JM;  
 XX  
 WPI; 1997-424972/39.  
 XX  
 SR Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX  
 PS Claim 22; Page 91; 131pp; English.  
 XX  
 XX The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the SH3 domain of Grb2. The purified  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

```

SQ Sequence 15 AA;
Query Match 71.4%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPPQ 6
Db 6 PPPPQ 10

RESULT 63
AAW45819
ID AAW45819 standard; peptide; 15 AA.
XX AC AAW45819;
XX XX
DT 25-JUN-1998 (first entry)
XX XX
DE Peptide recognised by anti HSV-2 glycoprotein G (gG) antibody E5.
XX XX
KW Glycoprotein G; herpes simplex virus type 2; HSV-2 gG; anti-gG2;
XX HSV-2 infection; vaccine; diagnosis.
XX OS Synthetic.
XX XX
XX WO9803544-A1.
XX XX
XX 29-JAN-1998.
XX XX
XX 24-JUL-1997; 97WO-GB02003.
XX XX
XX 24-JUL-1996; 96GB-0015533.
XX XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Grabowska AM, Irving WL, Laing P;
XX WPI; 1998-120696/11.
XX DR
XX PT Polypeptide antigen of Herpes simplex virus 2 glycoprotein G - used
XX to create antibodies for treating HSV-2 infection
XX PS Disclosure; Page 36; 63pp; English.
XX CC This sequence is shown in the specification. The invention relates to a
XX novel polypeptide which comprises 3-20 amino acids, or a peptidomimetic
XX analogue of it where the analogue is at least partly non-peptide in
XX nature and the analogue has a length equivalent to that determined by
XX 3-20 amino acid residues, which is a sequence not naturally occurring in
XX the native sequence of the Herpes simplex virus glycoprotein G (HSV-2 gG
XX protein), and has one of the following sequences: (X)n- alpha - beta -
XX gamma - (Y)m (I); or (X)n- delta - epsilon - theta - (Y)m (II); n = 0 or an
XX integer; m = 0 or an integer; n+m at most 17; alpha is E or may be
XX substituted in order of preference by D greater than T greater than S
XX greater than Q greater than N; beta is H; gamma is R or may be
XX substituted in order of preference by R greater than A or L greater than
XX T or P; epsilon is P; theta is L or may be substituted in order of
XX preference by B or Y; and X or Y are positively charged, negatively
XX charged or neutral amino acids or peptidomimetics thereof. The
XX polypeptide can be used in vaccine compositions, which can be used to
XX prevent HSV-2 infection. It can also be used to test for the presence
XX of type-specific HSV-2 gG2 antibodies in a fluid. This test can be used
XX to diagnose HSV-2 infection.
XX SQ Sequence 15 AA;

Query Match 71.4%; Score 5; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5
Db 6 PPPPQ 10

RESULT 64
AAW45614
ID AAW45614 standard; peptide; 15 AA.
XX AC AAW45614;
XX XX
DT 24-JUN-1998 (first entry)
XX XX
DE Peptide recognised by anti HSV-2 glycoprotein G (gG) antibody E5.
XX XX
KW Antigenic peptide; herpes simplex virus type 2; HSV-2; glycoprotein-G;
XX gG; vaccine; HSV-2 infection; diagnosis.
XX OS Synthetic.
XX XX
XX WO9803543-A1.
XX XX
XX 29-JAN-1998.
XX XX
XX 24-JUL-1997; 97WO-GB01990.
XX XX
XX 24-JUL-1996; 96GB-0015533.
XX XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Grabowska AM, Irving WL, Laing P;
XX WPI; 1998-120695/11.
XX DR
XX PT Polypeptide antigen of Herpes simplex virus 2 glycoprotein G - used
XX to create antibodies for treating HSV-2 infection
XX PS Disclosure; Page 32; 61pp; English.
XX CC Peptides AAW45608-15 represent antigenic peptides that are recognised
XX by antibodies against the herpes simplex virus type 2 (HSV-2)
XX glycoprotein-G (gG). They were isolated from a library of phage
XX containing random 15-mer peptide inserts that was screened with the
XX murine monoclonal antibody O1B90.E5 (E5). The peptides are not
XX recognised by anti-gG2 negative sera from patients with HSV-1 infection.
XX The specification describes a filamentous bacteriophage including
XX in a portion of its major coat protein sub-units multiple display of the
XX peptide (or its analogues). The peptides and the filamentous
XX bacteriophage can be used in vaccine compositions, which can be used to
XX prevent HSV-2 infection. The peptides and antibodies against them can be
XX used to test for the presence of type-specific HSV-2 gG2 antibodies in
XX a fluid. This test can be used to diagnose HSV-2 infection.
XX SQ Sequence 15 AA;

Query Match 71.4%; Score 5; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5
Db 5 DPPP 9

RESULT 65
AAW95144
ID AAW95144 standard; peptide; 15 AA.
XX AC AAW95144;
XX XX
DT 24-MAY-1999 (first entry)
XX XX
DE Phage peptide K5 binding to human IgG1 fragment.
XX XX
KW Modified phage library; screening; cell-surface associated protein;

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Wed Nov 26 09:06:42 2003

therapeutic; diagnostic; disease; ligand; drug; toxin; fractionation;  
noise elimination; bacteriophage.

Bacteriophage m13.

WO9906542-A1.

11-FEB-1999.

29-JUL-1998; 98WO-GB02269.

30-JUL-1997; 97GB-0016094.

(UNIU ) UNIV GLASGOW.

Allen JM, Laverty E;

WPI; 1999-153772/13.

Modified phage display library depleted in phage that react with  
native cellular proteins - provides reduced noise and higher  
signal-to-noise ratio when screened against cells transfected to  
express a specific heterologous protein, used to identify potential  
therapeutic and diagnostic agents

Example 1; Page 30; 49pp; English.

The invention relates to a modified phage library for use with a selected  
strain of cells that have been transformed to express a heterologous  
protein (I) in a screening procedure, to detect specific binding between  
individual phage and a recognition site on the heterologous protein. The  
modified library is produced as follows. The initial phage library is  
fractionated by contact with strain of cells that do not express (I) to  
bind any phage that bind to cellular proteins other than the (I). Bound  
and unbound phages are separated to produce the modified library.  
The library is depleted in components that bind to cell-surface associated (I),  
used to identify phage that bind to cell-surface associated (I),  
specifically receptors. Peptides identified by screening with the  
modified library are potentially useful as therapeutic and diagnostic  
agents, for diseases involving (I) or its ligands (including as carriers  
for delivering drugs, toxins or antibodies to cells), and their amino  
acid sequences can be used to design other agents for the same uses. The  
initial fractionation eliminates much of the noise caused by binding to  
other cell-surface proteins, and the use of transfected cells for  
screening (these express a far greater number of (I) than wild-type  
cells) improves the signal-to-noise ratio. The number of rounds of  
screening may thus be reduced.

Sequence 15 AA;

Query Match 71.4%; Score 5; DB 20; Length 15;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 PPPQS 7  
Db 8 PPPQS 12

RESULT 66

AAW95125  
ID AAW95125 standard; peptide; 15 AA.

XX AAW95125;

XX 24-MAY-1999 (first entry)

Peptide K5 expressed by a modified bacteriophage library.

Modified phage library; screening; cell-surface associated protein;  
therapeutic; diagnostic; disease; ligand; drug; toxin; fractionation;  
noise elimination; bacteriophage.

Bacteriophage m13.

WO9906542-A1.

11-FEB-1999.

29-JUL-1998; 98WO-GB02269.

30-JUL-1997; 97GB-0016094.

(UNIU ) UNIV GLASGOW.

Allen JM, Laverty E;

WPI; 1999-153772/13.

Modified phage display library depleted in phage that react with  
native cellular proteins - provides reduced noise and higher  
signal-to-noise ratio when screened against cells transfected to  
express a specific heterologous protein, used to identify potential  
therapeutic and diagnostic agents

Example 1; Page 29; 49pp; English.

The invention relates to a modified phage library for use with a selected  
strain of cells that have been transformed to express a heterologous  
protein (I) in a screening procedure, to detect specific binding between  
individual phage and a recognition site on the heterologous protein. The  
modified library is produced as follows. The initial phage library is  
fractionated by contact with strain of cells that do not express (I) to  
bind any phage that bind to cellular proteins other than the (I). Bound  
and unbound phages are separated to produce the modified library.  
The library is depleted in components that bind to cell-surface associated (I),  
used to identify phage that bind to cell-surface associated (I),  
specifically receptors. Peptides identified by screening with the  
modified library are potentially useful as therapeutic and diagnostic  
agents, for diseases involving (I) or its ligands (including as carriers  
for delivering drugs, toxins or antibodies to cells), and their amino  
acid sequences can be used to design other agents for the same uses. The  
initial fractionation eliminates much of the noise caused by binding to  
other cell-surface proteins, and the use of transfected cells for  
screening (these express a far greater number of (I) than wild-type  
cells) improves the signal-to-noise ratio. The number of rounds of  
screening may thus be reduced.

Sequence 15 AA;

Query Match 71.4%; Score 5; DB 20; Length 15;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 PPPQS 7  
Db 8 PPPQS 12

RESULT 67

AAAY93014  
ID AAAY93014 standard; peptide; 15 AA.

XX AAAY93014;

XX 08-NOV-2000 (first entry)

Transforming growth factor inhibitory peptide P60.

Hepatotropic; antagonist; transforming growth factor beta1;  
competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
extracellular matrix degradation inhibitor; minetope; cirrhosis.

Rattus sp.

WO200031135-A1.



```

XX PD 02-JUN-2000.
XX XX
XX PF 23-NOV-1999; 99WO-ES00375.
XX XX
XX PR 24-NOV-1998; 98ES-0002465.
XX XX
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX PI Borras Cuesta F;
XX DR WPI; 2000-411935/35.
XX XX
XX PT Peptides that antagonize binding of transforming growth factor betaf,
XX PT useful for treatment of liver disease, especially cirrhosis, are
XX PT partial sequences of the factor or its receptors -
XX XX
XX PS Disclosure; Page 27; 86pp; Spanish.
XX XX
XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor
XX CC in vivo which have partial amino acid sequences identical, or similar,
XX CC with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133
XX CC represent examples of the peptides of the invention. The peptides act
XX CC by competitive inhibition of the binding of TGF-b1 to its receptors,
XX CC e.g. they are inhibitors of stimulation of collagen synthesis in liver
XX CC cells and inhibitors of synthesis of proteolytic enzymes able to degrade
XX CC the extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of
XX CC liver disease, specifically cirrhosis.
XX XX
XX SQ Sequence 15 AA;
XX
XX Query Match 71.4%; Score 5; DB 21; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 47;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 PPPPQ 6
XX DB 10 PPPPQ 14
XX
XX RESULT 68
XX AAY93015
XX ID AAY93015 standard; peptide; 15 AA.
XX AC AAY93015;
XX XX
XX DT 08-NOV-2000 (first entry)
XX XX
XX DE Transforming growth factor inhibitory peptide P61.
XX XX
XX KW Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX XX
XX OS Rattus sp.
XX XX
XX PN WO200031135-A1.
XX XX
XX PD 02-JUN-2000.
XX XX
XX PF 23-NOV-1999; 99WO-ES00375.
XX XX
XX PR 24-NOV-1998; 98ES-0002465.
XX XX
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX XX
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX PI Borras Cuesta F;
XX DR WPI; 2000-411935/35.
XX
XX
XX PT Peptides that antagonize binding of transforming growth factor betaf,
XX PT useful for treatment of liver disease, especially cirrhosis, are
XX PT partial sequences of the factor or its receptors -
XX XX
XX PS Disclosure; Page 27; 86pp; Spanish.
XX XX
XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor
XX CC in vivo which have partial amino acid sequences identical, or similar,
XX CC with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133
XX CC represent examples of the peptides of the invention. The peptides act
XX CC by competitive inhibition of the binding of TGF-b1 to its receptors,
XX CC e.g. they are inhibitors of stimulation of collagen synthesis in liver
XX CC cells and inhibitors of synthesis of proteolytic enzymes able to degrade
XX CC the extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of
XX CC liver disease, specifically cirrhosis.
XX XX
XX SQ Sequence 15 AA;
XX
XX Query Match 71.4%; Score 5; DB 21; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 47;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 PPPPQ 6
XX DB 5 PPPPQ 9
XX
XX RESULT 69
XX AAB72252
XX ID AAB72252 standard; peptide; 15 AA.
XX AC AAB72252;
XX XX
XX DT 14-MAY-2001 (first entry)
XX XX
XX DE Colostinin derived cytokine inducing peptide SEQ ID 7.
XX XX
XX KW Colostinin; immune response; cytokine; blood cell proliferation;
XX KW central nervous system disorder; neurological disorder; mental disorder;
XX KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
XX KW neurosis; infection.
XX XX
XX OS Synthetic.
XX XX
XX PN WO200111937-A2.
XX XX
XX PD 22-FEB-2001.
XX XX
XX PF 17-AUG-2000; 200WO-US22818.
XX XX
XX PR 17-AUG-1999; 99US-0149311.
XX XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PA (REGE-) REGEN THERAPEUTICS PLC.
XX XX
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX XX
XX DR WPI; 2001-202804/20.
XX XX
XX PT Inducing a cytokine and modulating an immune response, useful for
XX PT treating central nervous system diseases and bacterial and viral
XX PT infections, comprises administering colostinin as an immunological
XX PT regulator -
XX XX
XX PS Claim 1; Page 34; 50pp; English.
XX XX
XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostinin,
XX CC a proline rich polypeptide aggregate contained in colostrum. The
XX CC peptides have immune response modulatory activity, and are capable of
XX CC inducing cytokines. Colostinin and its derived peptides are useful for

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Wed Nov 26 09:06:42 2003

CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.

XX SQ Sequence 15 AA;  
Query Match 71.4%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
Db 7 PPPPQ 11

RESULT 70  
AAB72506  
ID AAB72506 standard; Peptide; 15 AA.  
XX AC AAB72506;  
XX DT 09-MAY-2001 (first entry)  
XX DE Colostrinin peptide #7.  
XX KW Dermatological; oxidative stress regulator; colostrinin.  
XX OS Unidentified.  
XX PN WO200112650-A2.  
XX PD 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US222665.  
XX PR 17-AUG-1999; 99US-0149310.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PI Stanton GJ, Hughes TK, Boldogh I;  
XX PS WPI; 2001-218342/22.  
XX PT Modulating oxidative stress level in a cell, involves contacting the  
XX cell with an oxidative stress regulator selected from colostrinin, its  
XX constituent peptide, analog or their combinations -  
XX Claim 6; Page 25; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative  
XX stress level in a cell or a patient, comprising contacting the cell with,  
XX or administering to the patient, an oxidative stress regulator selected  
XX from colostrinin, or its constituent peptide (e.g. the present peptide),  
XX to change the level of an oxidising species in the cell. The method can  
XX be used to treat oxidative damage to skin, by decreasing or preventing an  
XX increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 15 AA;  
Query Match 71.4%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
Db 7 PPPPQ 11

RESULT 71

AAB72538  
ID AAB72538 standard; Peptide; 15 AA.  
XX AC AAB72538;  
XX DT 09-MAY-2001 (first entry)  
XX DE Colostrinin peptide #7.  
XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
XX colostrinum.  
XX OS Unidentified.  
XX PN WO200112651-A2.  
XX PD 22-FEB-2001.  
XX PF 17-AUG-2000; 2000WO-US22774.  
XX PR 17-AUG-1999; 99US-0149633.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PI Boldogh I;  
XX PS WPI; 2001-226545/23.  
XX CC Use of colostrinin, its constituent peptide or analog as a neural cell  
XX regulator, for promoting neural cell differentiation and treating  
XX damaged neural cells in a patient -  
XX Claim 6; Page 21; 35pp; English.

XX CC The present invention relates to a method for promoting neural cell  
XX differentiation and treating damaged neural cells, using colostrinin and  
XX colostrinin constituent peptides (e.g. the present peptide) as a neural  
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.

XX SQ Sequence 15 AA;  
Query Match 71.4%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
Db 7 PPPPQ 11

RESULT 72  
AAB59312  
ID AAB59312 standard; Peptide; 15 AA.  
XX AC AAB59312;  
XX DT 21-MAR-2001 (first entry)  
XX DE Ewe colostrinin peptide fragment A-3.  
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
XX central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX OS Ovis sp.  
XX PN WO2000075173-A2.  
XX PD 14-DEC-2000.  
XX PF 02-JUN-2000; 2000WO-GB02128.  
XX PR 02-JUN-1999; 99GB-0012852.

PA (REG- ) REGEN THERAPEUTICS PLC.  
XX Georgiades JA;  
XX WPI; 2001-071058/08.  
XX Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system  
PT and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -  
XX  
XX Claim 7; Page 27; 63pp; English.  
XX  
CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.  
XX  
SQ Sequence 15 AA;  
Query Match 71.4%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 PPPPQ 6  
Db 7 PPPPQ 11  
RESULT 73  
AAE20234  
ID AAE20234 standard; peptide; 15 AA.  
AC AAE20234;  
XX 18-JUN-2002 (first entry)  
DT  
DE Colostrinin constituent peptide #7.  
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnary.  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 15 /note= "Optionally C-terminal amide"  
FT  
XX WO200213850-A1.  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US22776.  
XX  
XX 17-AUG-2000; 2000WO-US22776.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2002-269151/31.  
XX Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog -  
XX  
XX Claim 6; Page 25; 51pp; English.

XX The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress  
CC level in a cell e.g. mammalian or human cell present in a cell culture,  
CC tissue, organ, or organism; or for treating oxidative damage to the skin  
CC of a patient e.g. animal or human; to modulate oxidative stress during/  
CC after a premature birth or normal birth, preventing/delaying aging in a  
CC patient, enhancing wound healing, and the reduction of side effects of  
CC cosmetic procedures. The method changes the level of an oxidising species  
CC in the cell, such as decreases or prevents increase in the level of  
CC damage to a biomolecule of the patient selected from DNA, protein and/or  
CC lipid, compared to the same conditions when the oxidative stress  
CC regulator is not present. The modulation of oxidative stress results in  
CC enhanced repair, regeneration, and replacement of cells, tissues and  
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
CC external organs), as well as enhanced preservation of such organs for  
CC transplantation, implantation, or scientific research. The present  
CC sequence is a colostrinin constituent peptide.  
XX  
SQ Sequence 15 AA;  
Query Match 71.4%; Score 5; DB 23; Length 15;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 PPPPQ 6  
Db 7 PPPPQ 11  
RESULT 74  
AAMS1042  
ID AAMS1042 standard; Peptide; 15 AA.  
XX AAMS1042;  
XX 30-MAY-2002 (first entry)  
DT  
DE Colostrinin constituent peptide.  
XX Colostrinin; colostrum; immunomodulator; cardiovascular;  
KW blood cell regulator; cytokine inducer; human.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 15 /note= "optional C-terminal amidation"  
FT  
XX WO200213849-A1.  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US22775.  
XX  
XX 17-AUG-2000; 2000WO-US22775.  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX (REG- ) REGEN THERAPEUTICS PLC.  
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX WPI; 2002-269150/31.  
XX Modulation of blood cell proliferation in a patient involves use of  
PT blood cell regulator selected from colostrinin, its constituent peptide  
PT and/or analogue -  
XX  
XX Claim 1; Page 34; 54pp; English.  
XX The present sequence is that of a colostrinin constituent peptide  
CC that is preferred for use as an immunological regulator and as a

CC blood cell regulator in claimed methods of the invention. Methods  
CC are claimed for: inducing a cytokine in a cell by contact with an  
CC immunological regulator, where the cell is present in a cell  
CC culture, a tissue, an organ or an organism, and the cell is  
CC mammalian, including human; modulating an immune response in a cell  
CC by contact with the immunological regulator under conditions  
CC effective to induce a cytokine; modulating an immune response in a  
CC patient by administering an immunological regulator under conditions  
CC effective to induce a cytokine, where the immunological regulator  
CC is administered topically or as part of a dietary supplement, and  
CC where the immune response is specific or non specific, an interferon  
CC response or an antibody response; modulating blood cell proliferation  
CC by contacting blood cells with a blood cell regulator, where the  
CC blood cells are present in a cell culture or an organism, are  
CC mammalian or human, and where the blood cells are increased in  
CC number or differentiated; and a method for modulating blood cell  
CC proliferation in a patent. A claimed cytokine-inducing composition  
CC comprises a pharmaceutical carrier and an active agent such as the  
CC present peptide. Cytokines induced by this peptide in human  
CC leucocyte cultures include interferon-gamma, tumour necrosis  
CC factor-alpha, interleukin-4, interleukin-6 and interleukin-10.  
XX  
SQ Sequence 15 AA;

Query Match 71.4%; Score 5; DB 23; Length 15;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
| | | | |  
Db 7 PPPPQ 11

Search completed: November 25, 2003, 18:15:58  
Job time : 23.6755 secs

CC The invention comprises a method for promoting cell differentiation (e.g.  
CC neural cell differentiation). The method involves contacting cells with a  
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
CC polypeptide aggregate that is present in colostrum. The method of the  
CC invention is useful for promoting the differentiation of cells and for  
CC treating damaged neural cells in a patient. The present amino acid  
CC sequence represents a specifically claimed colostrinin peptide used in  
CC the method of the invention.  
XX  
SQ Sequence 15 AA;

Query Match 71.4%; Score 5; DB 23; Length 15;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
| | | | |  
Db 7 PPPPQ 11

Search completed: November 25, 2003, 18:15:58  
Job time : 23.6755 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 13.9255 Seconds  
(without alignments)  
92.715 Million cell updates/sec

**Title:** US-09-641-801-14

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perfect score: 7
Sequence:      1 DPPPPQS 7

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Scoring table: OLIGO  
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Minimum DB seq length: 3
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Post-processing: Listing first 100 summaries

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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	7	100.0	7	15	US-10-231-652-14	Sequence 14, Appl
2	5	71.4	8	15	US-10-236-007-1037	Sequence 1037, Ap
3	5	71.4	8	15	US-10-236-007-1050	Sequence 1050, Ap
4	5	71.4	8	15	US-10-236-007-1063	Sequence 1063, Ap
5	5	71.4	8	15	US-10-236-007-1180	Sequence 1180, Ap
6	5	71.4	8	15	US-10-236-007-1193	Sequence 1193, Ap
7	5	71.4	9	15	US-10-236-007-1206	Sequence 1206, Ap
8	5	71.4	9	15	US-10-236-007-1036	Sequence 1036, Ap
9	5	71.4	9	15	US-10-236-007-1051	Sequence 1051, Ap
10	5	71.4	9	15	US-10-236-007-1064	Sequence 1064, Ap
11	5	71.4	9	15	US-10-236-007-1076	Sequence 1076, Ap
12	5	71.4	9	15	US-10-236-007-1181	Sequence 1181, Ap
13	5	71.4	9	15	US-10-236-007-1194	Sequence 1194, Ap
14	5	71.4	9	15	US-10-236-007-1207	Sequence 1207, Ap
15	5	71.4	9	15	US-10-236-007-1219	Sequence 1219, Ap

89 5 71.4 15 12 US-10-161-791-373 Sequence 373, App  
90 5 71.4 15 12 US-10-161-791-405 Sequence 405, App  
91 5 71.4 15 12 US-10-161-791-439 Sequence 439, App  
92 5 71.4 15 15 US-10-281-652-7 Sequence 7, Appli  
93 5 71.4 15 15 US-10-226-007-1044 Sequence 1044, Ap  
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97 5 71.4 15 15 US-10-226-007-1093 Sequence 1093, Ap  
98 5 71.4 15 15 US-10-226-007-1103 Sequence 1103, Ap  
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100 5 71.4 15 15 US-10-226-007-1120 Sequence 1120, Ap

## ALIGNMENTS

RESULT 1  
US-10-281-652-14 15 12 US-10-161-791-373 Sequence 373, App  
; Sequence 14, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide

US-10-281-652-14 15 12 US-10-161-791-373 Sequence 373, App  
; Sequence 14, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide

US-10-281-652-14 15 12 US-10-161-791-373 Sequence 373, App  
; Sequence 14, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
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; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide

US-10-281-652-14 15 12 US-10-161-791-373 Sequence 373, App  
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; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide

; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1037

Query Match 71.4%; Score 5; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 1 DPPP 5

RESULT 3  
US-10-226-007-1050  
; Sequence 1050, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1050  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1050

Query Match 71.4%; Score 5; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 2 DPPP 6

RESULT 4  
US-10-226-007-1063  
; Sequence 1063, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1063  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1063

Query Match 71.4%; Score 5; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5

Db 3 DDP PPP 7

RESULT 5

US-10-226-007-1180

; Sequence 1180, Application US/10226007

; Publication No. US20030105277A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

; FILE REFERENCE: 5005.01

; CURRENT APPLICATION NUMBER: US/10/226,007

; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/313,883

; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 1673

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1180

; LENGTH: 8

; TYPE: PRT

; ORGANISM: human herpesvirus 1

US-10-226-007-1180

Query Match 71.4%; Score 5; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDP PPP 5

Db 1 DDP PPP 5

RESULT 6

US-10-226-007-1193

; Sequence 1193, Application US/10226007

; Publication No. US20030105277A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

; FILE REFERENCE: 5005.01

; CURRENT APPLICATION NUMBER: US/10/226,007

; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/313,883

; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 1673

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1193

; LENGTH: 8

; TYPE: PRT

; ORGANISM: human herpesvirus 1

US-10-226-007-1193

Query Match 71.4%; Score 5; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDP PPP 5

Db 2 DDP PPP 6

RESULT 7

US-10-226-007-1206

; Sequence 1206, Application US/10226007

; Publication No. US20030105277A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

; FILE REFERENCE: 5005.01

; CURRENT APPLICATION NUMBER: US/10/226,007

; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/313,883

; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 1673

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1206

; LENGTH: 8

; TYPE: PRT

; ORGANISM: human herpesvirus 1

US-10-226-007-1206

Query Match 71.4%; Score 5; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDP PPP 5

Db 2 DDP PPP 6

RESULT 8

US-10-226-007-1038

; Sequence 1038, Application US/10226007

; Publication No. US20030105277A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

; FILE REFERENCE: 5005.01

; CURRENT APPLICATION NUMBER: US/10/226,007

; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/313,883

; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 1673

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1038

; LENGTH: 9

; TYPE: PRT

; ORGANISM: human herpesvirus 1

US-10-226-007-1038

Query Match 71.4%; Score 5; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDP PPP 5

Db 1 DDP PPP 5

RESULT 9

US-10-226-007-1051

; Sequence 1051, Application US/10226007

; Publication No. US20030105277A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

; FILE REFERENCE: 5005.01

; CURRENT APPLICATION NUMBER: US/10/226,007

; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/313,883

; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 1673

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1051

; LENGTH: 8

; TYPE: PRT

; ORGANISM: human herpesvirus 1

US-10-226-007-1051

Query Match 71.4%; Score 5; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDP PPP 5

Db 2 DDP PPP 6

; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1051  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1051

Query Match 71.4%; Score 5; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 2 DPPP 6

## RESULT 10

US-10-226-007-1064  
; Sequence 1064, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1064  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1064

Query Match 71.4%; Score 5; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 3 DPPP 7

## RESULT 11

US-10-226-007-1076  
; Sequence 1076, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1076  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1076

Query Match 71.4%; Score 5; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 4 DPPP 8

## RESULT 12

US-10-226-007-1181  
; Sequence 1181, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1181  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1181

Query Match 71.4%; Score 5; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 1 DPPP 5

## RESULT 13

US-10-226-007-1194  
; Sequence 1194, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1194  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1194

Query Match 71.4%; Score 5; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 2 DPPP 6



RESULT 14  
US-10-226-007-1207  
; Sequence 1207, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1207  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1207

Query Match 71.4%; Score 5; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 3 DPPP 7

RESULT 15  
US-10-226-007-1219  
; Sequence 1219, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1219  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1219

Query Match 71.4%; Score 5; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 4 DPPP 8

RESULT 16  
US-10-226-007-1039  
; Sequence 1039, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1039  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1039

Query Match 71.4%; Score 5; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 1 DPPP 5

RESULT 17  
US-10-226-007-1052  
; Sequence 1052, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1052  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1052

Query Match 71.4%; Score 5; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 2 DPPP 6

RESULT 18  
US-10-226-007-1065  
; Sequence 1065, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1065

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1085

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 3 DPPP 7

RESULT 19
US-10-226-007-1077
; Sequence 1077, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1077
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1077

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 4 DPPP 8

RESULT 20
US-10-226-007-1088
; Sequence 1088, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1088
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1088

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 2 DPPP 6

RESULT 23
US-10-226-007-1208
; Sequence 1208, Application US/10226007
; Publication No. US20030105277A1
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QY 1 DPPP 5
Db 5 DPPP 9

RESULT 21
US-10-226-007-1182
; Sequence 1182, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1182
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1182

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 1 DPPP 5

RESULT 22
US-10-226-007-1195
; Sequence 1195, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1195
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1195

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 2 DPPP 6

RESULT 23
US-10-226-007-1208
; Sequence 1208, Application US/10226007
; Publication No. US20030105277A1
```

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; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1208
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1208

Query Match
Best Local Similarity 71.4%; Score 5; DB 15; Length 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5
Db 3 DPPP 7

RESULT 24
US-10-226-007-1220
; Sequence 1220, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1220
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1220

Query Match
Best Local Similarity 71.4%; Score 5; DB 15; Length 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5
Db 4 DPPP 8

RESULT 25
US-10-226-007-1231
; Sequence 1231, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1231
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1231

Query Match
Best Local Similarity 71.4%; Score 5; DB 15; Length 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5
Db 4 DPPP 8

RESULT 26
US-10-226-007-1231
; Sequence 1231, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1231
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1231

Query Match
Best Local Similarity 71.4%; Score 5; DB 15; Length 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5
Db 5 DPPP 9

RESULT 27
US-10-226-007-1053
; Sequence 1053, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1053
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1053

Query Match
Best Local Similarity 71.4%; Score 5; DB 15; Length 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5
Db 1 DPPP 5

```

Query Match 71.4%; Score 5; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
 |||||  
 Db 2 DPPP 6

RESULT 28  
 US-10-226-007-1066  
 ; Sequence 1066, Application US/10226007  
 ; Publication No. US20030105277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
 ; FILE REFERENCE: 5005.01  
 ; CURRENT APPLICATION NUMBER: US/10/226,007  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/313,883  
 ; PRIOR FILING DATE: 2001-08-21  
 ; NUMBER OF SEQ ID NOS: 1673  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1066  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 1  
 US-10-226-007-1066

Query Match 71.4%; Score 5; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
 |||||  
 Db 3 DPPP 7

RESULT 29  
 US-10-226-007-1078  
 ; Sequence 1078, Application US/10226007  
 ; Publication No. US20030105277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
 ; FILE REFERENCE: 5005.01  
 ; CURRENT APPLICATION NUMBER: US/10/226,007  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/313,883  
 ; PRIOR FILING DATE: 2001-08-21  
 ; NUMBER OF SEQ ID NOS: 1673  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1078  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 1  
 US-10-226-007-1078

Query Match 71.4%; Score 5; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
 |||||  
 Db 4 DPPP 8

RESULT 30  
 US-10-226-007-1089  
 ; Sequence 1089, Application US/10226007  
 ; Publication No. US20030105277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
 ; FILE REFERENCE: 5005.01  
 ; CURRENT APPLICATION NUMBER: US/10/226,007  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/313,883  
 ; PRIOR FILING DATE: 2001-08-21  
 ; NUMBER OF SEQ ID NOS: 1673  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1089  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 1  
 US-10-226-007-1089

Query Match 71.4%; Score 5; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
 |||||  
 Db 5 DPPP 9

RESULT 31  
 US-10-226-007-1099  
 ; Sequence 1099, Application US/10226007  
 ; Publication No. US20030105277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
 ; FILE REFERENCE: 5005.01  
 ; CURRENT APPLICATION NUMBER: US/10/226,007  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/313,883  
 ; PRIOR FILING DATE: 2001-08-21  
 ; NUMBER OF SEQ ID NOS: 1673  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1099  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 1  
 US-10-226-007-1099

Query Match 71.4%; Score 5; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
 |||||  
 Db 6 DPPP 10

RESULT 32  
 US-10-226-007-1183  
 ; Sequence 1183, Application US/10226007  
 ; Publication No. US20030105277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton

```

; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1183
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1183

```

```

Query Match          71.4%; Score 5; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DPPP 5
    |||||
Db 1 DPPP 5

```

```

RESULT 33
US-10-226-007-1196
; Sequence 1196, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1196
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1196

```

```

Query Match          71.4%; Score 5; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DPPP 5
    |||||
Db 2 DPPP 6

```

```

RESULT 34
US-10-226-007-1209
; Sequence 1209, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1

```

```

; SEQ ID NO 1209
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1209

```

```

Query Match          71.4%; Score 5; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DPPP 5
    |||||
Db 3 DPPP 7

```

```

RESULT 35
US-10-226-007-1221
; Sequence 1221, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1221
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1221

```

```

Query Match          71.4%; Score 5; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DPPP 5
    |||||
Db 4 DPPP 8

```

```

RESULT 36
US-10-226-007-1232
; Sequence 1232, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1232
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1232

```

```

Query Match          71.4%; Score 5; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 DPPP 5  
|  
|  
|  
|  
|  
Db 5 DPPP 9

## RESULT 37

US-10-226-007-1242  
; Sequence 1242, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; PRIOR FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1242  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1242

Query Match 71.4%; Score 5; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
|  
Db 6 DPPP 10

## RESULT 38

US-10-226-007-1041  
; Sequence 1041, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; PRIOR FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1041  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1041

Query Match 71.4%; Score 5; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
|  
Db 1 DPPP 5

## RESULT 39

US-10-226-007-1054  
; Sequence 1054, Application US/10226007

; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; PRIOR FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1054  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1054

Query Match 71.4%; Score 5; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
|  
Db 2 DPPP 6

## RESULT 40

US-10-226-007-1067  
; Sequence 1067, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; PRIOR FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1067  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1067

Query Match 71.4%; Score 5; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
|  
Db 3 DPPP 7

## RESULT 41

US-10-226-007-1079  
; Sequence 1079, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007

; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/313,883  
 ; PRIOR FILING DATE: 2001-08-21  
 ; NUMBER OF SEQ ID NOS: 1673  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1079  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 1  
 US-10-226-007-1079

Query Match 71.4%; Score 5; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
 |||||  
 Db 4 DPPP 8

RESULT 42  
 US-10-226-007-1090  
 ; Sequence 1090, Application US/10226007  
 ; Publication No. US20030105277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
 ; FILE REFERENCE: 5005.01  
 ; CURRENT APPLICATION NUMBER: US/10/226,007  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/313,883  
 ; PRIOR FILING DATE: 2001-08-21  
 ; NUMBER OF SEQ ID NOS: 1673  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1090  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 1  
 US-10-226-007-1090

Query Match 71.4%; Score 5; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
 |||||  
 Db 5 DPPP 9

RESULT 43  
 US-10-226-007-1100  
 ; Sequence 1100, Application US/10226007  
 ; Publication No. US20030105277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
 ; FILE REFERENCE: 5005.01  
 ; CURRENT APPLICATION NUMBER: US/10/226,007  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/313,883  
 ; PRIOR FILING DATE: 2001-08-21  
 ; NUMBER OF SEQ ID NOS: 1673  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1100  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 1

US-10-226-007-1100

Query Match 71.4%; Score 5; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
 |||||  
 Db 6 DPPP 10

RESULT 44  
 US-10-226-007-1109  
 ; Sequence 1109, Application US/10226007  
 ; Publication No. US20030105277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
 ; FILE REFERENCE: 5005.01  
 ; CURRENT APPLICATION NUMBER: US/10/226,007  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/313,883  
 ; PRIOR FILING DATE: 2001-08-21  
 ; NUMBER OF SEQ ID NOS: 1673  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1109  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 1  
 US-10-226-007-1109

Query Match 71.4%; Score 5; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
 |||||  
 Db 7 DPPP 11

RESULT 45  
 US-10-226-007-1184  
 ; Sequence 1184, Application US/10226007  
 ; Publication No. US20030105277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
 ; FILE REFERENCE: 5005.01  
 ; CURRENT APPLICATION NUMBER: US/10/226,007  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/313,883  
 ; PRIOR FILING DATE: 2001-08-21  
 ; NUMBER OF SEQ ID NOS: 1673  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1184  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 1  
 US-10-226-007-1184

Query Match 71.4%; Score 5; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
 |||||  
 Db 1 DPPP 5

```
RESULT 46
US-10-226-007-1197
; Sequence 1197, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1197
; LENGTH: 12
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1197

Query Match          71.4%; Score 5; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 2 DPPP 6

RESULT 47
US-10-226-007-1210
; Sequence 1210, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1210
; LENGTH: 12
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1210

Query Match          71.4%; Score 5; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 3 DPPP 7

RESULT 48
US-10-226-007-1222
; Sequence 1222, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1222
; LENGTH: 12
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1222

Query Match          71.4%; Score 5; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 5 DPPP 9

RESULT 49
US-10-226-007-1233
; Sequence 1233, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1233
; LENGTH: 12
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1233

Query Match          71.4%; Score 5; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 4 DPPP 8

RESULT 50
US-10-226-007-1243
; Sequence 1243, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1243
; LENGTH: 12
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1243

Query Match          71.4%; Score 5; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 5 DPPP 9

RESULT 51
US-10-226-007-1254
; Sequence 1254, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1254
; LENGTH: 12
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1254

Query Match          71.4%; Score 5; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
Db 5 DPPP 9
```



; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1243  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1243

Query Match 71.4%; Score 5; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
Db 6 DPPP 10

## RESULT 51

US-10-226-007-1252  
; Sequence 1252, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; PRIOR FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1252  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1252

Query Match 71.4%; Score 5; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
Db 7 DPPP 11

## RESULT 52

US-10-226-007-1042  
; Sequence 1042, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1042  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1042

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DPPP 5  
|  
|  
|  
|  
Db 1 DPPP 5

## RESULT 53

US-10-226-007-1055  
; Sequence 1055, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1055  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1055

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
Db 2 DPPP 6

## RESULT 54

US-10-226-007-1068  
; Sequence 1068, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR FILING DATE: 2001-08-21  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1068  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1068

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
Db 3 DPPP 7

## RESULT 55

US-10-226-007-1080

; Sequence 1080, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1080  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1080

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
DB 4 DPPP 8

## RESULT 56

US-10-226-007-1091  
; Sequence 1091, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1091  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1091

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
DB 5 DPPP 9

## RESULT 57

US-10-226-007-1101  
; Sequence 1101, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01

; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1101  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1101

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
DB 6 DPPP 10

## RESULT 58

US-10-226-007-1110  
; Sequence 1110, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1110  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1110

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
DB 7 DPPP 11

## RESULT 59

US-10-226-007-1118  
; Sequence 1118, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1118  
; LENGTH: 13  
; TYPE: PRT

```
; ORGANISM: human herpesvirus 1
US-10-226-007-1118

Query Match          71.4%; Score 5; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
   |||||
Db 8 DPPP 12

RESULT 60
US-10-226-007-1185
; Sequence 1185, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1185
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1185

Query Match          71.4%; Score 5; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
   |||||
Db 1 DPPP 5

RESULT 61
US-10-226-007-1198
; Sequence 1198, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1198
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1198

Query Match          71.4%; Score 5; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
   |||||
Db 1 DPPP 5

RESULT 62
US-10-226-007-1211
; Sequence 1211, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1211
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1211

Query Match          71.4%; Score 5; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
   |||||
Db 3 DPPP 7

RESULT 63
US-10-226-007-1223
; Sequence 1223, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1223
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1223

Query Match          71.4%; Score 5; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
   |||||
Db 4 DPPP 8

RESULT 64
US-10-226-007-1234
; Sequence 1234, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
```

; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1234  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1234

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
Db 5 DPPP 9

RESULT 65  
US-10-226-007-1244  
; Sequence 1244, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1244  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1244

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
Db 6 DPPP 10

RESULT 66  
US-10-226-007-1253  
; Sequence 1253, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1253  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1253

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
Db 7 DPPP 11

RESULT 67  
US-10-226-007-1261  
; Sequence 1261, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1261  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1261

Query Match 71.4%; Score 5; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
Db 8 DPPP 12

RESULT 68  
US-10-226-007-1043  
; Sequence 1043, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226,007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1043  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1043

Query Match 71.4%; Score 5; DB 15; Length 14;

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Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
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Db 1 DPPP 5

RESULT 69
US-10-226-007-1056
; Sequence 1056, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1056
; LENGTH: 14
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1056

Query Match 71.4%; Score 5; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
   |||||
Db 4 DPPP 8

RESULT 70
US-10-226-007-1092
; Sequence 1092, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1092
; LENGTH: 14
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1092

Query Match 71.4%; Score 5; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
   |||||
Db 5 DPPP 9

RESULT 71
US-10-226-007-1102
; Sequence 1102, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1069
; LENGTH: 14
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1069

Query Match 71.4%; Score 5; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
   |||||
Db 3 DPPP 7

RESULT 72
US-10-226-007-1092
; Sequence 1092, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1092
; LENGTH: 14
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1092

Query Match 71.4%; Score 5; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
   |||||
Db 5 DPPP 9

RESULT 73
US-10-226-007-1102
; Sequence 1102, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1069
; LENGTH: 14
; TYPE: PRT
; ORGANISM: human herpesvirus 1
US-10-226-007-1069

Query Match 71.4%; Score 5; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5
   |||||
Db 3 DPPP 7
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; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226.007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1102  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1102

Query Match 71.4%; Score 5; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
|  
|  
|  
|  
Db 6 DPPP 10

## RESULT 74

US-10-226-007-1111  
; Sequence 1111, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226.007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1111  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1111

Query Match 71.4%; Score 5; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
|  
|  
|  
|  
Db 7 DPPP 11

## RESULT 75

US-10-226-007-1119  
; Sequence 1119, Application US/10226007  
; Publication No. US20030105277A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection  
; FILE REFERENCE: 5005.01  
; CURRENT APPLICATION NUMBER: US/10/226.007  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/313,883  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 1673  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1119  
; LENGTH: 14

; TYPE: PRT  
; ORGANISM: human herpesvirus 1  
US-10-226-007-1119

Query Match 71.4%; Score 5; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
|  
|  
|  
|  
Db 8 DPPP 12

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JOB time : 13.9255 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 7.63298 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-14

Perfect score: 7

Sequence: 1 DPPPPQS 7

Scoring table: OLIGO

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Searched: 328717 seqs, 42310858 residues

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Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Databases : Issued Patents AA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	4	US-09-641-803-14
2	5	71.4	15	1	US-08-302-771-1
3	5	71.4	15	3	US-08-602-999A-339
4	5	71.4	15	3	US-08-602-999A-349
5	5	71.4	15	3	US-08-602-999A-367
6	5	71.4	15	3	US-08-602-999A-373
7	5	71.4	15	3	US-08-602-999A-405
8	5	71.4	15	3	US-08-602-999A-439
9	5	71.4	15	4	US-09-500-124-339
10	5	71.4	15	4	US-09-500-124-349
11	5	71.4	15	4	US-09-500-124-367
12	5	71.4	15	4	US-09-500-124-373
13	5	71.4	15	4	US-09-500-124-405
14	5	71.4	15	4	US-09-500-124-439
15	5	71.4	15	4	US-09-641-803-7
16	5	71.4	16	3	US-08-602-999A-199
17	5	71.4	16	4	US-09-500-124-199
18	5	71.4	16	4	US-09-247-890-23
19	5	71.4	16	4	US-09-724-969-23
20	5	71.4	16	4	US-09-724-852-23
21	5	71.4	18	3	US-08-602-999A-409
22	5	71.4	18	4	US-09-500-124-409
23	5	71.4	20	3	US-08-602-999A-368
24	5	71.4	20	4	US-09-500-124-368
25	4	57.1	4	1	US-07-972-007-33
26	4	57.1	4	1	US-08-351-058A-1
27	4	57.1	4	1	US-08-647-618-33

4	57.1	4	2	US-08-358-556A-21	Sequence 21, Appl
4	57.1	4	4	US-09-295-996B-6	Sequence 6, Appl
4	57.1	4	4	US-09-057-162-33	Sequence 33, Appl
4	57.1	4	4	US-09-295-846B-9	Sequence 9, Appl
4	57.1	4	4	US-09-551-737C-9	Sequence 9, Appl
4	57.1	4	5	PCT-US92-09964-1	Sequence 1, Appl
4	57.1	5	1	US-08-351-058A-5	Sequence 5, Appl
5	57.1	5	1	US-08-477-509B-9	Sequence 9, Appl
5	57.1	5	2	US-08-358-556A-23	Sequence 23, Appl
5	57.1	5	3	US-08-630-916A-3	Sequence 3, Appl
5	57.1	5	3	US-08-482-085B-9	Sequence 9, Appl
5	57.1	5	3	US-08-476-509B-38	Sequence 38, Appl
4	57.1	5	4	US-09-444-791A-9	Sequence 9, Appl
4	57.1	5	4	US-09-295-996B-7	Sequence 7, Appl
4	57.1	5	4	US-09-119-507B-3	Sequence 3, Appl
5	57.1	5	4	US-09-295-846B-10	Sequence 10, Appl
5	57.1	5	4	US-09-551-737C-10	Sequence 10, Appl
5	57.1	5	4	US-08-897-556A-3	Sequence 3, Appl
5	57.1	5	4	US-08-897-556A-105	Sequence 105, App
5	57.1	5	5	PCT-US92-09964-5	Sequence 5, Appl
6	57.1	6	1	US-08-151-219-5	Sequence 4, Appl
6	57.1	6	1	US-08-188-223-4	Sequence 4, Appl
6	57.1	6	1	US-08-188-223-11	Sequence 11, Appl
6	57.1	6	2	US-08-358-556A-25	Sequence 25, Appl
6	57.1	6	3	US-08-968-466-4	Sequence 4, Appl
6	57.1	6	3	US-08-968-466-11	Sequence 11, Appl
6	57.1	6	4	US-08-478-546B-4	Sequence 4, Appl
6	57.1	6	4	US-08-478-546B-11	Sequence 11, Appl
6	57.1	6	4	US-09-119-507B-117	Sequence 117, App
6	57.1	6	5	PCT-US94-13205-5	Sequence 5, Appl
7	57.1	7	1	US-08-151-219-3	Sequence 3, Appl
7	57.1	7	1	US-08-188-223-9	Sequence 9, Appl
7	57.1	7	1	US-08-188-223-10	Sequence 10, Appl
7	57.1	7	2	US-08-893-853-71	Sequence 71, Appl
7	57.1	7	3	US-08-968-466-9	Sequence 9, Appl
7	57.1	7	3	US-08-968-466-10	Sequence 10, Appl
7	57.1	7	3	US-09-076-372-3	Sequence 3, Appl
7	57.1	7	5	PCT-US94-13205-3	Sequence 3, Appl
8	57.1	8	1	US-08-371-698-4	Sequence 4, Appl
8	57.1	8	1	US-08-468-596-4	Sequence 4, Appl
8	57.1	8	2	US-08-769-745-22	Sequence 22, Appl
8	57.1	8	4	US-09-343-011B-9	Sequence 9, Appl
8	57.1	8	4	US-09-295-996B-10	Sequence 10, Appl
8	57.1	8	4	US-09-295-996B-14	Sequence 14, Appl
8	57.1	8	4	US-09-295-846B-13	Sequence 13, Appl
8	57.1	8	4	US-09-295-846B-17	Sequence 17, Appl
8	57.1	8	4	US-09-551-737C-13	Sequence 13, Appl
8	57.1	8	4	US-09-551-737C-17	Sequence 17, Appl
9	57.1	9	3	US-09-001-984C-17	Sequence 17, Appl
9	57.1	9	3	US-09-203-921-7	Sequence 7, Appl
9	57.1	9	3	US-09-424-414C-9	Sequence 9, Appl
9	57.1	9	4	US-09-343-011B-6	Sequence 6, Appl
9	57.1	9	4	US-09-295-996B-29	Sequence 29, Appl
9	57.1	9	4	US-09-396-347F-17	Sequence 17, Appl
9	57.1	9	4	US-09-295-846B-32	Sequence 32, Appl
9	57.1	9	4	US-09-551-737C-32	Sequence 32, Appl
9	57.1	9	5	PCT-US92-10432-2	Sequence 2, Appl
10	57.1	10	1	US-08-230-047-11	Sequence 11, Appl
10	57.1	10	1	US-08-230-047-13	Sequence 13, Appl
10	57.1	10	1	US-08-212-190A-4	Sequence 4, Appl
10	57.1	10	2	US-08-146-028-444	Sequence 444, App
10	57.1	10	2	US-08-900-321-4	Sequence 4, Appl
10	57.1	10	3	US-08-476-509B-30	Sequence 30, Appl
10	57.1	10	3	US-08-476-509B-36	Sequence 36, Appl
10	57.1	10	3	US-08-899-595-8	Sequence 8, Appl
10	57.1	10	3	US-08-723-425A-444	Sequence 444, App
10	57.1	10	3	US-09-112-206-444	Sequence 444, App

## ALIGNMENTS

RESULT 1  
US-09-641-803-14  
; Sequence 14, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265-00220101  
; CURRENT APPLICATION NUMBER: US/09/641.803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-14

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPPPQS 7  
DB 1 DPPPQS 7

RESULT 2  
US-09-641-803-14  
; Sequence 1, Application US/08302771  
; Patent No. 5599541  
; GENERAL INFORMATION:  
; APPLICANT: MARCHAL, GILLES  
; APPLICANT: ROMAIN, FELIX  
; TITLE OF INVENTION: PEPTIDE SEQUENCE CAPABLE OF INDUCING  
; TITLE OF INVENTION: A  
; TITLE OF INVENTION: DELAYED-TYPE HYPERSENSITIVITY REACTION IN THE PRESENCE  
; TITLE OF INVENTION: OF  
; TITLE OF INVENTION: LIVING BACTERIA OF THE MYCOBACTERIUM TUBERCULOSIS  
; TITLE OF INVENTION: COMPLEX  
; TITLE OF INVENTION: AND ITS APPLICATIONS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &  
; ADDRESSEE: NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/302,771  
; FILING DATE: OCTOBER 17, 1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 92 03 286  
; FILING DATE: 19-MAR-1992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 4  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 12  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 14  
; US-08-302-771-1

Query Match 71.4%; Score 5; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PPPPQ 6  
DB 7 PPPPQ 11

RESULT 3  
US-08-602-999A-339  
; Sequence 339, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864



TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 339:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-339

Query Match 71.4%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPPQ 6  
Db 6 PPPPQ 10

RESULT 4  
US-08-602-999A-349  
Sequence 349, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Miarock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 349:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-349

Query Match 71.4%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPPQ 6  
Db 6 PPPPQ 10

## RESULT 5

US-08-602-999A-367  
Sequence 367, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Miarock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 367:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-367

Query Match 71.4%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPPQ 6  
Db 9 PPPPQ 13

## RESULT 6

US-08-602-999A-373  
Sequence 373, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:

RESULT 7  
US-08-602-999A-405  
; Sequence 405: Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/602,999A  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie

Query Match 71.4%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels

Qy 2 PPPPQ 6  
| | | | |  
Db 6 PPPPQ 10

## RESULT 9

US-09-500-124-339  
; Sequence 339, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 339:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-339

Query Match 71.4%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPPQ 6  
| | | | |  
Db 6 PPPPQ 10

## RESULT 10

US-09-500-124-349  
; Sequence 349, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 349:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-349

Query Match 71.4%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPPQ 6  
| | | | |  
Db 6 PPPPQ 10

## RESULT 11

US-09-500-124-367  
; Sequence 367, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 367:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-367

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPPQ 6
Db 9 PPPPQ 13

RESULT 12
US-09-500-124-373
; Sequence 373, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 367:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-367
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```
;
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-373

Query Match 71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPPQ 6
Db 6 PPPPQ 10

RESULT 13
US-09-500-124-405
; Sequence 405, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 405:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-405
```

Query Match 71.4%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
| | | | |  
Db 6 PPPPQ 10

## RESULT 14

US-09-500-124-439  
; Sequence 439, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 439:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-09-500-124-439

QY 2 PPPPQ 6  
| | | | |  
Db 6 PPPPQ 10

Query Match 71.4%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
| | | | |  
Db 6 PPPPQ 10

## RESULT 15

US-09-641-803-7  
; Sequence 7, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Ielvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
; US-09-641-803-7

Query Match 71.4%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6  
| | | | |  
Db 7 PPPPQ 11

## RESULT 16

US-08-602-999A-199  
; Sequence 199, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 199:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid

TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-199

Query Match 71.4%; Score 5; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 4 DPPP 8

## RESULT 17

US-09-500-124-199 , Application US/09500124  
Sequence 199, Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 199:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-199

Query Match 71.4%; Score 5; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 4 DPPP 8

## RESULT 18

US-09-247-890-23 ,  
Sequence 23, Application US/09247890  
Patent No. 6541011  
GENERAL INFORMATION:  
APPLICANT: Punnonen, Juha  
APPLICANT: Bass, Steven H.  
APPLICANT: Whalen, Robert Gerald  
APPLICANT: Howard, Russell  
APPLICANT: Stemmer, Willem P.C.  
APPLICANT: Maxygen, Inc.  
TITLE OF INVENTION: Antigen Library Immunization  
FILE REFERENCE: 018097-028710US  
CURRENT APPLICATION NUMBER: US/09/247,890  
CURRENT FILING DATE: 1999-02-10  
EARLIER APPLICATION NUMBER: US 60/074,294  
EARLIER FILING DATE: 1998-02-11  
EARLIER APPLICATION NUMBER: US 60/105,509  
EARLIER FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 23  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Plasmodium berghei  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(16)  
OTHER INFORMATION: circumsporozoite (CS) protein-based B-epitope  
US-09-247-890-23

Query Match 71.4%; Score 5; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5  
Db 8 DPPP 12

## RESULT 19

US-09-724-969-23 ,  
Sequence 23, Application US/09724969  
Patent No. 6569435  
GENERAL INFORMATION:  
APPLICANT: Punnonen, Juha  
APPLICANT: Bass, Steven H.  
APPLICANT: Whalen, Robert Gerald  
APPLICANT: Howard, Russell  
APPLICANT: Stemmer, Willem P.C.  
APPLICANT: Maxygen, Inc.  
TITLE OF INVENTION: Antigen Library Immunization  
FILE REFERENCE: 018097-028710US  
CURRENT APPLICATION NUMBER: US/09/724,969  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 09/247,890  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: US 60/105,509  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 23  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Plasmodium berghei  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(16)  
OTHER INFORMATION: circumsporozoite (CS) protein-based B-epitope  
US-09-724-969-23

Query Match 71.4%; Score 5; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
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|  
|  
|  
Db 8 DPPP 12

## RESULT 20

US-09-724-852-23  
; Sequence 23, Application US/09724852  
; Patent No. 6576757  
; GENERAL INFORMATION:  
; APPLICANT: Punnonen, Juha  
; APPLICANT: Bass, Steven H.  
; APPLICANT: Whalen, Robert Gerald  
; APPLICANT: Howard, Russell  
; APPLICANT: Stemmer, Willem P.C.  
; APPLICANT: Maxygen, Inc.  
; TITLE OF INVENTION: Antigen Library Immunization  
; FILE REFERENCE: 018097-028710US  
; CURRENT APPLICATION NUMBER: US/09/724,852  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/247,890  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Plasmodium berghei  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(16)  
; OTHER INFORMATION: circumsporozoite (CS) protein-based B-epitope  
US-09-724-852-23

Query Match 71.4%; Score 5; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
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|  
|  
|  
Db 8 DPPP 12

## RESULT 21

US-08-602-999A-409  
; Sequence 409, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 409:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-409

Query Match 71.4%; Score 5; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPPP 5  
|  
|  
|  
|  
Db 4 DPPP 8

## RESULT 22

US-09-500-124-409  
; Sequence 409, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 08/602,999  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 409:

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-409

Query Match 71.4%; Score 5; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPPP 5

Db 4 DPPP 8

RESULT 23

US-08-602-999A-368  
Sequence 368, Application US/08602999A  
Patent No. 6184205

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 368:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-368

Query Match 71.4%; Score 5; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6

Db 13 PPPPQ 17

RESULT 24

US-09-500-124-368  
Sequence 368, Application US/09500124  
Patent No. 6432920

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA: 08/602,999

APPLICATION NUMBER: 08/602,999

FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-202

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 368:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-09-500-124-368

Query Match 71.4%; Score 5; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPPQ 6

Db 13 PPPPQ 17

RESULT 25

US-07-972-007-33

Sequence 33, Application US/07972007

Patent No. 5527681

GENERAL INFORMATION:

APPLICANT: Holmes, Christopher P.

TITLE OF INVENTION: Cyclic and Substituted Immobilized

TITLE OF INVENTION: Molecular Synthesis

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California



; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/972,007  
; FILING DATE: 19921105  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5527681viel, Vernon A.  
; REGISTRATION NUMBER: 32,483  
; REFERENCE/DOCKET NUMBER: 11509-57-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-07-972-007-33

Query Match 57.1%; Score 4; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 2 PPPP 5  
DB 1 PPPP 4

RESULT 26  
US-08-351-058A-1  
; Sequence 1, Application US/08351058A  
; Patent No. 5550215  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/351,058A  
; FILING DATE: 28-NOV-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,940  
; FILING DATE: 19-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-015  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-351-058A-1

Query Match 57.1%; Score 4; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 2 PPPP 5  
DB 1 PPPP 4

RESULT 27  
US-08-647-618-33  
; Sequence 33, Application US/08647618  
; Patent No. 5770456  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Cyclic and Substituted Immobilized  
; TITLE OF INVENTION: Molecular Synthesis  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/647,618  
; FILING DATE: 13-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/972,007  
; FILING DATE: 05-NOV-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/805,727  
; FILING DATE: 06-DEC-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/624,120  
; FILING DATE: 06-DEC-1990  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/492,462  
; FILING DATE: 07-MAR-1990  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/362,901  
; FILING DATE: 07-JUN-1989  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy, Matthew B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 16528J-000141US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400

```
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-647-618-33

Query Match          57.1%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPP 5
DB      1 PPPP 4

RESULT 28
US-08-358-556A-21
; Sequence 21, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-358-556A-21

Query Match          57.1%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPP 5
DB      1 PPPP 4
```

```
RESULT 29
US-09-295-996B-6
; Sequence 6, Application US/09295996B
; Patent No. 6413530
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UP-230
; CURRENT APPLICATION NUMBER: US/09/295,996B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking region
US-09-295-996B-6

Query Match          57.1%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPP 5
DB      1 PPPP 4

RESULT 30
US-09-057-162-33
; Sequence 33, Application US/09057162
; Patent No. 6468740
; GENERAL INFORMATION:
; APPLICANT: Holmes, Christopher P.
; TITLE OF INVENTION: Cyclic and Substituted Immobilized
;                               Molecular Synthesis
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,162
; FILING DATE: 08-Apr-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,618
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: US 07/972,007
; FILING DATE: 05-NOV-1992
; APPLICATION NUMBER: US 07/796,727
; FILING DATE: 22-NOV-1991
; APPLICATION NUMBER: US 07/805,727
; FILING DATE: 06-DEC-1991
; APPLICATION NUMBER: US 07/624,120
; FILING DATE: 06-DEC-1990
; APPLICATION NUMBER: US 07/492,462
; FILING DATE: 07-MAR-1990
; APPLICATION NUMBER: US 07/362,901
; FILING DATE: 07-JUN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Matthew B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-000141US
```

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-057-162-33

Query Match 57.1%; Score 4; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 1 PPPP 4

## RESULT 31

US-09-295-846B-9  
; Sequence 9, Application US/09295846B  
; Patent No. 6562590  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UP-223  
; CURRENT APPLICATION NUMBER: US/09/295,846B  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: flanking  
; OTHER INFORMATION: region  
US-09-295-846B-9

Query Match 57.1%; Score 4; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 1 PPPP 4

## RESULT 32

US-09-551-737C-9  
; Sequence 9, Application US/09551737C  
; Patent No. 6566129  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; APPLICANT: Schlesinger, Yaagov  
; APPLICANT: Nauwelaers, Sabine M. I.  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UP-223C1  
; CURRENT APPLICATION NUMBER: US/09/551,737C  
; CURRENT FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 09/295,846  
; PRIOR FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Flanking region  
US-09-551-737C-9

Query Match 57.1%; Score 4; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 1 PPPP 4

## RESULT 33

PCT-US92-09964-1  
; Sequence 1, Application PC/TUS9209964  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/09964  
; FILING DATE: 19921119  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11509-51-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US92-09964-1

Query Match 57.1%; Score 4; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 1 PPPP 4

## RESULT 34

US-08-351-058A-5  
; Sequence 5, Application US/08351058A  
; Patent No. 5550215  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/351,058A  
FILING DATE: 28-NOV-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/978,940  
FILING DATE: 19-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,727  
FILING DATE: 22-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 000324-015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-7400  
TELEFAX: 415-854-8275  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-351-058A-5

Query Match 57.1%; Score 4; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 PPPP 5  
Db 1 PPPP 4  
  
RESULT 35  
US-08-477-509B-9  
Sequence 9, Application US/08477509B  
Patent No. 5770697  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W  
APPLICANT: Dorman, Mary A  
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,509B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-509B-9  
  
Query Match 57.1%; Score 4; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 PPPP 5  
Db 2 PPPP 5  
  
RESULT 36  
US-08-358-556A-23  
Sequence 23, Application US/08358556A  
Patent No. 5869643  
GENERAL INFORMATION:  
APPLICANT: Chatelain, Francois  
APPLICANT: Kumarev, Viktor  
TITLE OF INVENTION: Process for Preparing Polynucleotides on  
TITLE OF INVENTION: a Solid Support and Apparatus Permitting its  
TITLE OF INVENTION: Implementation  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,556A  
FILING DATE: 14-DEC-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 9315164  
FILING DATE: 16-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: 10577/P58418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-6666  
TELEFAX: (202) 393-5350

; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-358-556A-23

Query Match 57.1%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PPPP 5  
Db 1 PPPP 4

RESULT 37  
US-08-630-916A-3  
; Sequence 3, Application US/08630916A  
; Patent No. 601137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; APPLICANT: Kay, Brian K.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,916A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 10,872  
; REFERENCE/DOCKET NUMBER: 1101-203  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-916A-3

Query Match 57.1%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PPPP 5  
Db 1 PPPP 4

RESULT 38  
US-08-482-085B-9  
; Sequence 9, Application US/08482085B

; Patent No. 6018030  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; APPLICANT: Richardson, Charles  
; APPLICANT: Chambers, James  
; APPLICANT: Causey, Stuart  
; APPLICANT: Pollock, Thomas J.  
; APPLICANT: Cappello, Joseph  
; APPLICANT: Crissman, John W.  
; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,085B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/927,258  
; FILING DATE: 04-NOV-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/114,618  
; FILING DATE: 29-OCT-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/053,049  
; FILING DATE: 22-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,155  
; FILING DATE: 29-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Trecartin, Richard F.  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-482-085B-9

Query Match 57.1%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 2 PPPP 5

RESULT 39  
US-08-476-509B-38  
; Sequence 38, Application US/08476509B  
; Patent No. 6034212  
; GENERAL INFORMATION:  
; APPLICANT: SUDOL, MARIUS  
; APPLICANT: PEER, BORK  
; APPLICANT: HENRY, CHEN

;; TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A  
;; TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE  
;; TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES  
;; TITLE OF INVENTION: THEREOF  
;; NUMBER OF SEQUENCES: 50  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Klauber & Jackson  
;; STREET: 411 Hackensack Avenue  
;; CITY: Hackensack  
;; STATE: New Jersey  
;; COUNTRY: USA  
;; ZIP: 07601  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/476,509B  
;; FILING DATE: 01-DEC-1994  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Jackson Esq., David A.  
;; REGISTRATION NUMBER: 26,742  
;; REFERENCE/DOCKET NUMBER: 600-1-101 CIP  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201 487-5800  
;; TELEFAX: 201 343-1684  
;; TELEX: 133521  
;; INFORMATION FOR SEQ ID NO: 38:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 5 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
US-08-476-509B-38  
  
Query Match 57.1%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 PPPP 5  
Db 1 PPPP 4  
  
RESULT 40  
US-09-444-791A-9  
; Sequence 9, Application US/09444791A  
; Patent No. 6355776  
; GENERAL INFORMATION:  
; APPLICANT: Ferrari, Franco A.  
; Richardson, Charles  
; Chambers, James  
; Causey, Stuart  
; Pollock, Thomas J.  
; Cappello, Joseph  
; Crissman, John W.  
; TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive  
; Units of Amino Acids and DNA Sequences Encoding the Same  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr Hohnbach Test Albritton & Herbert LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/444,791A  
;; FILING DATE: 22-NOV-1999  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/482,085  
;; FILING DATE: 07-JUN-1995  
;; APPLICATION NUMBER: US 08/175,155  
;; FILING DATE: 29-DEC-1993  
;; APPLICATION NUMBER: US 08/053,049  
;; FILING DATE: 22-APR-1993  
;; APPLICATION NUMBER: US 07/114,618  
;; FILING DATE: 29-OCT-1987  
;; APPLICATION NUMBER: US 06/927,258  
;; FILING DATE: 04-NOV-1986  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Trecartin, Richard F.  
;; REGISTRATION NUMBER: 31,801  
;; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-781-1989  
;; TELEFAX: 415-398-3249  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 5 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-444-791A-9  
  
Query Match 57.1%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 PPPP 5  
Db 2 PPPP 5  
  
RESULT 41  
US-09-295-996B-7  
; Sequence 7, Application US/09295996B  
; Patent No. 6413530  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; TITLE OF INVENTION: PESTICIDAL PEPTIDES  
; FILE REFERENCE: UF-230  
; CURRENT APPLICATION NUMBER: US/09/295,996B  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flanking region  
US-09-295-996B-7  
  
Query Match 57.1%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 PPPP 5  
Db 1 PPPP 4  
  
RESULT 42

US-09-119-507B-3  
; Sequence 3, Application US/09119507B  
; Patent No. 6548642  
; GENERAL INFORMATION:  
; APPLICANT: Kieliszewski, Marcia J.  
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums  
; FILE REFERENCE: OHU-03417  
; CURRENT APPLICATION NUMBER: US/09/119,507B  
; CURRENT FILING DATE: 1998-07-20  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)..(5)  
; OTHER INFORMATION: The proline at these positions is a  
; OTHER INFORMATION: hydroxyproline.  
US-09-119-507B-3

Query Match 57.1%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 2 PPPP 5

## RESULT 43

US-09-295-846B-10  
; Sequence 10, Application US/09295846B  
; Patent No. 6562590  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UP-223  
; CURRENT APPLICATION NUMBER: US/09/295,846B  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: flanking  
; OTHER INFORMATION: region  
US-09-295-846B-10

Query Match 57.1%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 1 PPPP 4

## RESULT 44

US-09-551-737C-10  
; Sequence 10, Application US/09551737C  
; Patent No. 6566129  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; APPLICANT: Schlesinger, Yaakov  
; APPLICANT: Nauwelaers, Sabine M. I.  
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
; FILE REFERENCE: UP-223C1

; CURRENT APPLICATION NUMBER: US/09/551,737C  
; CURRENT FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: US 09/295,846  
; PRIOR FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flanking region  
US-09-551-737C-10

Query Match 57.1%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 1 PPPP 4

## RESULT 45

US-08-897-556A-3  
; Sequence 3, Application US/08897556A  
; Patent No. 6570062  
; GENERAL INFORMATION:  
; APPLICANT: KIELSEWSKI, MARCIA J.  
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER  
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/897,556A  
; FILING DATE: 21-JUL-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: OHU-02908  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 2..5  
; OTHER INFORMATION: /note= "The proline at these  
; OTHER INFORMATION: positions is a hydroxyproline."  
US-08-897-556A-3

Query Match 57.1%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 2 PPPP 5

## RESULT 46

US-08-897-556A-105  
; Sequence 105, Application US/08897556A  
; Patent No. 6570062  
; GENERAL INFORMATION:  
; APPLICANT: KIELSZEWSKI, MARCIA J.  
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER  
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/897,556A  
; FILING DATE: 21-JUL-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: OHU-02908  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 105:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 2..5  
; OTHER INFORMATION: /note= "The proline at positions 2,  
; OTHER INFORMATION: 3, 4, and 5 is a hydroxyproline."  
US-08-897-556A-105

QY 2 PPPP 5  
Db 2 PPPP 5

## RESULT 47

PCT-US92-09964-5  
; Sequence 5, Application PC/TUS9209964  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Christopher P.  
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA

; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/09964  
; FILING DATE: 19921119  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/796,727  
; FILING DATE: 22-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11509-51-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: both  
; MOLECULE TYPE: peptide  
PCT-US92-09964-5

Query Match 57.1%; Score 4; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 2 PPPP 5

## RESULT 48

US-08-151-219-5  
; Sequence 5, Application US/08151219  
; Patent No. 5468494  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Karr, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, White and Case  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 100036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/151,219  
; FILING DATE: 12-NOV-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas, Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-028  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 819-8286

QY 2 PPPP 5  
Db 2 PPPP 5

Query Match 57.1%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-151-219-5

Query Match 57.1%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
DB 2 PPPP 5

RESULT 49  
US-08-188-223-4  
Sequence 4, Application US/08188223  
Patent No. 5688506  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Immunogens Against Gonadotropin  
TITLE OF INVENTION: Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,223  
FILING DATE: 27-JAN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8286  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: C-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /note= "spacer"  
US-08-188-223-4

Query Match 57.1%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5

DB 2 PPPP 5

RESULT 50  
US-08-188-223-11  
Sequence 11, Application US/08188223  
Patent No. 5688506  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Immunogens Against Gonadotropin  
TITLE OF INVENTION: Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,223  
FILING DATE: 27-JAN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas Esq., Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8286  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: N-terminal  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /note= "spacer"  
US-08-188-223-11

Query Match 57.1%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
DB 2 PPPP 5

RESULT 51  
US-08-358-556A-25  
Sequence 25, Application US/08358556A  
Patent No. 5869643  
GENERAL INFORMATION:  
APPLICANT: Chatelain, Francois  
APPLICANT: Kumarev, Viktor  
TITLE OF INVENTION: Process for Preparing Polynucleotides on  
TITLE OF INVENTION: a Solid Support and Apparatus Permitting its  
TITLE OF INVENTION: Implementation  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern

```

; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
; US-08-968-466-4

Query Match 57.1%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels

QY - 2 PPPP 5
|||
Db 2 PPPP 5

RESULT 53
US-08-968-466-11
; Sequence 11, Application US/08968466
; Patent No. 6132720
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,466
; FILING DATE: 27-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
; US-08-968-466-11

Query Match 57.1%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
|||||  
Db 2 PPPP 5

## RESULT 54

US-08-478-546B-4  
; Sequence 4, Application US/08478546B  
; Patent No. 6303123  
; GENERAL INFORMATION:  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent  
; TUMORS WITH IMMUNOGENS AGAINST GONADOTROPIN-RELEASING HORMONE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, Esq.  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2787  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,546B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/188,223  
; FILING DATE: 27-JAN-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas Esq., Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-300  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-819-8286  
; TELEFAX: 212-354-8113  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: C-terminal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..6  
; OTHER INFORMATION: /note= "spacer"  
US-08-478-546B-4

Query Match 57.1%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
|||||  
Db 2 PPPP 5

## RESULT 55

US-08-478-546B-11  
; Sequence 11, Application US/08478546B  
; Patent No. 6303123  
; GENERAL INFORMATION:  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Scibienski, Robert

; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent  
; TUMORS WITH IMMUNOGENS AGAINST GONADOTROPIN-RELEASING HORMONE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, Esq.  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2787  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,546B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/188,223  
; FILING DATE: 27-JAN-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas Esq., Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-300  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-819-8286  
; TELEFAX: 212-354-8113  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..6  
; OTHER INFORMATION: /note= "spacer"  
US-08-478-546B-11  
  
Query Match 57.1%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 PPPP 5  
|||||  
Db 2 PPPP 5  
  
RESULT 56  
US-09-119-507B-117  
; Sequence 117, Application US/09119507B  
; Patent No. 6548642  
; GENERAL INFORMATION:  
; APPLICANT: Kieliszewski, Marcia J.  
; TITLE OF INVENTION: NO. 6548642el Synthetic Genes for Plant Gums  
; FILE REFERENCE: OHU-03417  
; CURRENT APPLICATION NUMBER: US/09/119,507B  
; CURRENT FILING DATE: 1998-07-20  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 117  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; NAME/KEY: SITE  
; LOCATION: (2)..(5)

OTHER INFORMATION: The Proline at these positions is a  
US-09-119-507B-117

Query Match 57.1%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PPPP 5  
Db 2 PPPP 5

## RESULT 57

PCT-US94-13205-5

Sequence 5, Application PC/TUS9413205  
GENERAL INFORMATION:  
APPLICANT: Gevas, Philip C.  
APPLICANT: Grimes, Stephen  
APPLICANT: Karr, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, White and Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 100036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/13205  
FILING DATE: 12-NOV-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal

Query Match 57.1%; Score 4; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PPPP 5  
Db 2 PPPP 5

## RESULT 58

US-08-151-219-3

Sequence 3, Application US/08151219  
Patent No. 5468494  
GENERAL INFORMATION:

APPLICANT: Gevas, Philip C.  
APPLICANT: Grimes, Stephen  
APPLICANT: Karr, Stephen  
APPLICANT: Michaeli, Dov  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, White and Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 100036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,219  
FILING DATE: 12-NOV-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal

US-08-151-219-3

Query Match 57.1%; Score 4; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PPPP 5  
Db 3 PPPP 6

## RESULT 59

US-08-188-223-9

Sequence 9, Application US/08188223  
Patent No. 5688506  
GENERAL INFORMATION:  
APPLICANT: Grimes, Stephen  
APPLICANT: Scibienski, Robert  
TITLE OF INVENTION: Immunogens Against Gonadotropin.  
TITLE OF INVENTION: Releasing Hormone  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dimitrios T. Drivas, Esq.  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /note= "spacer"
;
; US-08-188-223-9
;
; Query Match
; Best Local Similarity 57.1%; Score 4; DB 1; Length 7;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 PPPP 5
; DB 2 PPPP 5
;
; RESULT 60
; US-08-188-223-10
; Sequence 10, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-188-223-9
;
; Query Match
; Best Local Similarity 57.1%; Score 4; DB 1; Length 7;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 PPPP 5
; DB 2 PPPP 5
;
; RESULT 61
; US-08-893-853-71
; Sequence 71, Application US/08893853
; Patent No. 5891994
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; TITLE OF INVENTION: Methods and Compositions for Impairing
; TITLE OF INVENTION: Multiplication of HIV-1
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., P.O. Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,853
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GGP2USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-893-853-71
;
; Query Match
; Best Local Similarity 57.1%; Score 4; DB 2; Length 7;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 PPQS 7
; DB 3 PPQS 6
;
; RESULT 62
; US-08-968-466-9
; Sequence 9, Application US/08968466
; Patent No. 6132720
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
```

```
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,466
; FILING DATE: 27-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /note= "spacer"
;
; US-08-968-466-9
;
; Query Match 57.1%; Score 4; DB 3; Length 7;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 PPPP 5
; Db 2 PPPP 5
;
; RESULT 63
; US-08-968-466-10
; Sequence 10, Application US/08968466
; Patent No. 6132720
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/968,466
; FILING DATE: 27-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /note= "spacer"
;
; US-08-968-466-10
;
; Query Match 57.1%; Score 4; DB 3; Length 7;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 PPPP 5
; Db 3 PPPP 6
;
; RESULT 64
; US-09-147-933-35
; Sequence 35, Application US/09147933A
; Patent No. 6168917
; GENERAL INFORMATION:
; APPLICANT: Kilpatrick, David
; TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF
; FILE REFERENCE: 62242/US
; CURRENT APPLICATION NUMBER: US/09/147,933A
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: PCT/US97/17734
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: U. S. 60/027,353
; EARLIER FILING DATE: 1996-10-02
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: "RESIDUE 2 = LEU OR MET"
; OTHER INFORMATION: peptide
; US-09-147-933-35
;
; Query Match 57.1%; Score 4; DB 3; Length 7;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 DPPP 4
; Db 4 DPPP 7
;
; RESULT 65
; US-09-343-011B-8
; Sequence 8, Application US/09343011B
```

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; Patent No. 6300473
; GENERAL INFORMATION:
; APPLICANT: Stephane Richard
; TITLE OF INVENTION: SLM-1 AND SLM-2: NOVEL
; FILE REFERENCE: A32561
; CURRENT APPLICATION NUMBER: US/09/343,011B
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: CA 2265271
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-343-011B-8

Query Match      57.1%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPP 5
Db      3 PPPP 6

RESULT 66
US-08-478-546B-9
; Sequence 9, Application US/08478546B
; Patent No. 6303123
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienki, Robert
; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
; TITLE OF INVENTION: Tumors with Immunogens against Gonadotropin Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/478,546B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 8
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /note= "spacer"
US-08-478-546B-9

Query Match      57.1%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPP 5
Db      3 PPPP 6

RESULT 68
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; LOCATION: 1..7
; OTHER INFORMATION: /note= "spacer"
US-08-478-546B-9

Query Match      57.1%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPP 5
Db      2 PPPP 5

RESULT 67
US-08-478-546B-10
; Sequence 10, Application US/08478546B
; Patent No. 6303123
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienki, Robert
; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
; TITLE OF INVENTION: Tumors with Immunogens against Gonadotropin Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/478,546B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 10
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /note= "spacer"
US-08-478-546B-10

Query Match      57.1%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PPPP 5
Db      3 PPPP 6

RESULT 68
```

US-09-076-372-3  
; Sequence 3, Application US/09076372  
; Patent No. 6548066  
; GENERAL INFORMATION:  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Caplin, Martin E.  
; APPLICANT: Watson, Susan A.  
; APPLICANT: Grimes, Stephen  
; TITLE OF INVENTION: Immunogenic Compositions  
; TITLE OF INVENTION: to the Cck-B/Gastrin Receptor and Methods for  
; TITLE OF INVENTION: the Treatment of Tumors  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, White & Case LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10036-2787  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/076,372  
; FILING DATE: 12-MAY-1998  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/046,201  
; FILING DATE: 12-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Drivas, Dimitrios T.  
; REGISTRATION NUMBER: 32,218  
; REFERENCE/DOCKET NUMBER: 1102865-0032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 819-8200  
; TELEFAX: (212) 354-8113  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-076-372-3

Query Match 57.1%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 3 PPPP 6

RESULT 69  
PCT-US94-13205-3  
; Sequence 3, Application PC/TUS9413205  
; GENERAL INFORMATION:  
; APPLICANT: Gevas, Philip C.  
; APPLICANT: Grimes, Stephen  
; APPLICANT: Kart, Stephen  
; APPLICANT: Michaeli, Dov  
; APPLICANT: Scibienski, Robert  
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS  
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dimitrios T. Drivas, White and Case  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York

COUNTRY: U.S.A.  
ZIP: 100036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/13205  
FILING DATE: 12-NOV-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Drivas, Dimitrios T.  
REGISTRATION NUMBER: 32,218  
REFERENCE/DOCKET NUMBER: 1102865-028  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8286  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
PCT-US94-13205-3

Query Match 57.1%; Score 4; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 3 PPPP 6

RESULT 70  
US-07-989-290-4  
; Sequence 4, Application US/07989290  
; Patent No. 5358934  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; APPLICANT: Carlson, David A.  
; TITLE OF INVENTION: Materials and Methods for Control  
; TITLE OF INVENTION: of Pests  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/989,290  
; FILING DATE: 19921211  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: UF/S&S-127  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:



; LENGTH: 8 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-07-989-290-4

Query Match 57.1%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 5 PPPP 8

RESULT 71  
US-08-271-698-4  
; Sequence 4, Application US/08271698  
; Patent No. 5439821  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; APPLICANT: Carlson, David A.  
; TITLE OF INVENTION: Materials and Methods for Control  
; TITLE OF INVENTION: of Pests  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/271,698  
; FILING DATE: 07-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER: US/07/989,290  
; FILING DATE: 11-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: UF/S&S-127  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-271-698-4

Query Match 57.1%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 5 PPPP 8

RESULT 72  
US-08-468-596-4  
; Sequence 4, Application US/08468596  
; Patent No. 5629196  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; APPLICANT: Carlson, David A.  
; TITLE OF INVENTION: Materials and Methods for Control  
; TITLE OF INVENTION: of Pests  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,596  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER: US/08/271,698  
; FILING DATE: 07-JUL-1994  
; APPLICATION NUMBER: US/07/989,290  
; FILING DATE: 11-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: UF/S&S-127  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-468-596-4

Query Match 57.1%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPPP 5  
Db 5 PPPP 8

RESULT 73  
US-08-769-745-22  
; Sequence 22, Application US/08769745  
; Patent No. 5955259  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd C.  
; APPLICANT: Levitan, Irwin B.  
; APPLICANT: Brandeis University  
; TITLE OF INVENTION: Mechanism for the Regulation of Ion  
; TITLE OF INVENTION: Channel Activity  
; FILE REFERENCE: BRU96-02  
; CURRENT APPLICATION NUMBER: US/08/769,745  
; CURRENT FILING DATE: 1996-12-19  
; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Rat  
; US-08-769-745-22

Query Match 57.1%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPP 5  
|  
|  
|  
|  
Db 1 PPPP 4

RESULT 74  
US-09-343-011B-9  
; Sequence 9, Application US/09343011B  
; Patent No. 6300473  
; GENERAL INFORMATION:  
; APPLICANT: Stephane Richard  
; TITLE OF INVENTION: SLIM-1 AND SLIM-2; NOVEL  
; FILE REFERENCE: A32561  
; CURRENT APPLICATION NUMBER: US/09/343,011B  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: CA 2265271  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-343-011B-9

Query Match 57.1%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPP 5  
|  
|  
|  
|  
Db 2 PPPP 5

RESULT 75  
US-09-295-996B-10  
; Sequence 10, Application US/09295996B  
; Patent No. 6413530  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; TITLE OF INVENTION: PESTICIDAL PEPTIDES  
; FILE REFERENCE: UF-230  
; CURRENT APPLICATION NUMBER: US/09/295,996B  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TMOF peptide  
; US-09-295-996B-10

Query Match 57.1%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPPP 5  
|  
|  
|  
|  
Db 3 PPPP 6

Search completed: November 25, 2003, 20:16:10  
Job time : 7.63298 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 4.60106 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-15

Perfect score: 5

Sequence: 1 SEEMP 5

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR\_76:\*

1: pirl:\*

2: pirl:\*

3: pirl:\*

4: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	60.0	10	2 S39392	calpain (EC 3.4.22
2	3	60.0	12	2 A39233	myosin heavy chain
3	3	60.0	12	2 B47171	chondroitin sulfat
4	3	60.0	14	2 A49018	myosin heavy chain
5	3	60.0	15	2 S62620	protein disulfide-
6	3	60.0	16	2 JH0517	insulin-like growt
7	3	60.0	17	2 A34572	osteonectin - rat
8	3	60.0	18	2 I55453	zinc finger homeod
9	3	60.0	18	2 S54272	CTC 75 protein - h
10	3	60.0	19	2 S68194	alpha-1,6-mannosyl
11	3	60.0	20	2 A49164	chromogranin-B - r
12	3	60.0	20	2 A49164	chromogranin-B - r
13	3	60.0	20	2 S19618	globin - polychaet
14	3	60.0	20	2 H49164	chromogranin-B - r
15	3	60.0	20	2 A31516	lectin, galactose/
16	2	40.0	3	3 I78890	tyrosine protein k
17	2	40.0	4	2 I54357	schwannomin - mous
18	2	40.0	4	2 S55238	pallidipin - aspas
19	2	40.0	5	2 B37325	pap fibrial regul
20	2	40.0	5	2 A32014	traM protein - Esc
21	2	40.0	5	2 D60274	major protein anti
22	2	40.0	5	2 S53595	hypothetical prote
23	2	40.0	5	2 PT0610	T-cell receptor be
24	2	40.0	5	2 PT0535	T-cell receptor be
25	2	40.0	5	2 PT0684	T-cell receptor be
26	2	40.0	6	2 A61419	sarcosine dehydrog
27	2	40.0	6	2 S11556	hydrogensulfite re
28	2	40.0	6	2 PT0648	T-cell receptor be
29	2	40.0	7	2 ECMUCR	catch-relaxing pep

neuromodulatory pe  
neuromodulatory pe  
alpha-myosin heavy  
calsequestrin, fas  
T-cell receptor be  
T-cell receptor be  
T-cell receptor be  
carnocin U149 - Ca  
orf 4 para 5'-regi  
Na+-transporting A  
peptidyl-dipeptida  
acetylcholinestera  
aspartate transami  
enamelin f - bovin  
T-cell receptor be  
neural proteinase  
tocopherol-binding  
gene Tnfrslow prote  
aspartate kinase ( f  
ferredoxin a2 - Ja  
L-serine ammonia-1  
ribosomal protein  
caldesmon - rabbit  
calsequestrin, car  
fibrinogen beta ch  
fibrinogen beta ch  
chlorophyll a/b-bi  
cat gene leader pe  
chloramphenicol O-  
lg heavy chain CRD  
macrophage chemota  
gastrin - domestic  
late G1-69 protein  
N-methylpurine DNA  
Gene C-mpl protein  
T-cell receptor be  
T-cell receptor be  
T-cell receptor be  
T-cell receptor be  
orf 2 para 5'-regi  
cytochrome-c oxida  
sperm-activating p  
probable methionin  
ribosomal protein  
seed storage prote  
acetylcholinestera  
cytochrome-c oxida  
T-cell receptor be  
chromogranin-B - r  
photosystem I 17.5  
nifs protein - Bra  
luxC protein - Pho  
58K heat shock pro  
tetraenomycin A2  
hypothetical 1.5K  
hypothetical 1.5K  
39K protein 3225 -  
chemical-sense-rel  
cytochrome-c oxida  
major glycoprotein  
6-phosphofructokin  
complement C3b rec  
microtubule-associ  
T-cell receptor be  
ELAV-like neuronal  
hypothetical prote  
aminotransferase c  
tyrosine 3-monooxy  
tyrosine 3-monooxy  
tyrosine 3-monooxy

## ALIGNMENTS

## RESULT 1

S39392  
calpain (BC 3.4.22.17) II light chain - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 18-Feb-1994 #sequence\_revision 24-Jul-1998 #text\_change 29-Sep-1999  
C:Accession: S39392  
R:Crawford, C.; Brown, N.R.; Willis, A.C.  
Biochem. J. 296, 135-142, 1993  
A:Title: Studies of the active site of m-calpain and the interaction with calpastatin.  
A:Reference number: S39391; MUID:94071815; PMID:8250833  
A:Accession: S39392  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <CRA>  
C:Superfamily: calpain small chain; calmodulin repeat homology  
C:Keywords: cysteine proteinase; EF hand; hydrolase

Query Match 60.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 4 SEE 6

## RESULT 2

A39233  
myosin heavy chain 1, smooth muscle - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 20-Sep-1991 #sequence\_revision 20-Sep-1991 #text\_change 13-Feb-1998  
C:Accession: A39233  
R:Kelley, C.A.; Adelstein, R.S.  
J. Biol. Chem. 265, 17876-17882, 1990  
A:Title: The 204-kDa smooth muscle myosin heavy chain is phosphorylated in intact cells  
A:Reference number: A39233; MUID:91009254; PMID:2170399  
A:Accession: A39233  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <REL>  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: smooth muscle

Query Match 60.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 8 SEE 10

## RESULT 3

B47171  
chondroitin sulfate proteoglycan PG-M core protein, splice form V1 - chicken (fragment)  
N:Alternate names: versican-like chondroitin sulfate proteoglycan  
C:Species: Gallus gallus (chicken)  
C>Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Feb-1997  
C:Accession: B47171  
R:Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.  
J. Biol. Chem. 268, 14461-14469, 1993  
A:Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during

A:Reference number: A47171; MUID:93300846; PMID:8314802  
A:Accession: B47171  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-12 <SHI>  
A:Experimental source: CEF, embryo fibroblasts  
A>Note: sequence extracted from NCBI backbone (NCBIN:134459, NCBIIP:134462)

Query Match 60.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 3 SEE 5

## RESULT 4

A49018  
myosin heavy chain, fast skeletal muscle type X - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 13-Aug-1999  
C:Accession: A49018; S32161  
R:DeNardi, C.; Ausoni, S.; Moretti, P.; Gorza, L.; Velleca, M.; Buckingham, M.; Schiaff  
J. Cell Biol. 123, 823-835, 1993  
A:Title: Type 2X-myosin heavy chain is coded by a muscle fiber type-specific and develo  
A:Reference number: A49018; MUID:94043465; PMID:8227143  
A:Accession: A49018  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-14 <DEN>  
A:Cross-references: GB:X72591; NID:9288645; PIDN:CAA51189.1; PID:9288646  
R:DeNardi, C.; Ausoni, S.; Moretti, P.; Gorza, L.; Velleca, M.; Merlie, J.; Buckingham, M.; Schiaff  
submitted to the EMBL Data Library, March 1993  
A:Description: Type 2X myosin heavy chain is coded by a muscle fiber type-specific and develo  
A:Reference number: S32161  
A:Accession: S32161  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-14 <DEN2>  
A:Cross-references: EMBL:X72591; NID:9288645; PIDN:CAA51189.1; PID:9288646  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: skeletal muscle

Query Match 60.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 12 SEE 14

## RESULT 5

S62620  
protein disulfide-isomerase (EC 5.3.4.1) - castor bean (fragment)  
C:Species: Ricinus communis (castor bean)  
C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 17-Mar-1999  
C:Accession: S62620  
R:Coughlan, S.J.; Hastings, C.; Winfrey Jr., R.J.  
Eur. J. Biochem. 235, 215-224, 1996  
A:Title: Molecular characterisation of plant endoplasmic reticulum: identification of p  
A:Reference number: S62620; MUID:96202938; PMID:8631332  
A:Accession: S62620  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <COU>  
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 60.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 3 SEE 5

## RESULT 6

JH0517

```
insulin-like growth factor-binding protein 4 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995
C;Accession: JH0517
R;Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
A;Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth
A;Reference number: JH0515; NUID:92109718; PMID:1722398
A;Accession: JH0517
A;Molecule type: protein
A;Residues: 1-16 <COL>
A;Experimental source: serum

Query Match 60.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
DB 10 SEE 12

RESULT 7
A34572
osteonectin - rat (fragment)
N;Alternate names: BM-40; SPARC
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 17-Nov-2000
C;Accession: A34572
R;Cheng, C.Y.
Biochem. Biophys. Res. Commun. 167, 1393-1399, 1990
A;Title: Purification of a calcium binding protein (rat SPARC) from primary Sertoli cells
A;Reference number: A34572; NUID:90211328; PMID:2322281
A;Accession: A34572
A;Molecule type: protein
A;Residues: 1-17 <RES>
C;Superfamily: osteonectin; calmodulin repeat homology; Kazal proteinase inhibitor homol
C;Keywords: calcium binding; collagen binding; disulfide bond; EF hand; extracellular ma

Query Match 60.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4
DB 8 EEM 10

RESULT 8
I55453
zinc finger homeodomain protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 15-Oct-1999
C;Accession: I55453
R;Miura, Y.; Tam, T.; Ido, A.; Morinaga, T.; Miki, T.; Hashimoto, T.; Tanaoki, T.
J. Biol. Chem. 270, 26840-26848, 1995
A;Title: Cloning and characterization of an ATBF1 isoform that expresses in a neuronal d
A;Reference number: I55453; NUID:96070776; PMID:7592926
A;Accession: I55453
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-18 <RES>
A;Cross-references: GB:I32833; NID:976348; PIDN:AAC37582.1; PID:g976349
C;Superfamily: alpha-fetoprotein enhancer-binding protein; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 60.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
DB 10 SEE 12
```

## RESULT 9

S54272

CTC 75 protein - human

C;Species: Homo sapiens (man)

C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Mar-1999

C;Accession: S54272

R;Genersch, E.; Eckerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.

EMBO J. 14, 791-800, 1995

A;Title: Purification of the sequence-specific transcription factor CTCBP, involved in

A;Reference number: S54272; NUID:95188883; PMID:7882982

A;Accession: S54272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 &lt;GEN&gt;

Query Match

60.0%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3

DB 13 SEE 15

## RESULT 10

S68194

alpha-1,6-mannosyl-glycoprotein 6-beta-N-acetylglucosaminyltransferase (EC 2.4.1.155) V,

C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 03-Jun-2002

C;Accession: S68194

R;Saio, H.; Gu, J.; Nishikawa, A.; Ihara, Y.; Fujii, J.; Kohgo, Y.; Taniguchi, N.

Eur. J. Biochem. 233, 18-26, 1995

A;Title: Organization of the human N-acetylglucosaminyltransferase V gene.

A;Reference number: S68194; NUID:96061927; PMID:7588744

A;Accession: S68194

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-19 &lt;SN1&gt;

A;Cross-references: GB:S80050; NID:g1195562; PIDN:AAD14320.1; PID:g4262020

A;Experimental source: blood

C;Function:

A;Description: catalyzes the transfer of N-acetylglucosamine from UDP-N-acetylglucosam.

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match

60.0%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3

DB 5 SEE 7

## RESULT 11

D49164

chromogranin-B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-May-1997

C;Accession: D49164

R;Nielsen, E.; Wellinder, B.S.; Madsen, O.D.

Endocrinology 129, 3147-3156, 1991

A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides t

A;Reference number: A49164; NUID:92063871; PMID:1954895

A;Accession: D49164

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-20 &lt;NIE&gt;

A;Note: sequence extracted from NCBI backbone (NCBIP:66368)

C;Superfamily: chromogranin B precursor

Query Match

60.0%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 10 SEE 12

RESULT 12  
A49164  
chromogranin-B - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-May-1997  
C;Accession: A49164  
R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.  
Endocrinology 129, 3147-3156, 1991  
A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th  
A;Reference number: A49164; MUID:92063871; PMID:1954895  
A;Accession: A49164  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <NIE>  
A;Note: sequence extracted from NCBI backbone (NCBIP:66372)  
C;Superfamily: chromogranin B precursor

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 10 SEE 12

RESULT 13  
S19618  
globin - polychaete (Eudistyllia vancouveri) (fragment)  
N;Alternate names: chlorocruorin  
C;Species: Eudistyllia vancouveri  
C;Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 05-Dec-1998  
C;Accession: S19618  
R;Qabar, A.N.; Steirn, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O.H  
J. Mol. Biol. 222, 1109-1129, 1991  
A;Title: Hierarchy of globin complexes. The quaternary structure of the extracellular ch  
A;Reference number: S19532; MUID:92106333; PMID:1762147  
A;Accession: S19618  
A;Molecule type: protein  
A;Residues: 1-20 <QAB>  
A;Experimental source: plume  
A;Complex: dodecamers, each consisting of a trimer of tetramers of globin chains, dodeca  
C;Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 4 SEE 6

RESULT 14  
H49164  
chromogranin-B - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Dec-1994  
C;Accession: H49164  
R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.  
Endocrinology 129, 3147-3156, 1991  
A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th  
A;Reference number: A49164; MUID:92063871; PMID:1954895  
A;Accession: H49164  
A;Status: preliminary

A;Molecule type: protein  
A;Residues: 1-20 <NIE>  
A;Note: sequence extracted from NCBI backbone (NCBIP:66364)

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 10 EEM 12

RESULT 15  
A31516  
lectin, galactose/N-acetylgalactosamine-specific - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993  
C;Accession: A31516  
R;Li, M.; Kawasaki, T.; Yamashina, I.  
Biochem. Biophys. Res. Commun. 155, 720-725, 1988  
A;Title: Structural similarity between the macrophage lectin specific for galactose/N-a  
A;Reference number: A31516; MUID:88339956; PMID:3421964  
A;Accession: A31516  
A;Molecule type: protein  
A;Residues: 1-20 <IIX>

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 5 SEE 7

RESULT 16  
I78890  
tyrosine protein kinase - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: I78890  
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C  
Oncogene 9, 3437-3448, 1994  
A;Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine prote  
A;Reference number: I58407; MUID:95060800; PMID:7970703  
A;Accession: I78890  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <RES>  
A;Cross-references: GB:L33339; NID:9609536; PIDN:AAA64432.1; PID:9609538  
C;Genetics:  
A;Gene: p52ntk

Query Match 40.0%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5  
|||  
Db 1 MP 2

RESULT 17  
I54357  
schwannomin - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C;Accession: I54357  
R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.  
Hum. Mol. Genet. 3, 1075-1079, 1994  
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are c  
A;Reference number: I54357; MUID:95072570; PMID:7981675

A:Accession: I54357  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-4 <RES>  
A:Cross-references: GB:L28838; NID:9454836; PIDN:AAAS7150.1; PID:9601923  
C:Genetics:  
A:Gene: NF2

Query Match 40.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

QY 3 EM 4  
||  
Db 3 EM 4

RESULT 18  
S55238  
pallidipin - assassin bug (fragment)  
C:Species: Triatoma pallidipennis (assassin bug)  
C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000  
C:Accession: S55238  
R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin  
B:Ochem, J. 307, 465-470, 1995  
A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib  
A:Reference number: S55238; MUID:95251610; PMID:7733984  
A:Accession: S55238  
A:Molecule type: protein  
A:Residues: 1-4 <HAE>

Query Match 40.0%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

QY 2 EE 3  
||  
Db 1 EE 2

RESULT 19  
B37325  
pap fibmbrial regulatory protein papI - Escherichia coli (fragment)  
C:Species: Escherichia coli  
C:Date: 11-Sep-1992 #sequence\_revision 11-Sep-1992 #text\_change 23-Mar-1993  
C:Accession: B37325  
R:Bratzen, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.  
J. Bacteriol. 173, 1789-1800, 1991  
A:Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus ex  
A:Reference number: A37325; MUID:91154136; PMID:1671857  
A:Accession: B37325  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <BRA>  
A:Cross-references: GB:M63747

Query Match 40.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

QY 1 SE 2  
||  
Db 2 SE 3

RESULT 20  
A32014  
tram protein - Escherichia coli plasmid R100 (fragment)  
C:Species: Escherichia coli  
C:Date: 22-Jun-1989 #sequence\_revision 22-Jun-1989 #text\_change 16-Feb-1997  
C:Accession: A32014  
R:Inamoto, S.; Yoshioka, Y.; Ohtsubo, E.  
J. Bacteriol. 170, 2749-2757, 1988

A:Title: Identification and characterization of the products from the traJ and traY gene  
A:Reference number: A32014; MUID:88227859; PMID:2836369  
A:Accession: A32014  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <INA>  
C:Genetics:  
A:Gene: plasmid  
C:Keywords: DNA binding

Query Match 40.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

QY 2 EE 3  
||  
Db 4 EE 5

RESULT 21  
D60274  
major protein antigen MP746 - Mycobacterium tuberculosis (fragment)  
C:Species: Mycobacterium tuberculosis  
C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993  
C:Accession: D60274  
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.  
Infect. Immun. 59, 372-382, 1991  
A:Title: Isolation and partial characterization of major protein antigens in the cultur  
A:Reference number: A60274; MUID:91099989; PMID:1898899  
A:Accession: D60274  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <NAG>

Query Match 40.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

QY 1 SE 2  
||  
Db 3 SE 4

RESULT 22  
S53595  
hypothetical protein (upstream of transcription factor, CCAAT-binding) - chicken  
C:Species: Gallus gallus (Chicken)  
C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
C:Accession: S53595  
R:Calikhoven, C.P.; Bouwman, P.R.J.; Snippe, L.; Ab, G.  
Nucleic Acids Res. 22, 5540-5547, 1994  
A:Title: Translation start site multiplicity of the CCAAT/enhancer binding protein alph  
A:Reference number: S53595; MUID:95140613; PMID:7838705  
A:Accession: S53595  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <CAL>  
A:Cross-references: EMBL:X66844

Query Match 40.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

QY 4 MP 5  
||  
Db 1 MP 2

RESULT 23  
P10610  
T-cell receptor beta chain V-D-J region (100-2E) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0610

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

C:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0610

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

DB 3 SE 4

RESULT 24

PT0535

T-cell receptor beta chain V-D-J region (126-1AE) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0535

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

C:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0535

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

DB 3 SE 4

RESULT 25

PT0684

T-cell receptor beta chain V-D-J region (140-1BK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0684

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

C:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0684

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-5 <FEE>

A:Experimental source: day 18 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

DB 3 SE 4

RESULT 26

A61419

sarcosine dehydrogenase (EC 1.5.99.1) - Pseudomonas sp. (strain WRF) (fragment)

C:Species: Pseudomonas sp.

C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999

C:Accession: A61419

R:Pinto, J.T.; Frisell, W.R.

Arch. Biochem. Biophys. 169, 483-491, 1975

A:Title: Characterization of the peptide-bound flavin of a bacterial sarcosine dehydrog

A:Reference number: A61419; MUID:76038634; PMID:241294

A:Accession: A61419

A:Molecule type: protein

A:Residues: 1-6 <PIN>

C:Keywords: PAD; Flavoprotein; oxidoreductase; phosphoprotein

F;6/Modified site: 3'-PAD-histidine (His) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

DB 3 SE 4

RESULT 27

S11556

hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment)

N:Alternate names: bisulfite reductase; desulfocystidin

C:Species: Desulfovibrio thermophilus

C:Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998

C:Accession: S11556

R:Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.;

Biochim. Biophys. Acta 1040, 112-118, 1990

A:Title: Purification and characterization of bisulfite reductase (desulfocystidin) fro

A:Reference number: S11024; MUID:90335276; PMID:2165817

A:Accession: S11556

A:Molecule type: protein

A:Residues: 1-6 <FAU>

C:Keywords: oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SE 3

DB 2 SE 3

RESULT 28

PT0648

T-cell receptor beta chain V-D-J region (121-3BK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0648

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

C:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0648

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEE>

A:Experimental source: day 4 postnatal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

DB 3 SE 4



Db 3 SE 4

## RESULT 29

ECMUCR

catch-relaxing peptide - blue mussel

N;Alternate names: CARP

C;Species: Mytilus edulis (blue mussel)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: A29342

R;Hirata, T.; Kubota, I.; Takabatake, I.; Kawahara, A.; Shinamoto, N.; Muneoka, Y.

Brain Res. 422, 374-376, 1987

A;Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.

A;Reference number: A29342; MUID:88052022; PMID:3676797

A;Accession: A29342

A;Molecule type: protein

A;Residues: 1-7 &lt;HIR&gt;

C;Comment: This peptide exhibits both potentiating (contraction) and inhibitory (relaxat

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; hormone; retractor muscle

F;1/Modified site: amidated carboxyl end (Leu) #status experimental

## Query Match

Best Local Similarity 40.0%; Score 2; DB 2; Length 7;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5

||

Db 2 MP 3

## RESULT 30

S33244

neuromodulatory peptide Wamide-1 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C;Accession: S33244

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of b

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33244

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 &lt;MIN&gt;

## Query Match

Best Local Similarity 40.0%; Score 2; DB 2; Length 7;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4

||

Db 3 EM 4

## RESULT 31

S33245

neuromodulatory peptide Wamide-2 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C;Accession: S33245

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of b

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33245

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 &lt;MIN&gt;

## Query Match

Best Local Similarity 40.0%; Score 2; DB 2; Length 7;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4

||

Db 3 EM 4

## RESULT 32

I46868

alpha-myosin heavy chain - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 05-Nov-1999

C;Accession: I46868

R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Heu, H.

Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984

A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricul

A;Reference number: I46868; MUID:84221901; PMID:6328491

A;Accession: I46868

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-7 &lt;FRI&gt;

A;Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539

## Query Match

Best Local Similarity 40.0%; Score 2; DB 2; Length 7;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3

||

Db 6 EE 7

## RESULT 33

B39040

calsequestrin, fast skeletal muscle - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 23-Feb-1997

C;Accession: B39040

R;Calà, S.E.; Jones, L.R.

J. Biol. Chem. 266, 391-398, 1991

A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casei

A;Reference number: A39040; MUID:91093153; PMID:1985907

A;Accession: B39040

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 &lt;CAL&gt;

C;Keywords: phosphoprotein; skeletal muscle

## Query Match

Best Local Similarity 40.0%; Score 2; DB 2; Length 7;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3

||

Db 3 EE 4

## RESULT 34

PT0529

T-cell receptor beta chain V-D-J region (100-4K) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0529

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0529

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 &lt;FEE&gt;

A;Experimental source: adult thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 3 SE 4

RESULT 35  
 PT0667  
 T-cell receptor beta chain V-D-J region (121-21) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0667  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0667  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <FE>  
 A:Experimental source: day 4 postnatal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 3 SE 4

RESULT 36  
 PT0702  
 T-cell receptor beta chain V-D-J region (161-2AA) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0702  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0702  
 A>Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-7 <FE>  
 A:Experimental source: newborn thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 3 SE 4

RESULT 37  
 A58718  
 carnocin UI49 - Carnobacterium sp. (fragment)  
 C:Species: Carnobacterium sp.  
 C>Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
 C:Accession: A58718  
 R:Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.  
 Appl. Environ. Microbiol. 58, 1417-1422, 1992  
 A:Title: Purification and characterization of a new bacteriocin isolated from a Carnobac  
 A:Reference number: A58718; MUID:92321768; PMID:1622206  
 A:Accession: A58718  
 A>Status: preliminary

A:Molecule type: protein  
 A:Residues: 1-7 <STO>  
 C:Keywords: antibiotic; lanthionine

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 2 SE 3

RESULT 38  
 S45648  
 Na+-transporting ATP synthase (EC 3.6.1.-) alpha chain - Acetobacterium woodii (fragment)  
 N:Alternate names: ATPase alpha chain  
 C:Species: Acetobacterium woodii  
 C>Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07-May-1999  
 C:Accession: S45648  
 R:Reidlinger, J.; Mueller, V.  
 Eur. J. Biochem. 223, 275-283, 1994  
 A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as  
 A:Reference number: S45648; MUID:94307271; PMID:8033902  
 A:Accession: S45648  
 A:Molecule type: protein  
 A:Residues: 1-3; 4-7 <REI>  
 A:Experimental source: DSM 1030  
 C:Keywords: hydrolase

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SE 3  
 ||  
 Db 5 EE 6

RESULT 39  
 S15597  
 orf 4 rara 5'-region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 04-Jun-1999 #sequence\_revision 04-Jun-1999 #text\_change 28-Jun-1999  
 C:Accession: S15597  
 R:Brand, N.J.; Petkovich, M.; Chambon, P.  
 Nucleic Acids Res. 18, 6799-6806, 1990  
 A:Title: Characterization of a functional promoter for the human retinoic acid receptor  
 A:Reference number: S15594; MUID:91088249; PMID:2175878  
 A:Accession: S15597  
 A:Molecule type: DNA  
 A:Residues: 1-7 <BRA>  
 A:Cross-references: EMBL:X56058; NID:935876  
 A:Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0  
 C:Comment: This sequence is not thought to be translated.  
 C:Genetics:  
 \*A:Gene: GDB:RARA  
 A:Cross-references: GDB:120337; OMIM:180240  
 A:Map position: 17q12-17q12

Query Match 40.0%; Score 2; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5  
 ||  
 Db 1 MP 2

RESULT 40  
 A32523  
 peptidyl-dipeptidase A (EC 3.4.15.1) - bovine (fragment)  
 N:Alternate names: angiotensin I-converting enzyme; peptidyl-dipeptidase I

C;Species: Bos primigenius taurus (cattle)  
 C;Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 11-May-2000  
 C;Accession: A32523  
 R;Harris, R.B.  
 Adv. Exp. Med. Biol. 198, 513-521, 1986  
 A;Title: Isolation and sequencing of an active-site peptide from angiotensin I-converting enzyme from bovine aorta  
 A;Reference number: A32523; MUID:87123961; PMID:3028071  
 A;Accession: A32523  
 A;Molecule type: protein  
 A;Residues: 1-8 <HAR>  
 C;Superfamily: mammalian peptidyl-dipeptidase A  
 C;Keywords: alternative splicing; blood pressure control; peptidyl-dipeptide hydrolase; 2

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 DB 7 SE 8

RESULT 41  
 A41117  
 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)  
 C;Species: Naja naja oxianna (Asian cobra, Oxius cobra)  
 C;Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 23-Jun-1993  
 C;Accession: A41117  
 R;Kretzenkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a  
 A;Reference number: A41117; MUID:91296772; PMID:2068091  
 A;Accession: A41117  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-8 <KRE>  
 C;Keywords: carboxylic ester hydrolase

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4  
 ||  
 DB 3 EM 4

RESULT 42  
 A14683  
 aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragm  
 N;Alternate names: aspartate aminotransferase, mitochondrial  
 C;Species: Gallus gallus (chicken)  
 C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000  
 C;Accession: A14683  
 R;Wilson, K.J.; Hunziker, P.; Hughes, G.J.  
 FEBS Lett. 108, 98-102, 1979  
 A;Title: Microsequence analysis. IV. Automatic liquid-phase sequencing using DABITC.  
 A;Reference number: A14683; MUID:80092116; PMID:520566  
 A;Accession: A14683  
 A;Molecule type: protein  
 A;Residues: 1-8 <WIL>  
 C;Keywords: aminotransferase; mitochondrion

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 DB 1 SE 2

RESULT 43

enamelin f - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
 C;Accession: S10783  
 R;Strawich, E.; Glimcher, M.J.  
 Eur. J. Biochem. 191, 47-56, 1990  
 A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is alb  
 A;Reference number: S10780; MUID:90336641; PMID:2379503  
 A;Accession: S10783  
 A;Molecule type: protein  
 A;Residues: 1-8 <STR>  
 C;Keywords: enamel; phosphoprotein

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5  
 ||  
 DB 1 MP 2

RESULT 44  
 PT0595  
 T-cell receptor beta chain V-D-J region (100-2AA) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PT0595  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0595  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-8 <FEE>  
 C;Experimental source: newborn thymus, strain BALB/c  
 C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 DB 3 SE 4

RESULT 45  
 A35180  
 neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 21-Mar-1996  
 C;Accession: A35180  
 R;Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Vajima, H.; Satoh, M.  
 J. Biol. Chem. 265, 5809-5815, 1990  
 A;Title: Purification of a novel type of calcium-activated neutral protease from rat br.  
 A;Reference number: A35180; MUID:90202830; PMID:2318836  
 A;Accession: A35180  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-8 <YOS>  
 C;Keywords: hydrolase

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 DB 4 SE 5

## RESULT 46

S29272  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996  
 C:Accession: S29272  
 R;Nalecz, K.A.; Nalecz, M.J.; Azzi, A.  
 Eur. J. Biochem. 209, 37-42, 1992  
 A;Title: Isolation of tocopherol-binding proteins from the cytosol of smooth muscle A7r5  
 A;Reference number: S29272; MUID:93011150; PMID:1396710  
 A;Accession: S29272  
 A:Molecule type: protein  
 A;Residues: 1-8 <NAI>  
 A;Experimental source: smooth muscle A7r5 cells

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
 ||  
 Db 2 EE 3

## RESULT 47

S157532  
 gene Tn15low protein - rat (fragment)  
 C:Species: Rattus sp. (rat)  
 C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: I57532  
 R;Banerjee-Basu, S.; Buonanno, A.  
 Mol. Cell. Biol. 13, 7019-7028, 1993  
 A;Title: cis-acting sequences of the rat troponin I slow gene confer tissue- and develop  
 A;Reference number: I57532; MUID:94019373; PMID:8413291  
 A;Accession: I57532  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A;Residues: 1-8 <RES>  
 A;Cross-references: GB:S66172; NID:G432603  
 C;Genetics:  
 A;Gene: Tn15low

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5  
 ||  
 Db 1 MP 2

## RESULT 48

B47594  
 aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)  
 C:Species: Corynebacterium flavum  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 19-Dec-1997  
 C:Accession: B47594  
 R;Pollettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.  
 J. Bacteriol. 175, 4096-4103, 1993  
 A;Title: Gene structure and expression of the Corynebacterium flavum N13 ask-asd operon.  
 A;Reference number: A47594; MUID:93308089; PMID:8100567  
 A;Accession: B47594  
 A;Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A;Residues: 1-8 <FOL>  
 C;Keywords: phosphotransferase

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3

Db 2 EE 3  
 ||

## RESULT 49

S69165  
 ferredoxin a2 - Japanese radish (fragment)  
 C:Species: Kaiware daikon (Japanese radish)  
 C>Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 17-Apr-1998  
 C:Accession: S69165  
 R;Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.  
 Arch. Biochem. Biophys. 316, 797-802, 1995  
 A;Title: Four ferredoxins from Japanese radish leaves.  
 A;Reference number: S69164; MUID:95168867; PMID:7864635  
 A;Accession: S69165  
 A:Molecule type: protein

A;Residues: 1-8 <OBA>  
 C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
 ||  
 Db 4 EE 5

## RESULT 50

A25836  
 L-serine ammonia-lyase (EC 4.3.1.17) - Escherichia coli (fragment)  
 C:Species: Escherichia coli  
 C>Date: 24-Jan-1988 #sequence\_revision 24-Jan-1988 #text\_change 21-Jun-2002  
 C:Accession: A25836  
 R;Heincz, M.C.; McFall, E.  
 J. Bacteriol. 123, 1163-1168, 1975  
 A;Title: N-terminal amino acid sequences of D-serine deaminases of wild-type and operat  
 A;Reference number: A25836; MUID:76005414; PMID:1099073  
 A;Contents: K12  
 A;Accession: A25836  
 A:Molecule type: protein  
 A;Residues: 1-8 <HEI>  
 C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; ser

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 Db 2 SE 3

## RESULT 51

S35538  
 ribosomal protein S7 - Mycobacterium intracellulare (fragment)  
 C:Species: Mycobacterium intracellulare  
 C>Date: 09-Dec-1993 #sequence\_revision 14-Nov-1997 #text\_change 13-Aug-1999  
 C:Accession: S35538  
 R;Nair, J.; Rouse, D.; Morris, S.  
 Nucleic Acids Res. 21, 1039, 1993  
 A;Title: Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium intrac  
 A;Reference number: S35537; MUID:93197130; PMID:8451173  
 A;Accession: S35538  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A;Residues: 1-9 <NAI>

A;Cross-references: EMBL:L08171; NID:G149994; PID:AAA25376.1; PID:G551901  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1993  
 C;Superfamily: Escherichia coli ribosomal protein S7  
 C;Keywords: protein biosynthesis; ribosome

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5  
||  
Db 1 MP 2

RESULT 52  
A44873  
caldesmon - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997  
C;Accession: A44873  
R;Ikabe, M.; Hornick, T.  
Arch. Biochem. Biophys. 288, 538-542, 1991  
A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protein kinase C  
A;Reference number: A44873; MUID:91378498; PMID:1898046  
A;Accession: A44873  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <IKS>  
A;Experimental source: skeletal myosin  
A;Note: sequence extracted from NCBI backbone (NCBIP:63199)  
C;Superfamily: caldesmon

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
||  
Db 7 EE 8

RESULT 53  
A61230  
caldesmon, cardiac and slow skeletal muscle - northern leopard frog (fragment)  
N;Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin-  
C;Species: Rana pipiens (northern leopard frog)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 16-Jul-1999  
C;Accession: A61230  
R;McLeod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.  
Circ. Res. 69, 344-359, 1991  
A;Title: Frog cardiac caldesmon. Identification, characterization, and subcellular distribution.  
A;Reference number: A61230; MUID:91316784; PMID:1860177  
A;Accession: A61230  
A;Molecule type: protein  
A;Residues: 1-9 <MCL>  
C;Comment: Caldesmon is a high-capacity and moderate-affinity calcium binding protein  
C;Comment: Caldesmon acts as a calcium buffer, and the release of calcium bound to caldesmon  
C;Superfamily: caldesmon  
C;Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; skeletal muscle

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
||  
Db 1 EE 2

RESULT 54  
C24180  
fibrinogen beta chain - Japanese macaque (fragment)  
N;Contains: fibrinopeptide B  
C;Species: Macaca fuscata (Japanese macaque)  
C;Date: 05-Jun-1988 #sequence\_revision 10-Mar-1994 #text\_change 26-Jan-1996  
C;Accession: C24180  
R;Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 97, 1487-1492, 1985  
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Ptilinopus) and baboons.  
A;Reference number: A91990; MUID:85289140; PMID:3928610  
A;Accession: C24180  
A;Molecule type: protein  
A;Residues: 1-9 <NAK>  
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide isomerase

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
||  
Db 2 EE 3

RESULT 55  
D24180  
fibrinogen beta chain - red guenon (fragment)  
N;Contains: fibrinopeptide B  
C;Species: Erythrocebus patas (red guenon, hussar)  
C;Date: 05-Jun-1988 #sequence\_revision 10-Mar-1994 #text\_change 26-Jan-1996  
C;Accession: D24180  
R;Nakamura, S.; Takenaka, O.; Takahashi, K.  
J. Biochem. 97, 1487-1492, 1985  
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Ptilinopus) and baboons.  
A;Reference number: A91990; MUID:85289140; PMID:3928610  
A;Accession: D24180  
A;Molecule type: protein  
A;Residues: 1-9 <NAK>  
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide isomerase

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
||  
Db 2 EE 3

RESULT 56  
PW0002  
Chlorophyll a/b-binding protein 31K - green alga (Dunaliella tertiolecta) (fragment)  
N;Alternate names: photosystem II light-harvesting chlorophyll 31K protein  
C;Species: Dunaliella tertiolecta  
C;Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 24-Nov-1999  
C;Accession: PW0002  
R;LaRoche, J.; Bennett, J.; Falkowski, P.G.  
Gene 95, 165-171, 1990  
A;Title: Characterization of a cDNA encoding for the 28.5-kDa LHCII apoprotein from the green alga Dunaliella tertiolecta.  
A;Reference number: JW0040; MUID:91065528; PMID:2249775  
A;Accession: PW0002  
A;Molecule type: protein  
A;Residues: 1-9 <LAR>  
C;Superfamily: chlorophyll a/b-binding protein  
C;Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane protein

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4  
||  
Db 5 EM 6

RESULT 57  
S30494  
cat gene leader peptide - Streptococcus agalactiae plasmid pIP501

C;Species: Streptococcus agalactiae  
C;Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 24-Sep-1999  
C;Accession: S30494  
R;Trieu-Cuot, P.; de Cespedes, G.; Horaud, T.  
Plasmid 28, 272-276, 1992  
A;Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Streptococcus agalactiae plasmid pIP501  
A;Reference number: JQ1950; MUID:93096867; PMID:1461942  
A;Accession: S30494  
A;Molecule type: DNA  
A;Residues: 1-9 <TRI>  
A;Cross-references: EMBL:X65462; NID:G49071; PIDN:CAA46454.1; PID:G581554  
C;Genetics:  
A;Genome: plasmid pIP501  
C;Superfamily: unassigned leader peptides

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
DB 4 SE 5

RESULT 58  
B24362  
Chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus plasmid pIP501  
C;Species: Staphylococcus aureus  
C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 11-May-2000  
C;Accession: B24362  
R;Bruckner, R.; Matzura, H.  
EMBO J. 4, 2295-2300, 1985  
A;Title: Regulation of the inducible chloramphenicol acetyltransferase gene of the Staphylococcus aureus plasmid pIP501  
A;Reference number: A24362; MUID:86081739; PMID:3865770  
A;Accession: B24362  
A;Molecule type: DNA  
A;Residues: 1-9 <BRU>  
A;Cross-references: GB:X02872; NID:G46536; PIDN:CAA26630.1; PID:G581555  
C;Comment: Ribosome stalling in the translation of this leader peptide, caused by the effect of the chloramphenicol O-acetyltransferase from a ribosome binding site located upstream of the chloramphenicol O-acetyltransferase gene.  
C;Genetics:  
A;Genome: plasmid  
C;Superfamily: unassigned leader peptides

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
DB 4 SE 5

RESULT 59  
PT0272  
Ig heavy chain CRD3 region (clone 3-103B) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0272  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J region in the generation of the human Ig heavy chain CRD3 region.  
A;Reference number: PT0272; MUID:91108337; PMID:1899102  
A;Accession: PT0272  
A;Molecule type: DNA  
A;Residues: 1-9 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4  
DB 6 EM 7

RESULT 60  
A37027  
Macrophage chemotactic factor - human (fragment)  
N;Alternate names: T-cell hybridoma D6-18 protein  
C;Species: Homo sapiens (man)  
C;Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 23-Feb-1997  
C;Accession: A37027  
R;Yoshizuka, N.; Yoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.  
Cell. Immunol. 123, 212-225, 1989  
A;Title: Macrophage chemotactic factor (MCF) produced by a human T cell hybridoma clone A37027  
A;Reference number: A37027; MUID:89376581; PMID:2505934  
A;Accession: A37027  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <YOS>

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
DB 8 SE 9

RESULT 61  
C60070  
gastrin - domestic ferret (fragment)  
C;Species: Mustela putorius furo (domestic ferret)  
C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 18-Jun-1993  
C;Accession: C60070  
R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.  
Regul. Pept. 25, 223-231, 1989  
A;Title: The constitution and properties of phosphorylated and unphosphorylated C-terminal fragments of gastrin  
A;Reference number: A60070; MUID:89331947; PMID:2756156  
A;Accession: C60070  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <DES>

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SE 3  
DB 3 SE 4

RESULT 62  
PH0108  
late G1-69 protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C;Accession: PH0108  
R;Nikaido, T.; Bradley, D.W.; Pardee, A.B.  
Exp. Cell Res. 192, 102-109, 1991  
A;Title: Molecular cloning of transcripts that accumulate during the late G1 phase in cells synchronized at the G1/S boundary  
A;Reference number: PH0108; MUID:91078351; PMID:1984406  
A;Accession: PH0108  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-9 <NIK>

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
||  
Db 7 EE 8

## RESULT 63

A56029  
N-methylpurine DNA glycosylase - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 19-Jan-1996  
C:Accession: A56029  
R:Roy, R.; Brooks, C.; Mitra, S.  
Biochemistry 33, 15131-15140, 1994  
A:Title: Purification and biochemical characterization of recombinant N-methylpurine-DNA  
A:Reference number: A56029; MUID:95092772; PMID:7999773  
A:Accession: A56029  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <ROY>

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5  
||  
Db 8 MP 9

## RESULT 64

I58350  
gene c-mpl protein - mouse (fragment)  
C:Species: Mus sp. (mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 28-Feb-1997  
C:Accession: I58350  
R:Alexander, W.S.; Dunn, A.R.  
Oncogene 10, 795-803, 1995  
A:Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a receptor  
A:Reference number: I58350; MUID:95166571; PMID:7662460  
A:Accession: I58350  
A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-9 <RES>

A:Cross-references: GB:S76841; NID:gs12992

C:Genetics:

A:Gene: C-mpl

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5  
||  
Db 1 MP 2

## RESULT 65

PH0942  
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0942  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi  
A:Reference number: PH0891; MUID:92078857; PMID:1836012  
A:Accession: PH0942  
A:Molecule type: mRNA  
A:Residues: 1-9 <GOL>

A:Experimental source: complete Freund's adjuvant-immunized lymph node

A>Note: the authors translated the codon TGC for residue 2 as Ala

C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
||  
Db 7 EE 8

## RESULT 66

PH0935  
T-cell receptor beta chain V-D-J region (clone 6) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0935  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerg  
A:Reference number: PH0891; MUID:92078857; PMID:1836012  
A:Accession: PH0935  
A:Molecule type: mRNA  
A:Residues: 1-9 <GOL>

A:Experimental source: complete Freund's adjuvant-immunized lymph node

C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
Db 4 SE 5

## RESULT 67

PH0917  
T-cell receptor beta chain V-D-J region (isolate 3) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0917  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerg  
A:Reference number: PH0891; MUID:92078857; PMID:1836012  
A:Accession: PH0917  
A:Molecule type: mRNA  
A:Residues: 1-9 <GOL>

A:Experimental source: concanavalin A-activated lymphoblast

C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
Db 4 SE 5

## RESULT 68

PH0921  
T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0921  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerg  
A:Reference number: PH0891; MUID:92078857; PMID:1836012  
A:Accession: PH0921  
A:Molecule type: mRNA  
A:Residues: 1-9 <GOL>

A:Experimental source: concanavalin A-activated lymphoblast

**C;Keywords:** T-cell receptor

```
Query Match      40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	SE	2
Db	4	SE	5

RESULT 69

S15595  
 orf 2 rara 5'-region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Jun-1999 #sequence\_revision 04-Jun-1999 #text\_change 28-Jun-1999  
 C:Accession: S15595  
 R:Brand, N.J.; Petkovich, M.; Chambon, P.  
 Nucleic Acids Res. 18, 6799-6806, 1990  
 A:Title: Characterization of a functional promoter for the human retinoic acid receptor-1  
 A:Reference number: S15594; MUID:91089249; PMID:2175878  
 A:Accession: S15595  
 A:Molecule type: DNA  
 A:Residues: 1-9 <BR>  
 A:Cross-references: EMBL:X56057; NID:q35875  
 A:Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRAR1, release 111.0  
 C:Comment: This sequence is not thought to be translated.  
 C:Genetics:  
 A:Gene: GDB:RARA  
 A:Cross-references: GDB:120337; OMIM:180240  
 A:Map position: 17q12-17q12

Query Match 40.0%; Score 2; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels

Qy 4 MP 5  
D<sub>b</sub> 1 MP 2'

**RESULT 70**

S653388  
Cytochrome-c oxidase (EC 1.9.3.1) chain VII c, hepatic - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C:Accession: S653388; S653389  
R:Schaegger, H.; Noack, H.; Halingk, W.; Brandt, U.; von Jagow, G.  
Eur. J. Biochem. 230, 235-241, 1995  
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymatic properties and amino-term

```
Query Match      40.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
```

Qy 2 EE 3  
Db 4 EE 5

RESULT 71

885091  
T /  
RESUL I  
I60588

sperm-activating peptide (Glu-3, Met-4, Gly-5, Thr-7 SAP-I) - slate-pencil urchin (Hetero-  
 C/Species: Heterocentrotus mamillatus  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
 C/Accession: I60588  
 R/Yoshino, K.I.; Kajiwara, H.; Nomura, K.; Takeao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi,  
 Comp. Biochem. Physiol. B 94, 739-751, 1989  
 A/Title: A halogenated amino acid-containing sperm activating peptide and its related pro-  
 toms nudus, Echinometra mathaei and Heterocentrotus mamillatus.

```
Query Match      40.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	3	EM	4
Db	3	EM	4

RESULT 72

probable methionine-tRNA ligase attenuator peptide - *Thermus aquaticus*  
C:Species: *Thermus aquaticus*  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 18-Jun-1993  
C:Accession: B39517  
R:Nureki, O.; Muramatsu, T.; Suzuki, K.; Kohda, D.; Matsuzawa, H.; Ohca, T.; Miyazawa, T.  
J. Biol. Chem. 266, 3268-3277, 1991  
A:Title: Methionyl-tRNA synthetase gene from an extreme thermophile, *Thermus thermophilus*.  
A:Reference number: A39517; MUID:91131636; PMID:1993699  
A:Accession: B39517  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-10 <NUR>  
A:Cross-references: GB:J05744

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels

Qy 4 MP 5  
db 7 MP 8

RESULT 73

F41839 Ribosomal protein L16 - Acholeplasma laidlawii (fragment)  
 C:Species: Acholeplasma laidlawii  
 C:Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Nov-1994  
 C:Accession: F41839  
 R:Ljm, P.O.; Sears, B.B.  
 J. Bacteriol. 174, 2606-2611, 1992  
 A:Title: Evolutionary relationships of a plant-pathogenic mycoplasma-like organism and A  
 A:Reference number: A41839; MUID:92210505; PMID:1556079  
 A:Accession: F41839  
 A:Status: preliminary; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-10 <LJM>  
 A:Cross-references: GB:M74471  
 C:Genetics:  
 A:Gene: rpl16  
 C:Keywords: protein biosynthesis; ribosome

```
Query Match      40.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;
```

Qy 4 MP 5



Db           ||  
              3 MP 4

## RESULT 74

C38925  
seed storage protein beta-chain 6 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995  
C;Accession: C38925  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional  
A;Reference number: PA0001  
A;Accession: C38925  
A;Molecule type: protein  
A;Residues: 1-10 <KAM>  
A;Experimental source: seed  
C;Keywords: seed; storage protein

Query Match           40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           2 EE 3  
              ||  
Db           3 EE 4

## RESULT 75

A24196  
acetylcholinesterase (EC 3.1.1.7) - electric eel (fragment)  
C;Species: Electrophorus electricus (electric eel)  
C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 28-Apr-1993  
C;Accession: A24196  
R;Kieffer, B.; Goeldner, M.; Hirth, C.; Aebersold, R.; Chang, J.Y.  
FEBS Lett. 202, 91-96, 1986  
A;Title: Sequence determination of a peptide fragment from electric eel acetylcholinesterase  
A;Reference number: A24196  
A;Accession: A24196  
A;Molecule type: protein  
A;Residues: 1-10 <KIE>  
C;Keywords: carboxylic ester hydrolase

Query Match           40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           1 SE 2  
              ||  
Db           5 SE 6

Search completed: November 25, 2003, 18:28:23  
Job time : 4.60106 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 2.42021 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-15  
Perfect score: 5  
Sequence: 1 SEEMP 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	60.0	16	1BP4_PIG	P24854 sus scrofa
2	3	60.0	19	1TPIS_CLOPA	P81348 clostridium
3	3	60.0	20	1LECB_IRIHO	P36231 iris hollan
4	3	60.0	20	1OM4V_VIBAL	P83149 vibrio algi
5	2	40.0	4	1E0SI_HUMAN	P02731 homo sapien
6	2	40.0	5	1TRM3_ECOLI	P13973 escherichia
7	2	40.0	7	1CARP_MYTED	P10420 mytilus edu
8	2	40.0	7	1LANC_CARUI	P36960 carnobacter
9	2	40.0	7	1UF03_MOUSE	P38641 mus musculus
10	2	40.0	7	1WVA3_ACHFU	P35919 achatina fu
11	2	40.0	7	1WVA3_ACHFU	P35921 achatina fu
12	2	40.0	8	1UF06_MOUSE	P38644 mus musculus
13	2	40.0	9	1DI_NEPNO	P24816 nephrops no
14	2	40.0	9	1FAR5_PENMO	P83320 penaeus mon
15	2	40.0	9	1FIBB_ERYPA	P19346 erythrocebu
16	2	40.0	9	1FIBB_MACFU	P19345 macaca fusc
17	2	40.0	9	1LPCA_STAAU	P36894 staphylococ
18	2	40.0	9	1RT33_BOVIN	P82926 bos taurus
19	2	40.0	9	1UN19_CLOPA	P81355 clostridium
20	2	40.0	10	1COXA_ONCMY	P80328 oncorhynch
21	2	40.0	10	1COXO_RAT	P80432 rattus norv
22	2	40.0	10	1RL16_ACHLA	P29221 acholeplasm
23	2	40.0	10	1SPI_HALRO	Q10957 halocynthia
24	2	40.0	10	1SYK_CAMUP	Q46464 campylobact
25	2	40.0	10	1UPA4_HUMAN	P10090 homo sapien
26	2	40.0	10	1UR46_HUMAN	P32080 homo sapien
27	2	40.0	11	1COXA_CANFA	P99501 canis famil
28	2	40.0	12	1CALM_TETTH	Q05055 tetrahymena
29	2	40.0	12	1HS9A_RAT	P82995 rattus norv
30	2	40.0	12	1PA2B_VIPBO	P31859 vipera беру
31	2	40.0	12	1PVK2_PERAM	P81555 periplaneta
32	2	40.0	12	1UR2_POLSP	P81022 polyodon sp
33	2	40.0	13	1BP37_LEUMA	P81754 leucophaea

1	3	40.0	1	CPI_APLCA	Q10998 aplysia cal
2	2	40.0	1	ECDE_LYMDI	P80941 lymantria d
3	2	40.0	1	E121_LITRU	P82097 litoria rub
4	2	40.0	1	E122_LITRU	P82098 litoria rub
5	2	40.0	1	FARB_ASCSU	P43173 ascaris suu
6	2	40.0	1	LMT4_LOCOMI	P41490 locusta mig
7	2	40.0	1	PEDI_HYDAT	P80578 hydra atten
8	2	40.0	1	PSAE_PEA	P20118 pisum sativ
9	2	40.0	1	UHA1_HUMAN	P40928 homo sapien
10	2	40.0	1	UHA3_CANFA	P56535 canis famil
11	2	40.0	1	CX1A_CONBE	P58623 conus betul
12	2	40.0	1	DHSL_ANACY	P17874 anabaena cy
13	2	40.0	1	FIBA_HORSE	P14452 equus cabal
14	2	40.0	1	FIBB_WANLE	P14474 mandrillus
15	2	40.0	1	MARI_ALTSP	P29399 alteromonas
16	2	40.0	1	NSK2_SARBU	P41493 sarcophaga
17	2	40.0	1	PKK6_PERAM	P82993 periplaneta
18	2	40.0	1	UC15_MAIZE	P80621 zea mays (m
19	2	40.0	1	AFP3_MALPA	P83137 malva parvi
20	2	40.0	1	ARCA_STRP5	P58827 streptococc
21	2	40.0	1	ESTJ_WANSE	P19985 manduca sex
22	2	40.0	1	GR78_HORSE	P16392 equus cabal
23	2	40.0	1	METK_MAIZE	P80616 zea mays (m
24	2	40.0	1	MM01_ONCKE	P81037 oncorhynch
25	2	40.0	1	MM01_RAT	P81563 rattus norv
26	2	40.0	1	ODP3_SOLTU	P81420 solanum tub
27	2	40.0	1	RS20_BACST	P59681 bacillus st
28	2	40.0	1	UBL1_WONDO	P50103 monodelphis
29	2	40.0	1	UC13_MAIZE	P80619 zea mays (m
30	2	40.0	1	UN01_PINPS	P81106 pinus pinas
31	2	40.0	1	UN04_PINPS	P81673 pinus pinas
32	2	40.0	1	AF28_MALPA	P83142 malva parvi
33	2	40.0	1	AL11_CALVO	P41839 calliphora
34	2	40.0	1	FIBA_EQUAS	P14449 equus asinu
35	2	40.0	1	FIBA_MELME	P14456 meles meles
36	2	40.0	1	FIBA_MUSVI	P14458 mustela vis
37	2	40.0	1	HTPG_ACICA	P81876 acinetobact
38	2	40.0	1	ODPB_SOLTU	P81419 solanum tub
39	2	40.0	1	UPAB_HUMAN	P31935 homo sapien
40	2	40.0	1	ALYS_MYCPH	P81528 mycobacteri
41	2	40.0	1	GAST_MACMU	P33714 macaca mula
42	2	40.0	1	RM35_YEAST	P36530 saccharomyc
43	2	40.0	1	TRP2_LEUMA	P81733 leucophaea
44	2	40.0	1	AGI_EUPCH	P33888 euphorbia c
45	2	40.0	1	ALI2_CVDPO	P82153 cydia pomon
46	2	40.0	1	DRPH_UCAPU	P08871 uca pugilat
47	2	40.0	1	LUXB_KRYAS	P18300 kryptophana
48	2	40.0	1	OBP_LYMDI	P34173 lymantria d
49	2	40.0	1	RL23_HALCU	P05975 halobacteri
50	2	40.0	1	RL24_SERMA	P49624 serrattia ma
51	2	40.0	1	ADC_CLOPA	P81336 clostridium
52	2	40.0	1	AL22_HORSE	P81217 equus cabal
53	2	40.0	1	FIBA_CERNI	P14447 cervus nipp
54	2	40.0	1	FIBB_HORSE	P14471 equus cabal
55	2	40.0	1	FIBB_LAMGL	P14473 lama glama
56	2	40.0	1	FIBB_TAPTE	P14539 tapirus ter
57	2	40.0	1	FIBB_VULVU	P14482 vulpes vulp
58	2	40.0	1	OXLA_OPHFA	P81183 ophiophagus
59	2	40.0	1	RL10_CITFR	P43448 citrobacter
60	2	40.0	1	BIP_FHAVU	P80089 phaseolus v
61	2	40.0	20	1CATA_ACIRA	P81422 acinetobact
62	2	40.0	20	1COGC_PARC	P20734 paralithode
63	2	40.0	20	1COXA_THUOB	P80972 thunnus obe
64	2	40.0	20	1COXF_ONCMY	P80329 oncorhynch
65	2	40.0	20	1COXN_THUOB	P80980 thunnus obe
66	2	40.0	20	1CPXX_RHORH	P31718 rhodococcus
67	2	40.0	20	1CRTC_SPIOL	P30806 spinacia ol

ALIGNMENTS

RESULT 1

IBP4\_PIG  
ID IBP4\_PIG STANDARD; PRT; 16 AA.  
AC P24854;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Inulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)  
DE (IGF-binding protein 4) (Fragment).  
GN IGFBP4.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RN SEQUENCE.  
RP MEDLINE=92109719; PubMed=1722398;  
RX Coleman M.E., Pan Y.-C.E., Esherton T.D.;  
RA "Identification and NH2-terminal amino acid sequence of three  
RT insulin-like growth factor-binding proteins in porcine serum.";  
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).  
CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFS  
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH  
CC PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE  
CC INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Contains 1 IGFBP domain.  
CC -1- SIMILARITY: Contains 1 thyroglobulin type-I domain.  
DR PIR; JH0517; JH0517.  
DR InterPro; IPR000867; Insl\_gro\_fac\_pr.  
DR InterPro; IPR000716; Thyroglobulin\_1.  
DR PROSITE; PS00222; IGF BINDING; PARTIAL.  
DR PROSITE; PS00484; THYROGLOBULIN\_1; PARTIAL.  
KW Growth factor binding.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;  
  
Query Match 60.0%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SEE 3  
DB 10 SEE 12  
  
RESULT 2  
TPIS\_CLOPA STANDARD; PRT; 19 AA.  
AC P81348;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (CP 25) (Fragment).  
GN TPIA OR TPI.  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RN SEQUENCE.  
RP STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;  
RX Flengserud R., Skjeldestad L.;  
RA "Two-dimensional gel electrophoresis separation and N-terminal  
RT sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycero-  
CC phosphate.  
CC -1- PATHWAY: Plays an important role in several metabolic pathways.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.  
DR HAMAP; MF 00147; -; 1.  
DR InterPro; IPR000652; Triophos\_ismrse.

DR PROSITE; PS00171; TIM; PARTIAL.  
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;  
KW Pentose shunt.  
FT VARIANT 1 1 M -> S.  
FT VARIANT 3 3 T -> Y.  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2053 MW; 288C0350BAFB25AF CRC64;  
  
Query Match 60.0%; Score 3; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SEE 3  
DB 17 SEE 19  
  
RESULT 3  
LECB\_IRIHO STANDARD; PRT; 20 AA.  
ID LECB\_IRIHO  
AC P36231;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE N-acetyl-D-galactosamine-binding lectin subunit B (A-disaccharide-  
DE binding lectin subunit B) (Fragment).  
OS Iris hollandica (Dutch iris).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;  
OC Iris.  
OX NCBI\_TaxID=35876;  
RN [1]  
RN SEQUENCE.  
RP STRAIN=cv. Golden Harvest, and cv. Prof. Blaauw; TISSUP-Bulb;  
RX MEDLINE=94171801; PubMed=8125993;  
RX Mo H., van Damme E.J.M., Peumans W.J., Goldstein I.J.;  
RA "Isolation and characterization of an  
RT N-acetyl-D-galactosamine-binding lectin from Dutch iris bulbs which  
RT recognizes the blood group A disaccharide (GalNAc alpha 1-3Gal).";  
RL J. Biol. Chem. 269:7666-7673(1994).  
CC -1- FUNCTION: GAL / GALNAC-SPECIFIC LECTIN. AGGLUTINATES BOTH NATIVE  
CC AND TRYPSIN-TREATED RABBIT ERYTHROCYTES BUT NOT HUMAN ERYTHROCYTES  
CC IRRESPECTIVE OF BLOOD GROUP TYPE.  
CC -1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A AND B CHAINS.  
KW Lectin.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2246 MW; DE08DA025FD17D56 CRC64;  
  
Query Match 60.0%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SEE 3  
DB 8 SEE 10  
  
RESULT 4  
OM4V\_VIBAL STANDARD; PRT; 20 AA.  
ID OM4V\_VIBAL  
AC P83149;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Outer membrane protein 40Va (Omp40Va) (Fragment).  
OS Vibrio alginolyticus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=663;  
RN [1]  
RN SEQUENCE.  
RP STRAIN=NCIMB 19037;  
RX Onji M., Hirabayashi J., Suzuki S.;

```

RT "Characterization of major outer membrane proteins of Vibrio
RL alginolyticus and the stability against proteases.";
RL Microbes Environ. 0:0-0(2002).
CC -|- SUBCELLULAR LOCATION: Outer membrane.
CC -|- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
KW Transmembrane; Porin; Outer membrane.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2239 MW; 4FA95CB24FEC3CDE CRC64;

Query Match 60.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 1 SEE 3
DB 6 SEE 8

RESULT 5
EOSI_HUMAN
ID EOSI_HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Eosinophilic tetrapeptides.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -|- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR GO; GO:0030105; P:anaphylaxis; IDA.
DR GO; GO:0006935; P:chemotaxis; IDA.
FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
FT FTIDS=VAR_005201.
SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 1 SE 2
DB 3 SE 4

RESULT 6
TRM3_ECOLI
ID TRM3_ECOLI STANDARD; PRT; 5 AA.
AC PL3973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TrmM protein (Fragment).
GN TRAM.
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traJ
RT and traY genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).
CC -|- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: BELONGS TO THE TRAM FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M20941; -; NOT ANNOTATED_CDS.
DR PIR; A32014; A32014.
KW Conjugation; Plasmid; DNA-binding.
FT NON_TER 1
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 SE 3
DB 4 SE 5

RESULT 7
CARP_MYTED
ID CARP_MYTED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahata A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -|- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
CC RETRACTOR MUSCLE.
DR PIR; A29342; ECMUCR.
KW Hormone; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 4 MP 5
DB 2 MP 3

RESULT 8
LANC_CARUI
ID LANC_CARUI STANDARD; PRT; 7 AA.

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AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin U149 (Fragment).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92331768; PubMed=1622206;
RA Scoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -1- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
CC ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON TER
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 2 SE 3

RESULT 9
UF03_MOUSE
ID UF03_MOUSE STANDARD; PRT; 7 AA.
AC P38641;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Marrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
FT NON TER
SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DB1B1180 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 2 EE 3

RESULT 10
WWA1_ACHFU
ID WWA1_ACHFU STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)

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DE Wwamide-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RX TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
CC PIR; S33245; S33245.
DR Neuropeptide; Amidation.
KW Neuropeptide; Amidation.
FT MOD RES
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
DB 3 EM 4

RESULT 11
WWA3_ACHFU
ID WWA3_ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wwamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RX TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD RES
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
DB 3 EM 4

RESULT 12
UF06_MOUSE
ID UF06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX TISSUE=Fibroblast; PubMed=7523108;
RA MEDLINE=95009907; Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
  using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC NON_TER 8
FT PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B905B1 CRC64;

  Query Match 40.0%; Score 2; DB 1; Length 8;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
  ||
DB 2 SE 3

RESULT 13
DI_NEPNO
ID_D1_NEPNO STANDARD; PRT; 9 AA.
AC P24816;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Gastrin/cholecystokinin-like peptide D1.
OS Nephrops norvegicus (Norway lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Nephrops.
OC NCBI_TaxID=6829;
OX [1]
RP SEQUENCE.
RX TISSUE=Stomach; PubMed=1747388;
RA MEDLINE=92082847; Sedlmeier D., Keller R., van Wormhoudt A.;
RA Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.;
RT "Structure and biological activity of crustacean gastrointestinal
  peptides identified with antibodies to gastrin/cholecystokinin.";
RL Biochimie 73:1233-1239(1991).
CC -1- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; S47432; S47432.
KW Hormone.
SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;

  Query Match 40.0%; Score 2; DB 1; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
  ||
DB 1 SE 2

RESULT 14
FAR5_PENMO
ID_FAR5_PENMO STANDARD; PRT; 9 AA.
AC P83370;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP5 (SMPSLRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OC NCBI_TaxID=6687;

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RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
RA Chaivuthangkul P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
  of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

  Query Match 40.0%; Score 2; DB 1; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5
  ||
DB 2 MP 3

RESULT 15
FIBB_ERYPA
ID_FIBB_ERYPA STANDARD; PRT; 9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocytes patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
  patas monkey (Erythrocebus patas): their amino acid sequences,
  RT patas monkey (Erythrocebus patas): their amino acid sequences,
  RT restricted mutations, and a molecular phylogeny for macaques,
  RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D24180; D24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

  Query Match 40.0%; Score 2; DB 1; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
  ||
DB 2 EE 3

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RESULT 16
FIBB_MACFU
ID FIBB_MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE.
RA MEDLINE=85289140; PubMed=1928610;
RX Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COPOLYMER IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; C24180;
DR InterPro; IPR002181; Fibrinogen C.
DR POSITIVE; PS00514; FIBRIN AG_C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1038 MW; 69F65B9C735BB1B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 2 EE 3

RESULT 17
LPCA_STAUAU
ID LPCA_STAUAU STANDARD; PRT; 9 AA.
AC P36884;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OS Streptococcus agalactiae.
OG Plasmid pSCS6, Plasmid pSCS7, Plasmid pUB112, and Plasmid pIP501.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 1311;
RN [1]
RP SEQUENCE FROM N.A.
RA SPECIES=S. aureus; STRAIN=436; PLASMID=pSCS7;
RX MEDLINE=92027652; PubMed=1929326;
RA Schwarz S., Cardoso M.;
RT "Nucleotide sequence and phylogeny of a chloramphenicol
RT acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
RT aureus.";
RL Antimicrob. Agents Chemother. 35:1551-1556(1991).

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RN [2]
RP SEQUENCE FROM N.A.
RA SPECIES=S. aureus; PLASMID=pSCS6;
RX MEDLINE=92388047; PubMed=1517170;
RA Cardoso M., Schwarz S.;
RT "Nucleotide sequence and structural relationships of a
RT chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
RT Staphylococcus aureus.";
RL J. Appl. Bacteriol. 72:289-293(1992).
RN [3]
RP SEQUENCE FROM N.A.
RA SPECIES=S. aureus; PLASMID=pUB112;
RX MEDLINE=86081739; PubMed=3865770;
RA Brueckner R., Matzura H.;
RT "Regulation of the inducible chloramphenicol acetyltransferase gene
RT of the Staphylococcus aureus plasmid pUB112.";
RL EMBO J. 4:2295-2300(1985).
RN [4]
RP SEQUENCE FROM N.A.
RA SPECIES=S. agalactiae; PLASMID=pIP501;
RX MEDLINE=93096867; PubMed=1461942;
RA Trieu-Cuot P., de Cespedes G., Horaud T.;
RT "Nucleotide sequence of the chloramphenicol resistance determinant of
RT the streptococcal plasmid pIP501.";
RL Plasmid 28:272-276(1992).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; M58515; AAA26612.1; -
CC EMBL; M58516; AAA16528.1; -
CC EMBL; X02872; CAA26630.1; -
CC EMBL; X60827; CAA43217.1; -
CC EMBL; X65462; CAA46454.1; -
CC FIR; B24362; B24362.
CC FIR; S30494; S30494.
KW Leader peptide; Antibiotic resistance; Plasmid.
SQ SEQUENCE 9 AA; 1074 MW; 5D9CAB5AAB05B333 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 4 SE 5

RESULT 18
RT33_BOVIN
ID RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RT TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:

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RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 3 SE 4

RESULT 19
UN19_CLOPA STANDARD; PRT; 9 AA.
AC P8135;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 19 from 2D-page (Fragment).
OS Clostridium pasteurianum
OC Bacterii; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629919;
RA Flengrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.5, ITS MW IS: 38.0 kDa.
FT VARIANT 8 8 M -> D.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1128 MW; E33E9B0AF5BB19DA CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
DB 7 EM 8

RESULT 20
COXA_ONCMY STANDARD; PRT; 10 AA.
ID COXA_ONCMY
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa

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RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C33D CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 9 EE 10

RESULT 21
COXO_RAT STANDARD; PRT; 10 AA.
ID COXO_RAT
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1)
DE (VIIIA) (Fragment).
DE COX7C OR COX7C1.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 4 EE 5

RESULT 22
RL16_ACHLA STANDARD; PRT; 10 AA.
ID RL16_ACHLA
AC P29221;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 50S ribosomal protein L16 (Fragment).

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GN RPLP.  
OS Acholeplasma laidlawii;  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
OC Acholeplasmataceae; Acholeplasma.  
OX NCBI\_TaxID=2148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92210505; PubMed=1556079;  
RA Lim P.O., Sears B.B.;  
RA "Evolutionary relationships of a plant-pathogenic mycoplasma-like  
RT organism and Acholeplasma laidlawii deduced from two ribosomal protein  
RT gene sequences.";  
RL J. Bacteriol. 174:2606-2611(1992).  
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS  
CC LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER  
CC (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M74771; AAA21914.1; -;  
DR PIR; F41839; F41839.  
DR InterPro; IPR000114; Ribosomal L16.  
DR PROSITE; PS00586; RIBOSOMAL\_L16\_1; PARTIAL.  
DR PROSITE; PS00701; RIBOSOMAL\_L16\_2; PARTIAL.  
KW Ribosomal protein; rRNA-binding.  
FT NON\_TER 10  
FT SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;  
SQ

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MP 5  
DB 3 MP 4

## RESULT 23

SPI HALRO  
ID SPI HALRO STANDARD; PRT; 10 AA.  
AC Q10597;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Serine proteinase inhibitor (fragment).  
OS Halocynthia roretzi (Sea squirt).  
OS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
OC Stolidobranchia; Pyrosidae; Halocynthia.  
OX NCBI\_TaxID=7729;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Hemolymph;  
RX MEDLINE=96321313; PubMed=8759295;  
RA Shiehikura F., Abe T., Ohtake S.-I., Tanaka K.;  
RA "Purification and characterization of a 58,000-Da proteinase  
RT inhibitor from the hemolymph of a solitary ascidian, Halocynthia  
RT roretzi.";  
RL Comp. Biochem. Physiol. 114B:1-9(1996).  
CC -1- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.  
CC -1- SUBUNIT: Monomer.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR InterPro; IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.  
KW Serpin; Serine proteinase inhibitor; Glycoprotein; Plasma.  
FT NON\_TER 10  
FT SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;  
SQ

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EE 3  
DB 6 EE 7

## RESULT 24

SYK CAMUP  
ID SYK CAMUP STANDARD; PRT; 10 AA.  
AC Q46464;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LYSRS)  
DE (Fragment).  
GN LYSS  
OS Campylobacter upsaliensis.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Campylobacteraceae; Campylobacter.  
OX NCBI\_TaxID=28080;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=ATCC 43954;  
RX MEDLINE=97149302; PubMed=89961110;  
RA Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;  
RA "Characterization of Campylobacter upsaliensis fur and its  
RT localization in a highly conserved region of the Campylobacter  
RT genome.";  
RL Gene 183:219-224(1996).  
CC -1- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate  
CC + L-lysyl-tRNA(Lys).  
CC -1- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; L77076; AAB41342.1; -;  
DR HAMAP; MF 00252; -; 1.  
DR InterPro; IPR006195; tRNA\_ligase\_II.  
DR PROSITE; PS50862; AA\_TRNA\_LIGASE\_II; PARTIAL.  
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
KW Metal-binding; Magnesium.  
FT NON\_TER 1  
FT SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;  
SQ

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SE 2  
DB 3 SE 4

## RESULT 25

UPA4 HUMAN  
ID UPA4 HUMAN STANDARD; PRT; 10 AA.  
AC P30090;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
SQ

DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.8, ITS MW IS: 40.5 kDa.  
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF  
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT  
CC PROTEIN.  
DR SWISS-2DPAGE; P30090; HUMAN.  
FT NON\_TER 1 1  
FT UNSURE 4 4  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;  
  
Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SE 2  
DB 6 SE 7  
  
RESULT 26  
ID URA6\_HUMAN STANDARD; PRT; 10 AA.  
AC P32080;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of red blood cells (Spot 17) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Erythrocyte;  
RX MEDLINE=94147970; PubMed=8313871;  
RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,  
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,  
RA Balant L., Hochstrasser D.F.;  
RT "Plasma and red blood cell protein maps: update 1993."  
RL Electrophoresis 14:1223-1231(1993).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.4, ITS MW IS: 65 kDa.  
DR SWISS-2DPAGE; P32080; HUMAN.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 965 MW; 63DDC8D86AE1EDDB CRC64;  
  
Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SE 2  
DB 2 SE 3  
  
RESULT 27  
ID COXA\_CANFA STANDARD; PRT; 11 AA.  
ID COXA\_COXA\_CANFA

AC P99501;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 10-MAY-2000 (Rel. 39, Last annotation update)  
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).  
GN COX5A.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart;  
RX MEDLINE=98163340; PubMed=9504812;  
RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
RT dog heart proteins."  
RL Electrophoresis 18:2795-2802(1997).  
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C  
CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.  
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
DR HSC-2DPAGE; P99501; DOG.  
DR InterPro; IPR003204; Cyt\_c\_ox5A.  
DR Pfam; PF02284; COX5A; 1\_c\_ox5A.  
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1B1F5 CRC64;  
  
Query Match 40.0%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 SE 3  
DB 9 SE 10  
  
RESULT 28  
ID CALM\_TETTH STANDARD; PRT; 12 AA.  
AC Q05055;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Calmodulin (Fragment).  
OS Tetrahymena thermophila.  
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;  
OC Tetrahymenina; Tetrahymena.  
OX NCBI\_TaxID=5911;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93281388; PubMed=8506136;  
RA Katoh M., Hirano M., Takemasa T., Kimura M., Watanabe Y.;  
RT "A micronucleus-specific sequence exists in the 5'-upstream region of  
RT calmodulin gene in Tetrahymena thermophila."  
RL Nucleic Acids Res. 21:2409-2414(1993).  
CC -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF  
CC ENZYMES BY CA(++) . AMONG THE ENZYMES TO BE STIMULATED BY THE  
CC CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND  
CC PHOSPHATASES.  
CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING  
CC SITES.  
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.  
CC -----  
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CC EMBL; D12774; BAA02239.1; --  
 DR InterPro; IPR002048; EF-Hand.  
 DR PROSITE; PS00018; EF\_HAND; PARTIAL.  
 KW Calcium-binding; Repeat; Acetylation.  
 FT INIT MET 0 0 BY SIMILARITY.  
 FT MOD\_RES 1 1 ACETYLATION (BY SIMILARITY).  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1393 MW; 83F31CD43DB1B01 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EE 3  
 DB 6 EE 7

# RESULT 29

ID HS9A\_RAT STANDARD; PRT; 12 AA.  
 AC P8295;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Heat shock protein HSP 90-alpha (Fragment).  
 GN HSPCA.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.

RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=2158973; PubMed=11732320;  
 RA Langer T.; Fasold H.;  
 RT "Isolation and quantification of the heat shock protein 90 alpha and  
 RT beta isoforms from rat liver.";  
 RL Protoplasma 218:54-56(2001).  
 CC -1- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY  
 (BY SIMILARITY).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.

DR InterPro; IPR001404; Hsp90.  
 DR PROSITE; PS00298; HSP90; PARTIAL.  
 KW Chaperone; ATP-binding; Heat shock; Phosphorylation.  
 FT MOD\_RES 4 4 PHOSPHORYLATION (BY DS-DNA KINASE) (BY  
 SIMILARITY).  
 FT MOD\_RES 6 6 PHOSPHORYLATION (BY DS-DNA KINASE) (BY  
 SIMILARITY).

FT NON\_TER 12 12  
 FT SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EE 3  
 DB 2 EE 3

# RESULT 30

PA2B\_VIPBO STANDARD; PRT; 12 AA.  
 AC P31859;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phospholipase A2, basic (EC 3.1.1.4) (Phosphatidylcholine

DE 2-acylhydrolase) (Fragment).  
 OS Vipera berus orientalis (Viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Vipera.  
 OX NCBI\_TaxID=31157;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=74128698; PubMed=4206446;  
 RA Delori P.J.;  
 RT "Purification and physicochemical, chemical and biological properties  
 RT of a toxic A2 phospholipase isolated from the venom of viperidae  
 RT snakes: Vipera berus";  
 RL Biochimie 55:1031-1045(1973).  
 CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
 CC acyl groups in 3-sn-phosphoglycerides.  
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 CC acylglycerophosphocholine + a fatty acid anion.  
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II  
 CC SUBFAMILY.

DR InterPro; IPR001211; PhospholipaseA2.  
 DR PROSITE; PS00119; PA2\_ASP; PARTIAL.  
 DR PROSITE; PS00118; PA2\_HIS; PARTIAL.  
 KW Hydrolase; Lipid degradation; Calcium.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1412 MW; D054351A89969879 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EE 3  
 DB 11 EE 12

# RESULT 31

PVK2\_PERAM STANDARD; PRT; 12 AA.  
 ID PVK2\_PERAM  
 AC P81555;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Periviscerokinin-2 (Pea-PVK-2).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Abdominal periviscerokinin-producing organs;  
 RX MEDLINE=98326577; PubMed=9663444;  
 RA Predel R.; Raps J.; Eckert M.; Holman G.M.; Nachman R.J.; Wang Y.;  
 RA Penzlin H.;  
 RT "Isolation of periviscerokinin-2 from the abdominal periviscerokinin-  
 RT organs of the American cockroach, Periplaneta americana.";  
 RL Peptides 19:801-809(1998).  
 CC -1- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITATORY ACTIONS ON THE  
 CC HYPERNEURAL MUSCLE.  
 CC -1- MASS SPECTROMETRY: MW=1189.3; METHOD=WALDI.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 12 12  
 SQ SEQUENCE 12 AA; 1190 MW; 2F4D8EE1EB05728 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 MP 5

```

Db          9 MP 10
||
RESULT 32
UR2_POLSP
ID_UR2_POLSP STANDARD; PRT; 12 AA.
AC P81022;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urotensin II (U-II) (UII).
OS Polyodon spathula (North American paddlefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;
OC Polyodon.
OX NCBI_TaxID=7913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal Cord;
RX MEDLINE=96051494; PubMed=8536944;
RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;
RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea
RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon
RT spathula).";
RL Gen. Comp. Endocrinol. 99:323-332(1995).
CC -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
CC -!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
DR InterPro; IPR001483; Urotensin_II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11 BY SIMILARITY.
SQ SEQUENCE 12 AA; 1410 MW; 7551E9DBB879CEBB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 4 SE 5

RESULT 33
BP37_LEUMA
ID BP37_LEUMA STANDARD; PRT; 13 AA.
AC P81754;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Brain protein 37F3.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Brain;
RX MEDLINE=97269266; PubMed=9114447;
RA Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT maderia cockroach; evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).
CC -!- TISSUE SPECIFICITY: BRAIN.
CC -!- MASS SPECTROMETRY: MW=1435.7; METHOD=WALDI.
SQ SEQUENCE 13 AA; 1436 MW; 8E532C9DE9A7D1B5 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 4 EE 5

RESULT 34
CPI_APLCA
ID_CPI_APLCA STANDARD; PRT; 13 AA.
AC Q10998;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Cerebral peptide 1 (CPI).
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthynura; Opiathobranchia; Anaspidea;
OC Aplysioides; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=97001771; PubMed=8844763;
RA Phares G.A., Lloyd P.E.;
RT "Purification, primary structure, and neuronal localization of
RT cerebral peptide 1 from Aplysia.";
RL Peptides 17:753-761(1996).
CC -!- FUNCTION: MAY FUNCTION AS A PEPTIDE TRANSMITTER.
CC -!- TISSUE SPECIFICITY: FOUND PREDOMINANTLY IN THE CEREBRAL AND PEDAL
CC GLANDIA.
SQ SEQUENCE 13 AA; 1314 MW; 9DBC3CE82C667B05 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 6 SE 7

RESULT 35
ECDE_LYMDI
ID_ECDE_LYMDI STANDARD; PRT; 13 AA.
AC P80941;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis ecdysiotropin peptide E (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC OF LARVAE AND PUPAE.
SQ SEQUENCE 13 AA; 1357 MW; 1841B4CA3275B764 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 SE 2  
||  
12 SE 13

## RESULT 36

E121\_LITRU STANDARD; PRT; 13 AA.  
AC P82097; 2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 2.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog Litoria rubella".  
RL Aust. J. Chem. 52:639-645 (1999).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 13 13  
SQ SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
||  
2 EE 3

## RESULT 37

E122\_LITRU STANDARD; PRT; 13 AA.  
AC P82098; 2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 2.2.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog Litoria rubella".  
RL Aust. J. Chem. 52:639-645 (1999).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 13 13  
SQ SEQUENCE 13 AA; 1598 MW; C1808EF33B357322 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3

Db 2 EE 3  
||

## RESULT 38

FARB\_ASCSU STANDARD; PRT; 13 AA.  
AC P43173;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE PMRFamide-like neuropeptide AF11.  
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
OC Ascarididae; Ascaris.  
OX NCBI\_TaxID=6253;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=95380362; PubMed=7651904;  
RA Cowden C., Stretton A.O.W.;  
RT "Eight novel PMRFamide-like neuropeptides isolated from the nematode Ascaris suum".  
RL Peptides 16:491-500 (1995).  
CC -1- SIMILARITY: BELONGS TO THE FARP (PMRFAMIDE RELATED PEPTIDE) FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 13 13  
SQ SEQUENCE 13 AA; 1495 MW; 9CAEC650D6886B05 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
6 SE 7

## RESULT 39

LMT4\_LOCMI STANDARD; PRT; 13 AA.  
AC P41490;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Locustamyotropin 4 (LOM-Wt-4).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P., de Loof A.;  
RT "Isolation, identification and synthesis of locustamyotropin III and IV, two additional neuropeptides of Locusta migratoria: members of the locustamyotropin peptide family.";  
RT Insect Biochem. Mol. Biol. 22:447-452 (1992).  
CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY). LOM-WT IV SEEMS TO BE A MORE POTENT MUSCLE STIMULATOR THAN LOM-WT I, II AND III.  
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR PIR; B61620; B61620.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 13 13  
SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5  
||  
Db 7 MP 8

## RESULT 40

PEDI\_HYDAT STANDARD; PRT; 13 AA.  
AC P80578;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Pedin.  
OS Hydra attenuata (Hydra) (Hydra vulgaris).  
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;  
OC Hydridae; Hydra.  
OX NCBI\_TaxID=6087;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96232307; PubMed=8674432;  
RA Hoffmeister S.A.H.;  
RT "Isolation and characterization of two new morphogenetically active peptides from Hydra vulgaris."  
RT Development 122:1941-1948(1996).  
RL  
CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT DEVELOPMENT.  
CC  
KW Morphogen.  
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
Db 12 SE 13

## RESULT 41

PSAE\_PEA STANDARD; PRT; 13 AA.  
AC P20118;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Photosystem I reaction center subunit IV (PSI-E) (Photosystem I 13 kDa protein) (Fragment).  
DE  
GN PSAE.  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=88137587; PubMed=3277857;  
RA Dunn P.P.J., Packman L.C., Pappin D., Gray J.C.;  
RT "N-terminal amino acid sequence analysis of the subunits of pea photosystem I."  
RL FEBS Lett. 228:157-161(1988).  
CC -!- FUNCTION: Stabilizes the interaction between psac and the PSI core, assists the docking of the ferredoxin to PSI and interacts with ferredoxin-NADP oxidoreductase (By similarity).  
CC  
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.  
CC  
CC -!- SIMILARITY: BELONGS TO THE PSAE FAMILY.  
DR PIR; S00316; S00316.  
KW Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1190 MW; D895AG3A52D8DB1D CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
||  
Db 2 SE 3

## RESULT 42

UHA1\_HUMAN STANDARD; PRT; 13 AA.  
AC P40928;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of heart (Spot 4304) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart;  
RX MEDLINE=95203287; PubMed=7895732;  
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;  
RT "The human myocardial two-dimensional gel protein database: update 1994."  
RT  
RL Electrophoresis 15:1459-1465(1994).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.7, ITS MW IS: 35.5 kDa.  
CC  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1380 MW; 6617BA7A1E06AB1B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SE 3  
||  
Db 6 SE 7

## RESULT 43

UHA3\_CANFA STANDARD; PRT; 13 AA.  
AC P56335;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Heart;  
RX MEDLINE=98163340; PubMed=9504812;  
RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins."  
RL Electrophoresis 18:2795-2802(1997).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.9, ITS MW IS: 55.4 kDa.  
CC  
FT HSC-2DPAGE; P56535; DOG.  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

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Db      12 SE 13

RESULT 44
CX1A_CONBE          STANDARD;          PRT;          14 AA.
AC P58623;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conotoxin BetXia.
OS Conus betulinus (Beech cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89764;
RN [1]
RP SEQUENCE. AND MASS SPECTROMETRY.
RC TISSUE=VENOM.
RX MEDLINE=20058566; PubMed=10591037;
RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
RT "Studies on conotoxins of Conus betulinus.";
RL J. Nat. Toxins 8:341-349(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1589.3; METHOD=WALDI.
CC -1- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
KW Neurotoxin; Toxin.
FT DISULFID 1 9 PROBABLE.
FT DISULFID 2 12 PROBABLE.
FT DISULFID 6 13 PROBABLE.
SQ SEQUENCE 14 AA; 1597 MW; 95B725AA93432EB1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5.
DB 10 MP 11

RESULT 45
DHSL_ANACY          STANDARD;          PRT;          14 AA.
AC P17874;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Soluble hydrogenase 50 kDa subunit (EC 1.12.-.-) (Fragment).
OS Anabaena cylindrica.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1165;
RN [1]
RP SEQUENCE.
RX MEDLINE=90126821; PubMed=2129525;
RA Ewart G.D., Reed K.C., Smith G.D.;
RT "Soluble hydrogenase of Anabaena cylindrica. Cloning and sequencing
RT of a potential gene encoding the tritium exchange subunit.";
RL Eur. J. Biochem 187:215-223(1990).
CC -1- FUNCTION: SOLUBLE HYDROGENASE CATALYZES BOTH PRODUCTION AND
CC CONSUMPTION OF HYDROGEN FROM SUITABLE ARTIFICIAL ELECTRON DONORS
CC OR ACCEPTORS. THIS SUBUNIT (50 kDa) IS REQUIRED FOR HYDROGEN
CC PRODUCTION WITH REDUCED METHYL-VIOLEGEN.
CC -1- SUBUNIT: Heterodimer of a large and a small subunit.
CC PR; S07768; S07768.
KW Oxidoreductase.
FT NON TER 14
SQ SEQUENCE 14 AA; 1551 MW; 9254DAFB141CF2A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 2 EE 3

RESULT 46
FIBA_HORSE          STANDARD;          PRT;          14 AA.
AC P14452;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
OS FGA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 14 FIBRINOPEPTIDE A.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1517 MW; 4E998EB63C2A15E7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 2 EE 3

RESULT 47
FIBB_MANLE          STANDARD;          PRT;          14 AA.
AC P14474;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
OS FGB.
OS Mandrillus leucophaeus (Drill) (Papio leucophaeus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Mandrillus.
OX NCBI_TaxID=9568;
RN [1]
RP SEQUENCE.
RX MEDLINE=69115139; PubMed=4974768;
RA Doolittle R.F., Glasgow C., Mross G.A.;
RT "Characterization of fibrinopeptides A and B from a drill (Mandrillus
RT leucophaeus)";
RL Biochim. Biophys. Acta 175:217-219(1969).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.

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CC -|- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -|- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 DR InterPro: IPR002181; Fibrinogen C.  
 DR PROSITE: PS00514; FIBRIN\_AG\_C DOMAIN; PARTIAL.  
 KW Blood coagulation; Plasma; Pyrrolidone carboxylic acid.  
 FT PEPTIDE 1 14 FIBRINOPEPTIDE B.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1434 MW; 6695B0F11EF72E1B CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EE 3  
 DB 7 EE 8  
 RESULT 48  
 MARI\_ALTSP STANDARD; PRT; 14 AA.  
 AC P29399;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Marinosatin C-2 [Marinosatin C-1; Marinosatin D].  
 OS Alteromonas sp. (strain B-10-31).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Alteromonadaceae; Alteromonas.  
 OX NCBI\_TaxID=29456;  
 [1]  
 RN SEQUENCE, AND ACTIVE SITE.  
 RX MEDLINE=92176155; PubMed=1794974;  
 RA Takano R., Imada C., Kami K., Hara S.;  
 RT "The reactive site of marinosatin, a proteinase inhibitor from  
 RT marine Alteromonas sp. B-10-31.";  
 RL J. Biochem. 110:856-858(1991).  
 CC -|- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT  
 CC NOT TRYPSIN.  
 KW Serine protease inhibitor; Pyrrolidone carboxylic acid.  
 FT PEPTIDE 1 14 MARINOSTATIN C-2.  
 FT PEPTIDE 3 14 MARINOSTATIN C-1.  
 FT PEPTIDE 4 14 MARINOSTATIN D.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 6 7 REACTIVE BOND.  
 SQ SEQUENCE 14 AA; 1644 MW; 6E7CEEF92EF32E44 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SE 2  
 DB 13 SE 14  
 RESULT 49  
 NSK2\_SARBU STANDARD; PRT; 14 AA.  
 AC P41493;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Neosulfakinin-II (NEB-SK-II).  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.

OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Head;  
 RX MEDLINE=93083101; PubMed=1360367;  
 RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;  
 RT "Isolation and primary structure of two sulfakinin-like peptides from  
 RT the fleshfly, Neobellieria bullata.";  
 RL Comp. Biochem. Physiol. 103C:135-142(1992).  
 CC -|- FUNCTION: MYOTROPIC PEPTIDE.  
 CC -|- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 DR FIR; A56632; A56632.  
 DR InterPro: IPR001651; Gastrin.  
 DR PROSITE: PS00259; GASTRIN; 1.  
 KW Neuropeptide; Amidation; Sulfation.  
 FT MOD\_RES 9 9 SULFATION (POTENTIAL).  
 FT MOD\_RES 14 14 AMIDATION (POTENTIAL).  
 SQ SEQUENCE 14 AA; 1794 MW; 8B4E06D5B61C62AA CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EE 3  
 DB 3 EE 4  
 RESULT 50  
 PPK6\_PERAM STANDARD; PRT; 14 AA.  
 AC P82693;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinnin-6 (Pea-PK-6) (FXPRL-amide).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.  
 RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
 RT the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -|- FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.  
 CC -|- TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN  
 CC ABDOMINAL PERISYPHATHETIC ORGANS.  
 CC -|- MASS SPECTROMETRY: MW=1590.8; METHOD=MALDI.  
 CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro: IPR001484; Pyrokinnin.  
 DR PROSITE: PS00539; PYROKININ; 1.  
 KW Amidation; Pyrokinnin.  
 FT MOD\_RES 14 14 AMIDATION.  
 SQ SEQUENCE 14 AA; 1592 MW; 3966CC3FF384A998 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SE 2  
 DB 1 SE 2  
 RESULT 51  
 UC15\_MAIZE STANDARD; PRT; 14 AA.  
 ID UC15\_MAIZE  
 AC P80621;

DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)  
 DE (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program."  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.8, ITS MW IS: 35.7 kDa.  
 DR Maize-2DPAGE; P80621; COLEOPTILE.  
 DR MaizeDB; 123947; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EE 3  
 DB 11 EE 12

RESULT 52  
 APP3 MALPA  
 ID APP3 MALPA STANDARD; PRT; 15 AA.  
 AC P8137;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antifungal protein 3 (CW-3) (Fragment).  
 OS Malva parviflora (Little mallow) (Cheeseweed).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC euroids II; Malvales; Malvaceae; Malvoideae; Malva.  
 OX NCBI\_TaxID=145753;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Seed;  
 RX MEDLINE=21199399; PubMed=11302747;  
 RA Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;  
 RT "Purification and characterization of three antifungal proteins from  
 RT Cheeseweed (Malva parviflora)."  
 RL Biochem. Biophys. Res. Commun. 282:1224-1228(2001).  
 CC -1- FUNCTION: Possesses antifungal activity against P.infestans but  
 CC not F.graminearum.  
 CC -1- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
 CC concentration.  
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.  
 DR GO; GO:0007275; P:development; NAS.  
 KW Fungicide; Antibiotic.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EE 3  
 DB 10 EE 11

RESULT 53  
 ARCA\_STRPS  
 ID ARCA\_STRPS STANDARD; PRT; 15 AA.  
 AC P58827;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD)  
 DE (Streptococcal acid glycoprotein) (Fragment).  
 GN ARCA OR SAGP.  
 OS Streptococcus pyogenes (serotype M5).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus  
 OX NCBI\_TaxID=160491;  
 RN [1]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC STRAIN=Manfredo / Serotype M5;  
 RX MEDLINE=98298018; PubMed=9632565;  
 RA Degnan B.A., Palmer J.M., Robson T., Jones C.E.D., Fischer M.,  
 RA Glanville M., Mellor G.D., Diamond A.G., Kehoe M.A., Goodacre J.A.;  
 RT "Inhibition of human peripheral blood mononuclear cell proliferation  
 RT by Streptococcus pyogenes cell extract is associated with arginine  
 RT deiminase activity."  
 RL Infect. Immun. 66:3050-3058(1998).  
 CC -1- FUNCTION: Antitumor protein. Has a powerful and dose-dependent  
 CC inhibitory effect on antigen, superantigen, or mitogen-stimulated  
 CC human peripheral blood mononuclear cell (PBMC) proliferation. It  
 CC may inhibit cell proliferation by arresting cell cycle and  
 CC inducing apoptosis.  
 CC -1- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).  
 CC -1- PATHWAY: Arginine degradation via arginine deiminase; first step.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- SIMILARITY: Belongs to the arginine deiminase family.  
 DR HAMAP; MF 00242; -; 1.  
 KW Hydrolase; Arginine metabolism; Glycoprotein.  
 FT INIT\_MET 0 0  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1657 MW; D21150201B00EE46 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SE 2  
 DB 10 SE 11

RESULT 54  
 ESTJ\_MANSE  
 ID ESTJ\_MANSE STANDARD; PRT; 15 AA.  
 AC P19985;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Juvenile hormone esterase (EC 3.1.1.59) (JH esterase) (Fragment).  
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Sphingioidea;  
 OC Sphingidae; Sphinginae; Manduca.  
 OX NCBI\_TaxID=7130;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larval plasma;  
 RX MEDLINE=91072375; PubMed=2254326;  
 RA Venkatesh K., Abdel-Aal Y.A.I., Armstrong F.B., Roe R.M.;  
 RT "Characterization of affinity-purified juvenile hormone esterase from  
 RT the plasma of the tobacco hornworm, Manduca sexta."  
 RL J. Biol. Chem. 265:21727-21732(1990).  
 CC -1- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF

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CC JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL
CC ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.
CC -!- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-
CC trimethyltrideca-2,6-dienoate + H(2)O = (2E,6E)-(10R,11S)-10,11-
CC epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC PIR; A36527; A36527.
CC InterPro; IPR002018; CarbesteraseB.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
CC KW Hydrolase; Serine esterase.
CC FT NON_TER 15
CC SQ SEQUENCE 15 AA; 1659 MW; D321EA432E58848 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 6 EE 7

RESULT 55
GR78_HORSE
ID GR78_HORSE STANDARD; PRT; 15 AA.
AC P16392;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 78 kDa glucose-regulated protein (GRP 78) (Immunoglobulin heavy chain
DE binding protein) (BiP) (Fragment).
GN HSPA5 OR GRP78.
OS Equus caballus (Horse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
CC NCBI_TaxID=9796;
CC [1]
CC SEQUENCE.
CC MEDLINE=90147817; PubMed=1689156;
CC RA Ohlas B., Boyd N.D., Luber-Narod J., Reyes V.E., Leeman S.E.;
CC RT "Isolation and identification of a polypeptide in the Hsp 70 family
CC that binds substance P.";
CC RL Biochem. Biophys. Res. Commun. 166:978-983(1990).
CC -!- FUNCTION: Probably plays a role in facilitating the assembly of
CC multimeric protein complexes inside the ER.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC InterPro; IPR01023; Hsp70.
CC PROSITE; PS00297; HSP70_1; PARTIAL.
CC PROSITE; PS00329; HSP70_2; PARTIAL.
CC PROSITE; PS01036; HSP70_3; PARTIAL.
CC KW ATP-binding; Endoplasmic reticulum.
CC FT NON_TER 15
CC SQ SEQUENCE 15 AA; 1647 MW; 8119P21D0EC26DB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 1 EE 2

RESULT 56
METK_MAIZE
ID METK_MAIZE STANDARD; PRT; 15 AA.
AC P80616;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine

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DE adenosyltransferase) (AdoMet synthetase) (Spot 178) (Fragment).
OS Zea mays (Maize).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC PACCD clade; Panicoideae; Andropogoneae; Zea.
CC NCBI_TaxID=4577;
CC [1]
CC RN SEQUENCE.
CC RP TISSUE=Coleoptile;
CC RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
CC Pernellet J.-C., Zivy M., de Vienne D.;
CC RT "The maize two dimensional gel protein database: towards an integrated
CC genome analysis program.";
CC RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (Potential).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.9, ITS MW IS: 43.3 kDa.
CC -!- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC DR Maize-2DPAGE; P80616; COLEOPTILE.
CC DR MaizeDB; 123938;
CC DR InterPro; IPR002133; S-AdoMet synt.
CC DR Pfam; PF02772; S-AdoMet syntD2.1
CC DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; PARTIAL.
CC DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; PARTIAL.
CC KW Transferase; One-carbon metabolism; Multigene family; ATP-binding;
CC Mgnesium; Potassium; Metal-binding.
CC FT NON_TER 1
CC FT NON_TER 15
CC SQ SEQUENCE 15 AA; 1601 MW; 232B07E9AC328D32 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 3 EE 4

RESULT 57
MILT_ONCKE
ID MILT_ONCKE STANDARD; PRT; 15 AA.
AC P81037;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Miltpain (EC 3.4.22.-) (fragment).
OS Oncorhynchus keta (Chum salmon).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
CC NCBI_TaxID=8018;
CC [1]
CC RN SEQUENCE, AND CHARACTERIZATION.
CC RX MEDLINE=97397031; PubMed=9253183;
CC RA Kawabata C., Ichishima E.;
CC RT "Miltpain, new cysteine proteinase from the milt of chum salmon,
CC RT Oncorhynchus keta.";
CC RL Comp. Biochem. Physiol. 117B:445-452(1997).
CC -!- FUNCTION: CYSTEINE PROTEINASE THAT HYDROLYZES BASIC PROTEINS.
CC HYDROLYZE BASIC PROTEINS SUCH AS HISTONE, SALMINE AND CLUPAINE BUT
CC NOT MILK CASEIN.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage with basic residues at
CC P2 and P1.
CC MEROPS; C01.093; -.
CC KW Hydrolase.
CC FT NON_TER 15

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SQ SEQUENCE 15 AA; 1730 MW; 766B7771C0F888E7 CRC64;  
 Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4  
 ||  
 DB 8 EM 9

RESULT 58  
 MM01 RAT  
 ID MM01 RAT STANDARD; PRT; 15 AA.  
 AC P81563; 2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interstitial collagenase (EC 3.4.24.7) (Matrix metalloproteinase-1)  
 DE (MMP-1) (Fibroblast collagenase) (Myocardial collagenase) (Fragment).  
 GN MMP1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=96201136; PubMed=8605638;  
 RA Tyagi S.C.; Cleutjens J.P.M.;  
 RT "Myocardial collagenase: purification and structural  
 characterization.";  
 RL Can. J. Cardiol. 12:165-171(1996).  
 CC -1- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN  
 THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X. MAY  
 PLAY A ROLE IN THE DETERIORATION OF THE HEART WALL EXTRACELLULAR  
 MATRIX PROTEINS DURING THE ONSET OF DILATED CARDIOMYOPATHY.  
 CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
 collagen. Cleavage of the triple helix of collagen at about three-  
 quarters of the length of the molecule from the N-terminus, at  
 775-Gly-[Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
 substrates and alpha-macroglobulins at bonds where P1' is a  
 hydrophobic residue.  
 CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.  
 CC -1- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE  
 ACTIVATION PEPTIDE.  
 CC -1- PTM: THE N-TERMINAL IS BLOCKED.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.  
 KW Hydrolase; Metalloprotease; Zinc; Calcium; Collagen degradation;  
 KW Extracellular matrix.  
 FT NON\_TER 1  
 FT NON\_TER 15  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1787 MW; 15A57D24C0F6FD80 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 DB 5 SE 6

RESULT 59  
 ODP3 SOLTU  
 ID ODP3 SOLTU STANDARD; PRT; 15 AA.  
 AC P81420;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 55 kDa dihydropyrimidine acetyltransferase component of pyruvate  
 dehydrogenase complex (EC 2.3.1.12) (E2) (Fragment).  
 DE Solanum tuberosum (Potato).  
 OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Romano; TISSUE=Tuber;  
 RX MEDLINE=98399821; PubMed=9729464;  
 RA Millar A.H.; Knorr C.; Leaver C.J.; Hill S.A.;  
 RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and  
 identification of catalytic components in potato.";  
 RL Biochem. J. 334:571-576(1998).  
 CC -1- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall  
 conversion of pyruvate to acetyl-CoA and CO(2). It contains  
 multiple copies of three enzymatic components: pyruvate  
 dehydrogenase (E1), dihydropyrimidine acetyltransferase (E2) and  
 lipoyl dehydrogenase (E3).  
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + dihydropyrimidine = CoA + S-  
 acetyldihydropyrimidine.  
 CC -1- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL  
 COFACTOR.  
 CC -1- SUBUNIT: FORMS A 60-POLYPEPTIDE STRUCTURAL CORE (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 KW Glycolysis; Transferase; Acyltransferase; Lipoyl; Mitochondrion.  
 FT NON\_TER 15  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1447 MW; EA28B063799BE825 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5  
 ||  
 DB 14 MP 15

RESULT 60  
 RS20 BACST  
 ID RS20 BACST STANDARD; PRT; 15 AA.  
 AC P59681;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE 30S ribosomal protein S20 (BS20) (Fragment).  
 GN RPST.  
 OS Bacillus stearothermophilus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.  
 OX NCBI\_TaxID=1422;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=10;  
 RX PubMed=4607606;  
 RA Yaguchi M.; Matheson A.T.; Visentin L.P.;  
 RT "Prokaryotic ribosomal proteins: N-terminal sequence homologies and  
 structural correspondence of 30 S ribosomal proteins from Escherichia  
 coli and Bacillus stearothermophilus.";  
 RL FEBS Lett. 46:296-300(1974).  
 CC -1- FUNCTION: Binds directly to 16S ribosomal RNA (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE S20P FAMILY OF RIBOSOMAL PROTEINS.  
 DR HAMAP; MF 00500; -; 1.  
 KW Ribosomal protein; rRNA-binding.  
 FT INIT\_MET 0  
 FT NON\_TER 15  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1645 MW; 4E4646265E4C6206 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 DB 13 SE 14

```
RESULT 61
UBL1 MONDO
ID UBL1 MONDO STANDARD; PRT; 15 AA.
AC PS0103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
DE L1) Ubiquitin thiolesterase L1 (Neuron cytoplasmic protein 9.5)
DE (PGP 9.5) (PGP9.5) (Fragment).
DE UCHL1.
GN Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96102916; PubMed=8522974;
RA Mann D.A., Trowern A.R., Lavender F.L., Whittaker P.A.,
RA Thompson R.J.;
RT "Identification of evolutionary conserved regulatory sequences in the
RT 5' untranslated region of the neural-specific ubiquitin C-terminal
RT hydrolase (PGP9.5) gene.";
RL J. Neurochem. 66:35-46(1996).
CC -1- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS.
CC THIS ENZYME IS A THIOL PROTEASE THAT RECOGNIZE AND HYDROLYZE
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@lsb-sib.ch).
CC -----
CC EMBL; U32208; AAA89059.1; -.
CC InterPro; IPR001578; UCH_1.
CC PROSITE; PS00140; UCH_1; PARTIAL.
CC Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family.
KW NON_TER 15
FT SEQUENCE 15 AA; 1816 MW; 1B7A3B6E623F6E79 CRC64;
SQ
Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 EM 4
DB 11 EM 12
RESULT 62
UC13 MAIZE
ID UC13 MAIZE STANDARD; PRT; 15 AA.
AC PS0619;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 243)
DE (Fragment).
DE Zea mays (Maize).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN
RP SEQUENCE
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 62 kDa.
FT NON_TER 1
FT NON_TER 15
FT SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;
SQ
Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EE 3
DB 2 EE 3
RESULT 63
UN01 PINPS
ID UN01 PINPS STANDARD; PRT; 15 AA.
AC P81106;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Unknown protein from 2D-page of needles (S1247/S1248) (N150/N151)
DE (Fragment).
OS Pinus pinaster (Maritime pine).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN
RP SEQUENCE.
RC TISSUE=Needle;
RX Plomion C., Costa P., Bahrman N., Frigerio J.M.;
RA "Genetic analysis of needle proteins in maritime pine. 1. Mapping
RT dominant and codominant protein markers assayed on diploid tissue, in
RT a haploid-based genetic map.";
RL Silvae Genet. 46:161-165(1997).
RN (2)
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 62 kDa.
FT NON_TER 1
FT NON_TER 15
FT SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;
SQ
Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EE 3
DB 2 EE 3
RESULT 64
UN04 PINPS
```

ID UN04\_PINPS STANDARD; PRT; 15 AA.  
AC P81673;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DE Unknown protein from 2D-page of needles (N143) (Fragment).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=71647;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Needle; PubMed=10344291;  
RX MEDLINE=99274088; PubMed=10344291;  
RA Costa P., Plomieu C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
RA Frigerio J.-M., Plomieu C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins";  
RL Electrophoresis 20:1098-1108(1999).  
CC -I- INDUCTION: By water stress.  
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.2, ITS MW IS: 21 KDa.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1489 MW; CE4D85E99308227A CRC64;  
  
Query Match 40.0%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 EE 3  
DB 4 EE 5

RESULT 65  
AF25 MALPA STANDARD; PRT; 16 AA.  
ID AF25 MALPA  
AC P83142;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE Antifungal protein 2 small subunit (CW-2) (Fragment).  
OS Malva parviflora (Little mallow) (Cheeseweed).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.  
OX NCBI\_TaxID=145753;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Seed;  
RX MEDLINE=20568734; PubMed=11118343;  
RA Wang X., Bunkers G.J.;  
RT "Potent heterologous antifungal proteins from cheeseweed (Malva  
RT parviflora)";  
RL Biochem. Biophys. Res. Commun. 279:669-673(2000).  
CC -I- FUNCTION: Possesses antifungal activity against P.infestans but  
CC not F.graminearum.  
CC -I- SUBUNIT: Heterodimer of a large and a small subunit.  
CC -I- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
CC concentration.  
DR GO:0003799; F:antifungal peptide activity; IDA.  
KW Fungicide; Antibiotic.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 2027 MW; 9998D9EB8FB7EB65 CRC64;  
  
Query Match 40.0%; Score 2; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 EE 3  
DB 14 EE 15

UN04\_PINPS STANDARD; PRT; 15 AA.  
AC P81673;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DE Unknown protein from 2D-page of needles (N143) (Fragment).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=71647;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Needle; PubMed=10344291;  
RX MEDLINE=99274088; PubMed=10344291;  
RA Costa P., Plomieu C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
RA Frigerio J.-M., Plomieu C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins";  
RL Electrophoresis 20:1098-1108(1999).  
CC -I- INDUCTION: By water stress.  
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.2, ITS MW IS: 21 KDa.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1489 MW; CE4D85E99308227A CRC64;  
  
Query Match 40.0%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 EE 3  
DB 4 EE 5

RESULT 66  
ALL1-CALVO STANDARD; PRT; 16 AA.  
ID ALL1-CALVO  
AC P41839;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE Callatostatin 1 (Leu-callatostatin 1) [Contains: Callatostatin 2 (Leu-  
DE callatostatin 2) (Leu-callatostatin 3) (Leu-callatostatin 3)].  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain, Head, and Thoracic ganglion;  
RX MEDLINE=93211980; PubMed=8460157;  
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
RA Thorpe A.;  
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria  
RT with sequence homology to cockroach allatostatin";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
RN [2]  
RP CHARACTERIZATION.  
RX MEDLINE=94291167; PubMed=8020069;  
RA Duve H., Thorpe A.;  
RT "Distribution and functional significance of Leu-callatostatin in  
RT the blowfly Calliphora vomitoria";  
RL Cell Tissue Res. 276:367-379(1994).  
CC -I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY  
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
CC -I- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEBRAL  
CC COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY  
CC SYSTEM AND INTESTINE.  
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
DR PIR; A47393; A47393.  
KW Neuropeptide; Amidation.  
FT PEPTIDE 1 16 CALLATOSTATIN 1.  
FT PEPTIDE 3 16 CALLATOSTATIN 2.  
FT PEPTIDE 9 16 CALLATOSTATIN 3.  
FT MOD\_RES 16 16 AMIDATION.  
SQ SEQUENCE 16 AA; 1907 MW; A435B68C26EC3D09 CRC64;  
  
Query Match 40.0%; Score 2; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 EE 3  
DB 5 EE 6

RESULT 67  
FIBA-EQUAS STANDARD; PRT; 16 AA.  
ID FIBA-EQUAS  
AC P14439;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).  
OS Equus asinus (Donkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9793;  
RN [1]  
RP SEQUENCE.

RA Blomback B., Blomback M., Grondahl N.J.;  
 RT "Studies on fibrinopeptides from mammals."  
 RL Acta Chem. Scand. 19:1789-1791(1965).  
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 KW Blood coagulation; Plasma.  
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1696 MW; 09598EB63C2A5957 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.6e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3

DB 4 EE 5

#### RESULT 68

FIBA\_MELME STANDARD; PRT; 16 AA.  
 ID FIBA\_MELME  
 AC P14456;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).  
 GN FGA.  
 OS Meles meles (Eurasian badger).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Carnivora; Fissipedia; Mustelidae; Melinae;  
 OC Meles.  
 OX NCBI\_TaxID=9662;  
 RN [1]  
 RP SEQUENCE.  
 RA Blomback B., Blomback M., Grondahl N.J.;  
 RT "Studies on fibrinopeptides from mammals."  
 RL Acta Chem. Scand. 19:1789-1791(1965).  
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 KW Blood coagulation; Plasma.  
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1708 MW; 09433547919EC7C4 CRC64;

Query Match

Best Local Similarity 40.0%; Score 2; DB 1; Length 16;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

DB 6 SE 7

#### RESULT 69

FIBA\_MUSVI STANDARD; PRT; 16 AA.  
 ID FIBA\_MUSVI  
 AC P14456;  
 DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).  
 GN FGA.  
 OS Mustela vison (American mink).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
 OC Mustela.  
 OX NCBI\_TaxID=9667;  
 RN [1]  
 RP SEQUENCE.  
 RA Blomback B., Blomback M., Grondahl N.J.;  
 RT "Studies on fibrinopeptides from mammals."  
 RL Acta Chem. Scand. 19:1789-1791(1965).  
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 KW Blood coagulation; Plasma.  
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1679 MW; 09432A57919ECF66 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.6e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

DB 6 SE 7

#### RESULT 70

HTPG\_ACICA STANDARD; PRT; 16 AA.  
 ID HTPG\_ACICA  
 AC F81876;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Chaperone protein htpg (Heat shock protein htpg) (High temperature  
 DE protein G) (Fragment).  
 GN HTPG.  
 OS Acinetobacter calcoaceticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 OX NCBI\_TaxID=471,  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=69-V;  
 RX MEDLINE=99274045; PubMed=10344248;  
 RA Bendorff D., Loffhagen N., Babel W.;  
 RT "Induction of heat shock proteins in response to primary alcohols in  
 RT Acinetobacter calcoaceticus."  
 RL Electrophoresis 20:781-789(1999).  
 CC -!- FUNCTION: Molecular chaperone. Has ATPase activity (By  
 CC similarity).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- INDUCTION: BY HEAT SHOCK AND PRIMARY ALCOHOLS.  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.  
 DR HAMAP; MF\_00505; -; 1.  
 DR InterPro; IPR001404; Hsp90.  
 DR PROSITE; PS00298; HSP90; PARTIAL.  
 KW Chaperone; ATP-binding; Heat shock.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1769 MW; 316C70D8928CB482 CRC64;

Query Match

40.0%; Score 2; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
DB 1 SE 2

RESULT 71  
ODPB\_SOLU STANDARD; PRT; 16 AA.  
AC P81419;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial  
DE (EC 1.2.4.1) (PDHE1-B) (Fragment).  
DE Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; Lamids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=cv. Romano; TISSUE=Tuber;  
RX MEDLINE=9839821; PubMed=9729464;  
RA Millar A.H., Knorr C., Leaver C.J., Hill S.A.;  
RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and  
identification of catalytic components in potato.";  
RL Biochem. J. 334:571-576(1998).  
CC -I- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall  
conversion of pyruvate to acetyl-CoA and CO(2). It contains  
multiple copies of three enzymatic components: pyruvate  
dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and  
lipoamide dehydrogenase (E3).  
CC -I- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-  
acetyldihydrolipoamide + CO(2).  
CC -I- COFACTOR: THIAMINE PYROPHOSPHATE.  
CC -I- SUBUNIT: Tetramer of two alpha and two beta subunits (by  
similarity).  
CC -I- SUBCELLULAR LOCATION: Mitochondrial matrix.  
KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;  
KW Phosphorylation; Mitochondrion.  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1705 MW; FFED80EC804F797 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4  
DB 6 EM 7

RESULT 72  
UPAB\_HUMAN STANDARD; PRT; 16 AA.  
AC P31935;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 53) (Fragments).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=94147970; PubMed=8313871;  
RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,  
RA Pasqualetti C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,

RA Balant L., Hochstrasser D.F.;  
RT "Plasma and red blood cell protein maps: update 1993.";  
RL Electrophoresis 14:1223-1231(1993).  
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.9, ITS MW IS: 41 KDa.  
DR SWISS-2DPAGE; P31935; HUMAN.  
FT NON\_TER 1  
FT NON\_CONS 7  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1879 MW; D63C5047818114B2 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
DB 11 EE 12

RESULT 73  
ALYS\_MYCPH STANDARD; PRT; 17 AA.  
ID Alys\_MycPH  
AC P81528;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 38 kDa autolysin (EC 3.2.1.-) (Beta-glycosidase) (Peptidoglycan  
dehydrolyase) (Fragment).  
GN LYTA.  
OS Mycobacterium phlei.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1771;  
RN [1]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC STRAIN=425;  
RX MEDLINE=99140149; PubMed=10206696;  
RA Li Z.S., Beveridge T.J., Betts J., Clarke A.J.;  
RT "Partial characterization of a major autolysin from Mycobacterium  
phlei.";  
RL Microbiology 145:169-176(1999).  
CC -I- FUNCTION: HYDROLYZES THE CELL WALLS OF MYCOBACTERIA. MAY PLAY AN  
IMPORTANT ROLE IN CELL WALL GROWTH AND CELL SEPARATION.  
CC -I- SUBUNIT: Monomer.  
CC -I- PTM: THE N-TERMINUS IS BLOCKED (PROBABLE).  
CC -I- MISCELLANEOUS: THE OPTIMUM PH OF THIS ENZYME IS 7.5.  
KW Hydrolase; Glycosidase; Bacteriolytic enzyme; Cell wall;  
KW Cell division; Septation.  
FT NON\_TER 1  
FT UNSURE 1 2. OR AV OR IG OR LG OR GI OR GL.  
FT UNSURE 14 14 OR L.  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1817 MW; 1FAC3240F5C4EC5 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
DB 9 EE 10

RESULT 74  
GAST\_MACMU STANDARD; PRT; 17 AA.  
ID GAST\_MACMU  
AC P33714;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gastrin.  
GN GAS.



Search completed: November 25, 2003, 18:17:34  
Job time : 3.42021 secs

OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91164506; PubMed=2003150;  
RA Yu J., Xin Y., Eng J., Yalow R.S.;  
RT "Rhesus monkey gastroenteropancreatic hormones: relationship to human  
RT sequences.";  
RL Regul. Pept. 32:39-45(1991).  
CC -!- FUNCTION: Gastrin stimulates the stomach mucosa to produce and  
CC secrete hydrochloric acid and the pancreas to secrete its  
CC digestive enzymes. It also stimulates smooth muscle contraction  
CC and increases blood circulation and water secretion in the stomach  
CC and intestine.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
DR PIR; A60071; A60071.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Hormone; Amidation; Sulfation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 12 12 SULFATION.  
FT MOD\_RES 17 17 AMIDATION.  
SQ SEQUENCE 17 AA; 2076 MW; 6F6E92C73611D39A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8e+03; 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 2 EE 3  
DB 6 EE 7

RESULT 75  
RM35 YEAST  
ID RM35 YEAST STANDARD; PRT; 17 AA.  
AC P36530;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE Mitochondrial 60S ribosomal protein L35 (YML35) (Fragment).  
GN MRPL35.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91285106; PubMed=2060626;  
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,  
RA Kitakawa M.;  
RT "Extended N-terminal sequencing of proteins of the large ribosomal  
RT subunit from yeast mitochondria.";  
RL FEBS Lett. 284:51-56(1991).  
DR PIR; S17274; S17274.  
DR SGD; S0002730; MRPL35.  
KW .Ribosomal protein; Mitochondrion.  
FT NON TER 17 17  
SQ SEQUENCE 17 AA; 1826 MW; 6CE89CB415483EE8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8e+03; 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 1 SE 2  
DB 5 SE 6

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 12.0479 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-15

Perfect score: 5

Sequence: 1 SEEMP 5

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp Vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	80.0	13	5	Q812E2
2	3	60.0	13	6	Q9TU76
3	3	60.0	14	5	P82209
4	3	60.0	14	11	Q06415
5	3	60.0	14	11	Q06414
6	3	60.0	15	2	Q9R5Z5
7	3	60.0	15	6	Q8H279
8	3	60.0	15	10	Q9S8D4
9	3	60.0	15	13	Q9PS61
10	3	60.0	15	15	Q9PXC1
11	3	60.0	17	4	Q96RT4
12	3	60.0	17	10	Q9S8E7
13	3	60.0	17	15	Q85705
14	3	60.0	18	4	Q16173
15	3	60.0	18	4	Q15912
16	3	60.0	18	6	Q9TRT2

17	3	60.0	18	6	Q9TRF1
18	3	60.0	18	10	Q39829
19	3	60.0	18	11	Q8CG31
20	3	60.0	19	4	Q95598
21	3	60.0	19	4	Q16408
22	3	60.0	19	13	Q8U0H2
23	3	60.0	19	13	Q9PS14
24	3	60.0	20	4	Q9BRP3
25	3	60.0	20	5	Q9UAM4
26	3	60.0	20	6	P79256
27	3	60.0	20	10	Q9S8C2
28	3	60.0	20	11	Q9CV29
29	3	60.0	20	11	Q9QVH4
30	3	60.0	20	11	Q9QVG7
31	3	60.0	20	13	Q9PSD3
32	2	40.0	7	2	Q8KMS9
33	2	40.0	7	6	Q28742
34	2	40.0	8	2	Q8KSR3
35	2	40.0	8	2	Q9ZIE9
36	2	40.0	8	2	Q47273
37	2	40.0	8	4	Q16428
38	2	40.0	8	4	Q9P285
39	2	40.0	8	5	Q02032
40	2	40.0	8	6	Q9MYL5
41	2	40.0	8	8	Q8W8G2
42	2	40.0	8	8	Q8W8G4
43	2	40.0	8	8	Q8W8G6
44	2	40.0	8	8	Q8W8G5
45	2	40.0	8	8	Q8W8G3
46	2	40.0	8	8	Q8W8R5
47	2	40.0	8	10	Q42507
48	2	40.0	8	11	Q62721
49	2	40.0	8	11	Q9P40
50	2	40.0	8	11	Q8CJ03
51	2	40.0	8	12	Q83349
52	2	40.0	8	12	Q9WJ33
53	2	40.0	8	12	Q89498
54	2	40.0	8	13	Q90ZV5
55	2	40.0	9	2	P72345
56	2	40.0	9	2	Q43960
57	2	40.0	9	6	Q8WJ77
58	2	40.0	9	6	Q8WJ78
59	2	40.0	9	6	Q9XSL0
60	2	40.0	9	6	Q9TRS0
61	2	40.0	9	6	Q9TRW2
62	2	40.0	9	8	Q8WFT4
63	2	40.0	9	8	Q8WFS4
64	2	40.0	9	8	Q8W8X4
65	2	40.0	9	8	P92072
66	2	40.0	9	8	Q8W875
67	2	40.0	9	8	Q8W8W5
68	2	40.0	9	8	Q8W8W6
69	2	40.0	9	9	Q8H9Z1
70	2	40.0	9	10	Q9FXL0
71	2	40.0	9	10	P82440
72	2	40.0	9	11	Q9QW2
73	2	40.0	9	11	Q93MG3
74	2	40.0	9	11	Q9QZ8
75	2	40.0	9	12	Q83622
76	2	40.0	9	12	Q67605
77	2	40.0	9	12	Q67606
78	2	40.0	9	12	Q84333
79	2	40.0	9	15	Q8AEW8
80	2	40.0	10	2	P74843
81	2	40.0	10	2	Q9ZIB1
82	2	40.0	10	2	P83064
83	2	40.0	10	2	P82588
84	2	40.0	10	3	Q8JOC2
85	2	40.0	10	4	Q8NER0
86	2	40.0	10	4	Q00493
87	2	40.0	10	4	Q9UCQ8
88	2	40.0	10	4	Q9UCP3
89	2	40.0	10	4	Q9UCQ4

Q9trf1 bos taurus	
Q39829 glycine max	
Q8cg31 mus sp. ret	
Q95598 homo sapien	
Q16408 homo sapien	
Q8uuh2 gallus gall	
Q9ps14 gallus gall	
Q9brp3 homo sapien	
Q9uam4 euplates cr	
P79256 actus trivi	
Q9s8c2 pinus sylve	
Q9cv29 rattus sp.	
Q9qvh4 rattus sp.	
Q9qvg7 rattus sp.	
Q9psd3 gallus gall	
Q8kms9 enterobacte	
Q28742 oryctolagus	
Q8rsr3 lactobacill	
Q9zie9 neisseria m	
Q47273 escherichia	
Q16428 homo sapien	
Q9p285 homo sapien	
Q02032 lytechinus	
Q9myl5 pongo pygma	
Q8w8g2 diadema sav	
Q8w8g4 diadema mex	
Q8w8g6 diadema mex	
Q8w8g5 diadema ant	
Q8w8g3 diadema pau	
Q8w8r5 diadema pau	
Q42507 tritum ae	
Q62721 rattus norv	
Q9p40 mus musculu	
Q8cj03 mus musculu	
Q83349 murine coro	
Q9wj33 pseudorabie	
Q89498 murine hepa	
Q90zv5 fulica leuc	
P72345 pseudomonas	
Q43960 azotobacter	
Q8mj77 eulemur ful	
Q8mj78 eulemur ful	
Q9xsl0 capra hircu	
Q9trs0 oryctolagus	
Q9trw2 oryctolagus	
Q8wft4 diadema ant	
Q8wfs4 diadema mex	
Q8w8x4 diadema mex	
P92072 euhadra her	
Q8w875 bostrychia	
Q8w8w5 diadema set	
Q8w8w6 diadema ant	
Q8h9z1 cyanophage	
Q9fxl0 lilium long	
P82440 nicotiana t	
Q9qwg2 mus musculu	
Q93mg3 mus musculu	
Q9qza8 mus musculu	
Q83622 murray vall	
Q67605 squash leaf	
Q67606 squash leaf	
Q84333 simian viru	
Q8sew8 human immun	
P74843 streptomyc	
Q9zib1 clostridium	
P83064 bacillus ce	
P82588 streptococ	
Q8joc2 encephalito	
Q8ner0 homo sapien	
Q00493 homo sapien	
Q9ucq8 homo sapien	
Q9ucp3 homo sapien	
Q9ucq4 homo sapien	

90 Q96QT9 homo sapien  
 91 Q8WXB5 homo sapien  
 92 Q8WTT4 homo sapien  
 93 Q81ZA2 homo sapien  
 94 Q8WPL6 oikopleura  
 95 Q82384 drosophila  
 96 Q82217 bombyx mori  
 97 Q9T47 bos taurus  
 98 Q9GKI5 pan troglod  
 99 Q9GKI4 macaca arct  
 100 Q8WBR7 chaitophoru

## ALIGNMENTS

RESULT 1  
 Q812E2 PRELIMINARY; PRT; 13 AA.  
 AC Q812E2  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN PPA0655W  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=36329;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22255708; PubMed=12368867;  
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,  
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,  
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,  
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,  
 RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,  
 RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,  
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,  
 RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,  
 RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,  
 RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,  
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,  
 RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,  
 RA Seeger K., Sharp S., Smith R., Squares S., Stevens K.,  
 RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,  
 RA Sulston J.E., Craig A., Newbold C., Barrell B.G;  
 RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."  
 RL Nature 419:527-531(2002).  
 DR EMBL: AL031744; CAD48947.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 13 AA; 1619 MW; 50E352E2F7FED1A7 CRC64;

Query Match 80.0%; Score 4; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
 Db 10 SEEM 13

RESULT 2  
 Q9TU76 PRELIMINARY; PRT; 13 AA.  
 AC Q9TU76  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE Interleukin 1 alpha (Fragment).  
 GN IL1A.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99397042; PubMed=10467711;  
 RA Maddox J.F., Hawken R.J., Matthew P., Davies K.P.;  
 RT "Single strand conformational polymorphisms (SSCPs) in the ovine IL1A  
 and IL6 genes";  
 RL Anim. Genet. 30:317-318(1999).  
 DR EMBL; AF117652; AAD25050.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1520 MW; C36BC6198305DB5D CRC64;

Query Match 60.0%; Score 3; DB 6; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 Db 9 SEE 11

RESULT 3  
 P82209 PRELIMINARY; PRT; 14 AA.  
 AC P82209  
 DT 01-OCT-2001 (TREMBLrel. 18, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Unknown protein from 2D-page (Fragment).  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;  
 RX MEDLINE=21177481; PubMed=11280994;  
 RA Zhong B.X.;  
 RT "Protein database for several tissues derived from five instar of  
 RT silkworm."  
 RL I Chuan Hsueh Pao 28:217-224(2001).  
 DR InterPro; IPR000886; ER\_TARGET.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1584 MW; 297C915A81EC1DC8 CRC64;

Query Match 60.0%; Score 3; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 Db 11 SEE 13

RESULT 4  
 Q06415 PRELIMINARY; PRT; 14 AA.  
 AC Q06415  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE 2X myosin heavy chain (Fragment).  
 OS Rattus rattus (Black rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10117;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=diaphragm;  
 RX MEDLINE=94043465; PubMed=8227143;  
 RA DeNardi C., Ausoni S., Moretti P., Gorza L., Velleca M.,  
 RA Buckingham M., Schiaffino S.  
 RT "Type 2X Myosin Heavy Chain is coded by a muscle fiber type-specific  
 RT and developmentally regulated gene."  
 RL J. Cell Biol. 123:823-835(1993).  
 DR EMBL; X72591; CAA51189.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 14 AA; 1655 MW; FIC0536CD7B6AFA1 CRC64;

Query Match 60.0%; Score 3; DB 11; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 DB 12 SEE 14

RESULT 5  
 Q06414 PRELIMINARY; PRT; 14 AA.  
 ID Q06414; Q06918;  
 AC Q06414; Q06918; PubMed=8227143;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Myosin heavy chain, 2B (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Diaphragm;  
 RX MEDLINE=94043465; PubMed=8227143;  
 RA DeNardi C., Ausoni S., Moretti P., Gorza L., Velleca M.,  
 RA Buckingham M., Schiaffino S.  
 RT "Type 2X-myosin heavy chain is coded by a muscle fiber type-specific  
 RT and developmentally regulated gene."  
 RL J. Cell Biol. 123:823-835(1993).  
 DR EMBL; X72590; CAA51188.1; -.  
 DR EMBL; X72589; CAA51187.1; -.  
 KW Muscle protein; Myosin.  
 FT NON TER 1 1  
 SQ SEQUENCE 14 AA; 1641 MW; FIC0536CC526AFA1 CRC64;

Query Match 60.0%; Score 3; DB 11; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 DB 12 SEE 14

RESULT 6  
 Q9R525 PRELIMINARY; PRT; 15 AA.  
 ID Q9R525  
 AC Q9R525;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Streptolysin O (Fragment).  
 OS Streptococcus equisimilis.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OC NCBI\_TaxID=119602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93273535; PubMed=8500915;  
 RA Gerlach D., Kohler W., Gunther E., Mann K.;  
 RT "Purification and characterization of streptolysin O secreted by

RT Streptococcus equisimilis (group C).";  
 RL Infect. Immun. 61:2727-2731(1993).  
 SQ SEQUENCE 15 AA; 1716 MW; 7C02547F72FF85BE CRC64;

Query Match 60.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5  
 DB 4 EMP 6

RESULT 7  
 Q8HZ79 PRELIMINARY; PRT; 15 AA.  
 ID Q8HZ79  
 AC Q8HZ79;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Alpha-synuclein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tompkins M.M., Gai W.P., Douglas S., Bunn S.J.;  
 RT "Alpha-synuclein expression localizes to the Golgi apparatus in bovine  
 RT adrenal medullary chromaffin cells."  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AV124580; AAM94359.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 15 AA; 1774 MW; 1715433C9115DADA CRC64;

Query Match 60.0%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5  
 DB 1 EMP 3

RESULT 8  
 Q9S8D4 PRELIMINARY; PRT; 15 AA.  
 ID Q9S8D4  
 AC Q9S8D4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE CARDOSIN A (Fragment).  
 OS Cynara cardunculus (Cardoon).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; campanulids; Asterales; Asteraceae; Carduoideae; Cardueae;  
 OC Cynara.  
 OC NCBI\_TaxID=4265;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96073661; PubMed=8540346;  
 RA Faro C., Verissimo P., Lin Y., Tang J., Pires E.;  
 RT "Cardosin A and B, aspartic proteases from the flowers of cardoon.";  
 RL Adv. Exp. Med. Biol. 362:373-377(1995).  
 SQ SEQUENCE 15 AA; 1687 MW; 157040FE9E75F39B CRC64;

Query Match 60.0%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 DB 1 SEE 3

Db 1 SEE 3

## RESULT 9

Q9PS61 ID Q9PS61 PRELIMINARY; PRT; 15 AA.  
 AC Q9PS61;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Factor XA light CHAIN, VAPAM light CHAIN=23 kDa PARAMYXOVIRUS-  
 DE activating endoprotease light chain (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=92164779; PubMed=1537403;  
 RA Gotoh B., Yamauchi F., Ogasawara T., Nagai Y.;  
 RT "Isolation of factor Xa from chick embryo as the amniotic endoprotease  
 RT responsible for paramyxovirus activation.";  
 RL FEBS Lett. 296:274-278(1992).  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1766 MW; B84F5F7ED0E57533 CRC64;

Query Match 60.0%; Score 3; DB 13; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4

Db 6 EEM 8

## RESULT 10

Q9PXC1 ID Q9PXC1 PRELIMINARY; PRT; 15 AA.  
 AC Q9PXC1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Unidentified 42 kDa polypeptide (Fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=92348600; PubMed=1379251;  
 RA Bhikhabhai R., Joelson T., Strandberg B., Carlsson T.,  
 RA Lovgren S.;  
 RT "Purification, characterization and crystallization of recombinant  
 RT HIV-1 reverse transcriptase.";  
 RL J. Chromatogr. 604:157-170(1992).  
 SQ SEQUENCE 15 AA; 1633 MW; C58B99E98F7C23C8 CRC64;

Query Match 60.0%; Score 3; DB 15; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4

Db 2 EEM 4

## RESULT 11

Q96RT4 ID Q96RT4 PRELIMINARY; PRT; 17 AA.  
 AC Q96RT4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Tuberos sclerosis 1 (Fragment).  
 GN TSCI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fang L., Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Chao D.R.,  
 RA Fang Z.M.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF274228; AAK60415.1;  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1742 MW; 12BBAPFFB9766FDF CRC64;

Query Match 60.0%; Score 3; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3

Db 7 SEE 9

## RESULT 12

Q9S8E7 ID Q9S8E7 PRELIMINARY; PRT; 17 AA.  
 AC Q9S8E7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE STIGMATIC glycoprotein (Fragment).  
 OS Brassica oleracea (Cauliflower).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3712;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=95322861; PubMed=7599529;  
 RA Hiscok S.J., Doughty J., Willis A.C., Dickinson H.G.;  
 RT "A 7-kDa pollen coating-borne peptide from Brassica napus interacts  
 RT with S-locus glycoprotein and S-locus-related glycoprotein.";  
 RL Planta 196:367-374(1995).  
 SQ SEQUENCE 17 AA; 1848 MW; B542AEA23C317DFF CRC64;

Query Match 60.0%; Score 3; DB 10; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3

Db 6 SEE 8

## RESULT 13

Q85705 ID Q85705 PRELIMINARY; PRT; 17 AA.  
 AC Q85705;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PRCII, fps gene (Fragment).  
 OS Avian sarcoma virus (strain PRCII).  
 OC Viruses; Retroviridae; Avian type C retroviruses.  
 OX NCBI\_TaxID=11880;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PRCII;  
 RX MEDLINE=84225820; PubMed=6328746;  
 RA Carlberg K., Chamberlin M.E., Beemon K.;

RT "The avian sarcoma virus PRCII lacks 1020 nucleotides of the fps  
 RT transforming gene."  
 RL Virology 135:157-167(1984).  
 DR EMBL; K01829; AAA42419.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1868 MW; 7FA99A79368E5458 CRC64;

Query Match 60.0%; Score 3; DB 15; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEE 3  
 Db 13 SEE 15

RESULT 14  
 Q16173 PRELIMINARY; PRT; 18 AA.  
 AC Q16173;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
 DE Dystrophin protein (Fragment).  
 GN DYSTROPHIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94258162; PubMed=8199594;  
 RA Wilton S.D., Chandler D.C., Kakulas B.A., Laing N.G.;  
 RT "Identification of a point mutation and germinal mosaicism in a  
 RT Duchenne muscular dystrophy family."  
 RL Hum. Mutat. 3:133-140(1994).  
 DR EMBL; S71486; AAD14085.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 18 AA; 2159 MW; C33D41084760ED6E CRC64;

Query Match 60.0%; Score 3; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEM 4  
 Db 6 EEM 8

RESULT 15  
 Q15912 PRELIMINARY; PRT; 18 AA.  
 AC Q15912;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Zinc finger homeodomain protein (Fragment).  
 GN ATBF1-B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=96070776; PubMed=7592926;  
 RA Miura Y., Tam T., Ido A., Morinaga T., Miki T., Hashimoto T.,  
 RA Tamaoki T.;  
 RT "Cloning and characterization of an ATBF1 isoform that expresses in a  
 RT neuronal differentiation-dependent manner."  
 RL J. Biol. Chem. 270:26840-26848(1995).  
 DR EMBL; L32833; AAC37582.1; -.

KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1960 MW; 5176F62C445BE7DE CRC64;

Query Match 60.0%; Score 3; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEE 3  
 Db 10 SEE 12

RESULT 16  
 Q9TRT2 PRELIMINARY; PRT; 18 AA.  
 AC Q9TRT2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE EXO1 T27 PEPTIDE-CYTOSOLIC protein factor (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92168136; PubMed=1538762;  
 RA Morgan A., Burgoyne R.D.;  
 RT "Exol and Exo2 proteins stimulate calcium-dependent exocytosis in  
 RT permeabilized adrenal chromaffin cells."  
 RL Nature 355:833-836(1992).  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2141 MW; 5659FFCE50AE198F CRC64;

Query Match 60.0%; Score 3; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEE 3  
 Db 7 SEE 9

RESULT 17  
 Q9TRF1 PRELIMINARY; PRT; 18 AA.  
 AC Q9TRF1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Soluble N-ethylmaleimide-sensitive attachment protein SNAP-25  
 DE (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93374072; PubMed=8365494;  
 RA Horikawa H.P., Saisu H., Ishizuka T., Sekine Y., Tsugita A., Odani S.,  
 RA Abe T.;  
 RL FEBS Lett. 330:236-240(1993).  
 SQ SEQUENCE 18 AA; 2120 MW; 371FC93766C4A7BB CRC64;

Query Match 60.0%; Score 3; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEM 4

```
Db          |||| 2 EEM 4
RESULT 18
Q39829      PRELIMINARY; PRT; 18 AA.
ID Q39829;
AC Q39829;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lipoxigenase (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolidae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ransom;
RX MEDLINE=96151505; PubMed=8587989;
RA Saravitz D.M., Siedow J.N.;
RT "The differential expression of wound-inducible lipoxigenase genes in
RL soybean leaves.";
RI Plant Physiol. 110:287-299(1996).
DR ENBL; U36442; AAC49161.1; -.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1850 MW; F372E99F9F99240F CRC64;

Query Match 60.0%; Score 3; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db |||| 3 SEE 5

RESULT 19
Q8CG31      PRELIMINARY; PRT; 18 AA.
ID Q8CG31;
AC Q8CG31;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Retinoic acid receptor isoform RAR-beta 4 (fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92212900; PubMed=1313565;
RA Nagpal S., Zelent A., Chambon P.;
RT "RAR-beta 4, a retinoic acid receptor isoform is generated from RAR-
RT beta 2 by alternative splicing and usage of a CUG initiator codon.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2718-2722(1992).
DR ENBL; S92180; AAN86725.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1952 MW; 7651E8E27A5078FC CRC64;

Query Match 60.0%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db |||| 12 SEE 14

RESULT 20
O95598      PRELIMINARY; PRT; 19 AA.
ID O95598;
AC O95598;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE <Delta>Fas/APO-1/CD95 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95346908; PubMed=7542559;
RA Owen-Schaub L.B., Angelo L.S., Radinsky R., Ware C.F., Gesner T.G.,
RA Barcos D.P.;
RT "Soluble Fas/APO-1 in tumor cells: a potential regulator of
RT apoptosis?";
RI Cancer Lett. 94:1-8(1995).
DR ENBL; S78781; AAD14292.1; -.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2144 MW; 8ABA3CE543C3DD6B CRC64;

Query Match 60.0%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db |||| 7 SEE 9

RESULT 21
Q16408      PRELIMINARY; PRT; 19 AA.
ID Q16408;
AC Q16408;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE UDP-N-acetylglucosamine: alpha-6-D-mannoside beta-1,6-N-
DE acetylglucosaminyltransferase V[GlcNAc transferase V protein
DE (fragment)].
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96061927; PubMed=7588744;
RA Saito H., Gu J., Nishikawa A., Ihara Y., Fujii J., Kohgo Y.,
RA Taniguchi N.;
RT "Organization of the human N-acetylglucosaminyltransferase V gene.";
RL Eur. J. Biochem. 233:18-26(1995).
DR ENBL; S80050; AAD14320.1; -.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2096 MW; 23D23C06B929C3622 CRC64;

Query Match 60.0%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db |||| 5 SEE 7

RESULT 22
Q8UHU2      PRELIMINARY; PRT; 19 AA.
ID Q8UHU2;
AC Q8UHU2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE TGF-beta4 (Fragment).
DE
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OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Li H., Deeb N., Zhou H., Ashwell C.M., Lamont S.J.;
RT "Chicken OTUs for Growth and Body Composition Traits Associated with
  TGF-beta Family Genes.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF459837; AAL67517.1; -.
DR EMBL; AF459838; AAL67518.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2046 MW; 1250C1CBFE03C2F7 CRC64;

Query Match
Best Local Similarity 60.0%; Score 3; DB 13; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4
Db 11 EEM 13

RESULT 23
Q9PS14 ID Q9PS14 PRELIMINARY; PRT; 19 AA.
AC Q9PS14;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Pyromycin-sensitive aminopeptidase isozyme I (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=93250542; PubMed=8485450;
RA Hui K.S., Saito M., Hui M., Saito M., Lajtha A., Yamamoto K.,
RA Osawa T.;
RL Neurochem. Int. 22:445-453(1993).
DR HSP; P29312; IQJA.
SQ SEQUENCE 19 AA; 2132 MW; 8091278C9478E774 CRC64;

Query Match
Best Local Similarity 60.0%; Score 3; DB 13; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db 14 SEE 16

RESULT 24
Q9BRP3 ID Q9BRP3 PRELIMINARY; PRT; 20 AA.
AC Q9BRP3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;

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RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006143; AA06143.1; -.
KW Hypochemical protein.
SQ SEQUENCE 20 AA; 2080 MW; DEE42194EE428FE4 CRC64;

Query Match
Best Local Similarity 60.0%; Score 3; DB 4; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db 6 SEE 8

RESULT 25
Q9UAM4 ID Q9UAM4 PRELIMINARY; PRT; 20 AA.
AC Q9UAM4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Developmental-specific protein conZa8 (Fragment).
GN CONZa8.
OS Euplotes crassus.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Moneuplotes.
OX NCBI_TaxID=5936;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=G1;
RX MEDLINE=97206572; PubMed=9172827;
RA Ling Z., Ghosh S., Jacobs M.E., Klobutcher L.A.;
RT "Conjugation-specific genes in the ciliate Euplotes crassus: gene
  expression from the old macronucleus.";
RL J. Eukaryot. Microbiol. 44:1-11(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=G1;
RX MEDLINE=98391748; PubMed=9722644;
RA Klobutcher L.A., Gyax S.E., Podoloff J.D., Vermeesch J.R.,
RA Price C.M., Tebeau C.M., Jahn C.L.;
RT "Conserved DNA sequences adjacent to chromosome fragmentation and
  telomere addition sites in Euplotes crassus.";
RL Nucleic Acids Res. 26:4230-4240(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=G1;
RA Ling Z., Klobutcher L.A.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF063083; AAD31725.1; -.
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2115 MW; 0816E1176FCS01AC CRC64;

Query Match
Best Local Similarity 60.0%; Score 3; DB 5; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db 2 SEE 4

RESULT 26
P79256 ID P79256 PRELIMINARY; PRT; 20 AA.
AC P79256;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE S-cone pigment gene/opsin protein (Fragment).
OS Aotus trivirgatus (Night monkey) (Douroucoulis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
 OX NCBI\_TaxID=9505;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96288974; PubMed=8763792;  
 RX Jacobs G.H., Neitz M., Neitz J.;  
 RT "Mutations in S-cone pigment genes and the absence of colour vision in  
 two species of nocturnal primate."  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 263:705-710(1996).  
 DR ENBL; S82618; AAD14408.1;  
 FT NON TER 20  
 SQ SEQUENCE 20 AA; 2325 MW; 1F017A36C0C4101E CRC64;

Query Match 60.0%; Score 3; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 Db [1]  
 5 SEE 7

RESULT 27

Q9S8C2 PRELIMINARY; PRT; 20 AA.  
 AC Q9S8C2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Glutathione reductase (EC 1.6.4.2) (Fragment).  
 OS Pinus sylvestris (Scots pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=3349;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96158490; PubMed=8580767;  
 RA Wangele G., Karpinski S.;  
 RT "Differential redox regulation by glutathione of glutathione reductase  
 and CuZn-superoxide dismutase gene expression in Pinus sylvestris L.  
 needles."  
 RL Planta 198:151-157(1996).  
 SQ SEQUENCE 20 AA; 2079 MW; 752934DEB4C4DAFB CRC64;

Query Match 60.0%; Score 3; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 Db [1]  
 3 SEE 5

RESULT 28

Q9QV29 PRELIMINARY; PRT; 20 AA.  
 AC Q9QV29;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Procarboxypeptidase B (EC 3.4.17.2) (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94255059; PubMed=8200353;  
 RA Opezzo O., Ventura S., Bergman T., Vendrell J., Jornvall H.,  
 RA Aviles F.X.;  
 RT "Procarboxypeptidase in rat pancreas. Overall characterization and  
 comparison of the activation processes."  
 RL Eur. J. Biochem. 222:55-63(1994).

SQ SEQUENCE 20 AA; 2369 MW; 17690B6201C31AA0 CRC64;  
 Query Match 60.0%; Score 3; DB 11; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 Db [1]  
 1 SEE 3

RESULT 29

Q9QVH4 PRELIMINARY; PRT; 20 AA.  
 AC Q9QVH4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Chromogranin-B, CGB=GLUCAGONOMA peptide (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92063871; PubMed=1954895;  
 RA Nielsen E., Welinder B.S., Madsen O.D.;  
 RT "Chromogranin-B, a putative precursor of eight novel rat glucagonoma  
 peptides through processing at mono-, di-, or tribasic residues."  
 RL Endocrinology 129:3147-3156(1991).  
 DR InterPro; IPR001990; Granin.  
 DR Pfam; PF01271; Granin; 1.  
 FT NON TER 1  
 FT NON TER 20  
 SQ SEQUENCE 20 AA; 2298 MW; A4E86C9A9A33FC97 CRC64;

Query Match 60.0%; Score 3; DB 11; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 Db [1]  
 10 SEE 12

RESULT 30

Q9QVG7 PRELIMINARY; PRT; 20 AA.  
 AC Q9QVG7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Chromogranin-B, CGB=GLUCAGONOMA peptide (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92063871; PubMed=1954895;  
 RA Nielsen E., Welinder B.S., Madsen O.D.;  
 RT "Chromogranin-B, a putative precursor of eight novel rat glucagonoma  
 peptides through processing at mono-, di-, or tribasic residues."  
 RL Endocrinology 129:3147-3156(1991).  
 FT NON TER 1  
 FT NON TER 20  
 SQ SEQUENCE 20 AA; 2321 MW; 2ED94F21F4E80274 CRC64;

Query Match 60.0%; Score 3; DB 11; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4

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Db      10 EEM 12

RESULT 31
Q9PSD3 PRELIMINARY; PRT; 20 AA.
ID Q9PSD3
AC Q9PSD3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Bone sialoprotein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95209705; PubMed=7695644;
RA Gotoh Y., Salih E., Glimcher M.J., Gerstenfeld L.C.;
RT "Characterization of the major non-collagenous proteins of chicken
RT bone: identification of a novel 60 kDa non-collagenous
RT phosphoprotein.";
RL Biochem. Biophys. Res. Commun. 208:863-870(1995).
SQ SEQUENCE 20 AA; 2306 MW; F7AD275D51E18525 CRC64;

Query Match 60.0%; Score 3; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db 15 SEE 17

RESULT 32
Q8KMS9 PRELIMINARY; PRT; 7 AA.
ID Q8KMS9
AC Q8KMS9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative transposase (Fragment).
GN TNIA.
OS Enterobacter sp. CH2-4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=143777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH2-4;
RX MEDLINE=21604134; PubMed=11763242;
RA Mindlin S.Z., Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.,
RA Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Mercury resistance transposons of Gram-negative environmental
RT bacteria and their classification.";
RL Res. Microbiol. 152:811-822(2001).
DR EMBL; AJ302778; CAC83058.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DAA9A0 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
Db 5 EE 6

RESULT 33
Q28742 PRELIMINARY; PRT; 7 AA.
ID Q28742
AC Q28742;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hau H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E6932680 CRC64;

Query Match 40.0%; Score 2; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
Db 6 EE 7

RESULT 34
Q8RSR3 PRELIMINARY; PRT; 8 AA.
ID Q8RSR3
AC Q8RSR3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PduG protein (Fragment).
GN PDUG.
OS Lactobacillus collinoides.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33960;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LMG 18850;
RA Sauvageot N., Gouffi K., Laplace J.M., Auffray Y.;
RT "Characterisation of the diol dehydratase pdu operon of Lactobacillus
RT collinoides.";
RL FEMS Microbiol. Lett. 0:0-0(0).
DR EMBL; AJ297723; CAD01093.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 882 MW; ECA40B05BAB5BDD6 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 5 SE 6

RESULT 35
Q9ZIE9 PRELIMINARY; PRT; 8 AA.
ID Q9ZIE9
AC Q9ZIE9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Carbamoyl-phosphate synthase subunit B (Fragment).

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GN CARB.
OS Neisseria meningitidis
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
ON NCBI_TaxID=487;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=1527; PubMed=7773412;
RX MEDLINE=95291461;
RA Lawson F.S., Billowes F.M., Dillon J.A.;
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
RT gonorrhoeae includes a large, variable intergenic sequence which is
RT also present in other Neisseria species.";
RL Microbiology 141:0-0(0).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=1527;
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT "Complexity of the variable sequence between the carbamoyl-phosphate
RT synthase genes of Neisseria species.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029361; AAC78449.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 988 MW; FA372AB1B4032766 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5
DB 1 MP 2

RESULT 36
Q47273 PRELIMINARY; PRT; 8 AA.
AC Q47273;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf33, orf151, orf56, orf96, rus, orf45, orf127, and nmpc
DE genes.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=K-12;
RX MEDLINE=96196428; PubMed=8648624;
RA Mandi A.A., Sharples G.J., Mandal T.N., Lloyd R.G.;
RT "Holiday Junction Resolvases encoded by homologous rusa genes in
RT Escherichia coli K-12 and Phage 32.";
RL J. Mol. Biol. 257:561-573(1996).
DR EMBL; X92587; CAA63323.1; -
SQ SEQUENCE 8 AA; 935 MW; FD4041A05B05B336 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 3 SE 4

RESULT 37
Q16428 PRELIMINARY; PRT; 8 AA.
AC Q16428;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Dystrophin protein (Fragment).
GN DYSTROPHIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=96163501; PubMed=8566960;
RX Holder E., Maeda M., Bies R.D.;
RA "Expression and regulation of the dystrophin Purkinje promoter in
RT human skeletal muscle, heart, and brain.";
RL Hum. Genet. 97:232-239(1996).
RN [2]
RN SEQUENCE FROM N.A.
RP Kitano T., Kobayakawa H., Saitou N.;
RA "Silver Project.";
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; S81419; AAD14363.1; -
DR EMBL; AB037493; BAA90413.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CB05B6 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 2 SE 3

RESULT 38
Q9P285 PRELIMINARY; PRT; 8 AA.
AC Q9P285;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Clotting factor VIII (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP Shibata M., Shima M., Morichika S., Yoshiola A.;
RA "Human clotting factor VIII gene, junction regions of the deletion of
RT exon 4 through 7.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040872; BAA94312.1; -
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 3 SE 4

RESULT 39
O02032 PRELIMINARY; PRT; 8 AA.
AC O02032;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Metallothionein (Fragment).
```

GN LPM2.  
 OS *Lytechinus pictus* (Painted sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;  
 OC Lytechinus.  
 OX NCBI\_TaxID=7653;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97264487; PubMed=9110313;  
 RA Caerjesi P., Fang H., Brandhorst B.P.;  
 RT "Metallothionein gene expression in embryos of the sea urchin  
 RT *Lytechinus pictus*.";  
 RL Mol. Reprod. Dev. 47:39-46(1997).  
 DR EMBL; U83400; AAB58320.1; -;  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 823 MW; EBD5A2C1F7686766 CRC64;  
 Query Match 40.0%; Score 2; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MP 5  
 DB 1 MP 2  
 RESULT 40  
 Q9MYL5 PRELIMINARY; PRT; 8 AA.  
 AC Q9MYL5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Dystrophin.  
 OS Pongo pygmaeus (Orangutan),  
 OS Pan troglodytes (Chimpanzee), and  
 OS Gorilla gorilla (gorilla).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 OX NCBI\_TaxID=9600, 9598, 9593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-P.pygmaeus, P.troglodytes, and G.gorilla;  
 RA Kitano T., Kobayakawa H., Saitou N.;  
 RT "Silver Project."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB037496; BAA90419.1; -;  
 DR EMBL; AB037494; BAA90415.1; -;  
 DR EMBL; AB037495; BAA90417.1; -;  
 SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CB05B6 CRC64;  
 Query Match 40.0%; Score 2; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SE 2  
 DB 2 SE 3  
 RESULT 41  
 Q8W8G2 PRELIMINARY; PRT; 8 AA.  
 AC Q8W8G2;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 GN COII.  
 OS Diadema savignyi (Longspine black urchin).  
 OS Mitochondrion.  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;

OC Diadema.  
 OX NCBI\_TaxID=105360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=DP751, SA2, SA7, SA10, GSA1, GSA3, GSA4, DOK17, and DOK105;  
 RX MEDLINE=21323357; PubMed=11430656;  
 RA Lessios H.A., Kessing B.D., Pearse J.S.;  
 RT "Population structure and speciation in tropical seas: global  
 RT phylogeography of the sea urchin *Diadema*.";  
 RL Evolution 55:955-975(2001).  
 DR EMBL; AY013065; AAL33860.1; -;  
 DR EMBL; AY013080; AAL33861.1; -;  
 DR EMBL; AY013083; AAL33862.1; -;  
 DR EMBL; AY013086; AAL33863.1; -;  
 DR EMBL; AY013088; AAL33864.1; -;  
 DR EMBL; AY013090; AAL33866.1; -;  
 DR EMBL; AY013091; AAL33867.1; -;  
 DR EMBL; AY013102; AAL33868.1; -;  
 DR EMBL; AY013103; AAL33869.1; -;  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 8 AA; 1037 MW; 701B173B46DDC2D3 CRC64;  
 Query Match 40.0%; Score 2; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SE 3  
 DB 7 SE 8  
 RESULT 42  
 Q8W8G4 PRELIMINARY; PRT; 8 AA.  
 ID Q8W8G4;  
 AC Q8W8G4;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 GN COII.  
 OS Diadema mexicanum.  
 OS Mitochondrion.  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;  
 OC Diadema.  
 OX NCBI\_TaxID=105359;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C15, D3, D5, D6, CC66, G123, DM1, DM3, and DM71;  
 RX MEDLINE=21323357; PubMed=11430656;  
 RA Lessios H.A., Kessing B.D., Pearse J.S.;  
 RT "Population structure and speciation in tropical seas: global  
 RT phylogeography of the sea urchin *Diadema*.";  
 RL Evolution 55:955-975(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C15, D3, D5, D6, CC66, G123, DM1, DM3, and DM71;  
 RX MEDLINE=21561594; PubMed=11703875;  
 RA Lessios H.A., Garrido M.J., Kessing B.D.;  
 RT "Demographic history of *Diadema antillarum*, a keystone herbivore on  
 RT Caribbean reefs.";  
 RL Proc. R. Soc. Lond. B. Biol. Sci. 268:2347-2353(2001).  
 DR EMBL; AY012908; AAL33837.1; -;  
 DR EMBL; AY012911; AAL33838.1; -;  
 DR EMBL; AY012913; AAL33839.1; -;  
 DR EMBL; AY012914; AAL33840.1; -;  
 DR EMBL; AY012919; AAL33842.1; -;  
 DR EMBL; AY012940; AAL33847.1; -;  
 DR EMBL; AY012949; AAL33849.1; -;  
 DR EMBL; AY012950; AAL33850.1; -;  
 DR EMBL; AY012951; AAL33851.1; -;  
 KW Mitochondrion.



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Query Match      40.0%; Score 2; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EE 3
Db      5 EE 6

RESULT 46
Q8WFRS      PRELIMINARY;      PRT;      8 AA.
AC Q8WFR5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema paucispinum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;
OC Diadema.
OX NCBI_TaxID=145530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H11;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
DR EMBL; AY012959; AALJ3852.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 8 AA; 954 MW; C41B173B46DDC2CE CRC64;

Query Match      40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EE 3
Db      7 EE 8

RESULT 47
Q42507      PRELIMINARY;      PRT;      8 AA.
AC Q42507;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Heat shock protein (Fragment).
GN HSP70C OR HSP70A OR HSP70B.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV MUSTANG;
RX MEDLINE=96189275; PubMed=8605312;
RA Joshi C.P., Kumar S., Nguyen H.T.;
RT "Application of modified differential display technique for cloning
RT and sequencing of the 3' region from three putative members of wheat
RT HSP70 gene family.";
RL Plant Mol. Biol. 30:641-646(1996).
DR EMBL; L41507; AAB02333.1; -.
DR EMBL; L41505; AAB02331.1; -.
DR EMBL; L41506; AAB02332.1; -.
KW Heat shock.
FT NON_TER
SQ SEQUENCE 8 AA; 886 MW; 71B2CB1B10532768 CRC64;

Query Match      40.0%; Score 2; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SE 2
Db      4 SE 5

RESULT 49
Q99P40      PRELIMINARY;      PRT;      8 AA.
AC Q99P40;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Repressor of GATA (Fragment).
GN ROG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B6;
RX Milaw S., HO I.;
RT "ROG is a NF-AT target gene that partly rescues the phenotype of NF-
RT ATC2/NF-ATc3 deficient Th cells.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335542; AAG59843.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 943 MW; FE3411B771B6C766 CRC64;

Query Match      40.0%; Score 2; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 MP 5

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Db      1 MP 2
||
ID Q8CJ03 PRELIMINARY; PRT; 8 AA.
AC Q8CJ03
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein inhibitor of activated STAT X (Fragment).
GN PIASX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=129/SVJ;
RA Santti H., Mikkonen L., Hirvonen-Santti S., Toppari J., Janne O.A.,
RA Palvimäki J.J.;
RT "Germ cell -specific transcription of the murine PIASX gene is
RT governed by a short GC-rich proximal promoter region.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF539748; AAN31759.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1010 MW; ED072B1B19CAADD6 CRC64;

Query Match 40.0%; Score 2; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
||
Db 5 EE 6

RESULT 51:
Q83349 PRELIMINARY; PRT; 8 AA.
ID Q83349
AC Q83349
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 0.8 kDa protein.
OS Murine coronavirus MHV (strain A59).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11142;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=A59;
RX MEDLINE=89299451; PubMed=2545027;
RA Pachuk C.J., Bredenbeek P.J., Zoltick P.W., Spaan W.J., Weiss S.R.;
RT "Molecular cloning of the gene encoding the putative polymerase of
RT mouse hepatitis coronavirus, strain A59.";
RL Virology 171:141-148(1989).
DR EMBL: M27198; AAA74010.1; -.
KW Hypothetical protein.
SQ SEQUENCE 8 AA; 787 MW; ECB732C7287DC766 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5
||
Db 1 MP 2

RESULT 52
Q9WJ33 PRELIMINARY; PRT; 8 AA.
ID Q9WJ33
AC Q9WJ33
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Suid herpesvirus 1 putative UL47 and UL46 genes and partial gB
DE (Fragment).
GN GB.
OS Pseudorabies virus (strain Kaplan) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=33703;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Kaplan;
RX MEDLINE=99239778; PubMed=10225272;
RA Bras F., Dezelee S., Simonet B., Nguyen X., Vende P., Flaman A.,
RA Masse M.J.;
RT "The left border of the genomic inversion of pseudorabies virus
RT contains genes homologous to the UL46 and UL47 genes of Herpes Simplex
RT Virus type 1, but no UL45 gene.";
RL Virus Res. 60:29-40(1999).
DR EMBL: AJ010303; CAA09075.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 875 MW; 262DDAB76AAB05BB CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
Db 2 SE 3

RESULT 53
Q89498 PRELIMINARY; PRT; 8 AA.
ID Q89498
AC Q89498
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CORONAVIRUS proviral defective INTERFERING PARTICLE (DLSSE) OBTAINED
DE AFTER SERIAL PASSAGE 17, with 2 recombination sites and ORFs (DLSSE).
OS Murine hepatitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11138;
RN [1]
RC SEQUENCE FROM N.A.
RP MEDLINE=89020822; PubMed=2845661;
RX Makino S., Shieh C.K., Soe L.H., Baker S.C., Lai M.M.;
RA "Primary structure and translation of a defective interfering RNA of
RT murine coronavirus.";
RL Virology 166:550-560(1988).
RN [2]
RC SEQUENCE FROM N.A.
RP MEDLINE=88062951; PubMed=2824826;
RX Soe L.H., Shieh C.K., Baker S.C., Chang M.F., Lai M.M.C.;
RA "Sequence and translation of the murine coronavirus 5'-end genomic RNA
RT reveals the N-terminal structure of the putative RNA polymerase.";
RL J. Virol. 61:3968-3976(1987).
DR EMBL: M23258; AAA91862.1; -.
DR EMBL: M8040; AAA46455.1; -.
SQ SEQUENCE 8 AA; 815 MW; ECB732C72862D766 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5
||
Db 1 MP 2

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RESULT 54
Q902V5 PRELIMINARY; PRT; 8 AA.
AC Q902V5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adenylate kinase (Fragment).
OS Pulica leucopetra.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Fulica.
OX NCBI_TaxID=156758;
RN [1]
RP SEQUENCE FROM N.A.
RA Shapiro L.H., Dumbacher J.P.;
RT "Adenylate kinase intron 5: a new nuclear locus for avian
RT systematics.";
RL Auk 118:248-255(2001).
DR EMBL; AF307898; AAK4337.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 994 MW; 96333B19CB1B1866 CRC64;

Query Match 40.0%; Score 2; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB |||
3 EE 4

RESULT 55
P72345 PRELIMINARY; PRT; 9 AA.
AC P72345;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TabA (Fragment).
GN TABA.
OS Pseudomonas syringae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=317;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BR2R;
RX MEDLINE=93167809; PubMed=7679566;
RA Barta T.M., Kinscherf T.G., Uchtyl T.P., Willis D.K.;
RT "DNA sequence and transcriptional analysis of the tliA gene required
RT for tabtoxin biosynthesis by Pseudomonas syringae.";
RL Appl. Environ. Microbiol. 59:458-466(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=BR2R;
RC Kinscherf T.G., Willis D.K.;
RT "Sequence analysis of the tabtoxin biosynthetic region.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF519896; AAB25381.2; -.
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1037 MW; 2B34D9D5BB05B047 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5
DB |||
1 MP 2

RESULT 56
Q43960 PRELIMINARY; PRT; 9 AA.
AC Q43960;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hydrogenase-related protein (Fragment).
OS HUPA.
OC Azotobacter chroococcum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=353;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MCD1;
RX MEDLINE=95055698; PubMed=7966281;
RA Du L., Tibelius K.H., Souza E.M., Garg R.P., Yates M.G.;
RT "Sequences, organization and analysis of the hupZMNOQRTV genes from
RT the Azotobacter chroococcum hydrogenase gene cluster.";
RL J. Mol. Biol. 243:549-557(1994).
DR EMBL; L25315; AAA64455.1; -.
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1004 MW; EF421DD045B69B11 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
DB |||
3 EM 4

RESULT 57
Q8MJT7 PRELIMINARY; PRT; 9 AA.
AC Q8MJT7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hemopexin (Fragment).
OS Eulemur fulvus (brown lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Eulemur.
OX NCBI_TaxID=13515;
RN [1]
RP SEQUENCE FROM N.A.
RA Wyner Y.M., Johnson S.E., Stumpf R., DeSalle R.;
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
RT zone at Andringitra, Madagascar.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258049; AAM43870.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;

Query Match 40.0%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB |||
2 EE 3

RESULT 58
Q8MJT8 PRELIMINARY; PRT; 9 AA.
AC Q8MJT8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hemopexin (Fragment).
OS Eulemur fulvus albocollaris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Eulemur.
OX NCBI_TaxID=122224;
RN [1]
RP SEQUENCE FROM N.A.
RA Wyner Y.M., Johnson S.E., Stumpf R., Desalle R.;
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
RT zone at Andringitra, Madagascar."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258028; AA043849.1;
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;

Query Match 40.0%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EE 3
Db 2 EE 3

RESULT 59
Q9XSLO PRELIMINARY; PRT; 9 AA.
AC Q9XSLO;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha s2-casein (Fragment).
GN CSN182.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=21313038; PubMed=11419340;
RA Ramunno L., Longobardi E., Pappalardo M., Rando A., Di Gregorio P.,
RA Cosenza G., Mariani P., Pastore N., Masina P.;
RT "An allele associated with a non detectable amount of as2 casein in
RT goat milk."
RL Anim. Genet. 32:19-26(2001).
DR EMBL; AJ238475; CAB44298.1;
FT NON_TER 1 1
FT VARIANT 5 5 I -> V.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1047 MW; AAA2A5A5B051EB16 CRC64;

Query Match 40.0%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 8 SE 9

RESULT 60
Q9TRSO PRELIMINARY; PRT; 9 AA.
AC Q9TRSO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcyclin-associated protein, CAP50-CA2+/phospholipid-binding protein
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DE L-7 fragment (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=92250478; PubMed=1533622;
RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
RT "A calcyclin-associated protein is a newly identified member of the
RT Ca2+/phospholipid-binding proteins, annexin family."
RL J. Biol. Chem. 267:8919-8924(1992).
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1010 MW; 64E419C44865B72B CRC64;

Query Match 40.0%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 1 SE 2

RESULT 61
Q9TRW2 PRELIMINARY; PRT; 9 AA.
AC Q9TRW2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CALDESIN=PHOSPHORYLATION site (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378498; PubMed=1898046;
RA Ikebe M., Hornick T.;
RT "Determination of the phosphorylation sites of smooth muscle caldesmon
RT by protein kinase C."
RL Arch. Biochem. Biophys. 288:538-542(1991).
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1018 MW; 8C901B10533735A5 CRC64;

Query Match 40.0%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EE 3
Db 7 EE 8

RESULT 62
Q8WFT4 PRELIMINARY; PRT; 9 AA.
AC Q8WFT4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematoidea; Diadematoidea; Diadematoidea;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=DCA3;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DCA3;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012941; AAL33848.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1151 MW; 2CED173B46DDC2D3 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 6 EE 7

RESULT 63
Q8WFS4 PRELIMINARY; PRT; 9 AA.
ID Q8WFS4;
AC Q8WFS4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Cytochrome oxidase subunit II (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G125;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=G125;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012941; AAL33848.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1151 MW; 2CED173B46DDC2D3 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 6 EE 7

RESULT 64
Q8W8X4 PRELIMINARY; PRT; 9 AA.
ID Q8W8X4;
AC Q8W8X4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Cytochrome oxidase subunit II (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CC70, and CC117;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CC70, and CC117;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012920; AAL33843.1; -.
DR EMBL; AY012921; AAL33844.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1174 MW; 2B73173B46DDC2D3 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3
DB 8 EE 9

RESULT 65
P92072 PRELIMINARY; PRT; 9 AA.
ID P92072;
AC P92072;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE ATPase subunit 8 (Fragment).
OS Euhadra herklotsi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Helicoidea; Bradybaenidae; Euhadra.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatopancreas;
RA Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
RA Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
RA Watanabe K., Thomas R.H.;
RT "Evolution of pulmonate gastropod mitochondrial genomes: comparisons
RT of complete gene organization of Euhadra, Cepaea and Albinaria and
RT implications of unusual tRNA secondary structures.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; 271697; CAA96373.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 9

```

SQ SEQUENCE 9 AA; 1009 MW; 380CB1F775B736C7 CRC64;  
 Query Match 40.0%; Score 2; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5  
 ||  
 1 MP 2

Db

RESULT 66  
 Q8W875 PRELIMINARY; PRT; 9 AA.  
 ID Q8W875  
 AC Q8W875; 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Ribulose-1,5-bisphosphate large subunit (Fragment).  
 GN RBCL.  
 OS Bostrychia calliptera.  
 OG Chloroplast.  
 OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Rhodomelaceae;  
 OC Bostrychia.  
 OX NCBI\_TaxID=161377;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=P.E350.PA, and P3999.NT;  
 RA Zuccarello G.C., West J.A.;  
 RT "Phylogeography of the Bostrychia calliptera/B. pinnata complex (Rhodomelaceae, Rhodophyta) and divergence rates based on nuclear, mitochondrial, and plastid DNA markers."  
 RT Submitted (May-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF382914; AAL67249.1; -.  
 DR EMBL; AF382916; AAL67253.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 9 AA; 981 MW; 93B94DC1B771AB05 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2  
 ||  
 2 SE 3

Db

RESULT 67  
 Q8W8W5 PRELIMINARY; PRT; 9 AA.  
 ID Q8W8W5  
 AC Q8W8W5; 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 GN COII.  
 OS Diadema setosum (Sea urchin).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;  
 OC Diadema.  
 OX NCBI\_TaxID=31175;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DEL1, DEL2, DEL3, and DEL5;  
 RX MEDLINE=21323357; PubMed=11430656;  
 RA Lessios H.A., Kessing B.D., Pearse J.S.;  
 RT "Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema."  
 RL Evolution 55:955-975 (2001).  
 DR EMBL; AY012890; AAL33833.1; -.  
 DR EMBL; AY012891; AAL33834.1; -.  
 DR EMBL; AY012892; AAL33835.1; -.

DR EMBL; AY012892; AAL33835.1; -.  
 DR EMBL; AY012893; AAL33836.1; -.  
 KW Mitochondrion.  
 FT NON\_TER  
 SQ SEQUENCE 9 AA; 1151 MW; 2CED173B46DC2D3 CRC64;  
 Query Match 40.0%; Score 2; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
 ||  
 8 EE 9

Db

RESULT 68  
 Q8W8W6 PRELIMINARY; PRT; 9 AA.  
 ID Q8W8W6  
 AC Q8W8W6; 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Cytochrome oxidase subunit II (Fragment).  
 GN COII.  
 OS Diadema antillarum.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;  
 OC Diadema.  
 OX NCBI\_TaxID=105358;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CN3, and CN5;  
 RX MEDLINE=21323357; PubMed=11430656;  
 RA Lessios H.A., Kessing B.D., Pearse J.S.;  
 RT "Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema."  
 RL Evolution 55:955-975 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CN3, and CN5;  
 RX MEDLINE=21561594; PubMed=11703875;  
 RA Lessios H.A., Garrido M.J., Kessing B.D.;  
 RT "Demographic history of Diadema antillarum, a keystone herbivore on Caribbean reefs."  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353 (2001).  
 DR EMBL; AY012853; AAL33827.1; -.  
 DR EMBL; AY012855; AAL33829.1; -.  
 KW Mitochondrion.  
 FT NON\_TER  
 SQ SEQUENCE 9 AA; 1151 MW; 2CED173B46DC2D3 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EE 3  
 ||  
 8 EE 9

Db

RESULT 69  
 Q8H9Z1 PRELIMINARY; PRT; 9 AA.  
 ID Q8H9Z1  
 AC Q8H9Z1; 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Capsid protein.  
 GN G20.  
 OS Cyanophage S-KM1.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.  
 OX NCBI\_TaxID=187678;

RN SEQUENCE FROM N.A.  
 RC STRAIN=S-KMI;  
 RA Okuniehi S., Maeda H.;  
 RT "Cyanophage in Kagoshima Bay."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB080247; BAC54112.1; -  
 SQ SEQUENCE 9 AA; 1167 MW; DB9205AB59DB42D6 CRC64;  
  
 Query Match 40.0%; Score 2; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 SE 2  
 Db 7 SE 8  
  
 RESULT 70  
 Q9FXL0 PRELIMINARY; PRT; 9 AA.  
 ID Q9FXL0  
 AC Q9FXL0  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE LfM8 protein (Fragment).  
 GN LfM8.  
 OS Lilium longiflorum (Trumpet lily).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.  
 OX NCBI\_TaxID=4690;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Hinomoto;  
 RA Uefuji H., Takase H., Hiratsuka K.;  
 RT "Lilium longiflorum LfM8 gene, promoter region and partial sequence."  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB050987; BAB17856.1; -  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;  
  
 Query Match 40.0%; Score 2; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 MP 5  
 Db 6 MP 7  
  
 RESULT 71  
 P82440 PRELIMINARY; PRT; 9 AA.  
 ID P82440  
 AC P82440  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 42 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RN SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed tobacco culture."  
 RL Planca 0:0-0(2000).  
 CC -/- SUBCELLULAR LOCATION: CELL WALL.  
 CC -/- TISSUE SPECIFICITY: XYLEM.

KW Cell wall.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2D5BB1B07 CRC64;  
  
 Query Match 40.0%; Score 2; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 EE 3  
 Db 3 EE 4  
  
 RESULT 72  
 Q9QWG2 PRELIMINARY; PRT; 9 AA.  
 ID Q9QWG2  
 AC Q9QWG2  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Protein G beta-2 subunit (Fragment).  
 GN GNB2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=9803028; PubMed=9365246;  
 RX Christien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,  
 RA Lacombe C.;  
 RT "Abnormal erythropoietin (Epo) gene expression in the murine erythroleukemia Iw32 cells is issued from a rearrangement between the G-protein b2 gene subunit and the Epo genes."  
 RL Oncogene 15:1995-1999(1997).  
 DR EMBL; Y11970; CAA72706.1; -  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1133 MW; 86FD0736DB172B05 CRC64;  
  
 Query Match 40.0%; Score 2; DB 11; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 SE 2  
 Db 2 SE 3  
  
 RESULT 73  
 Q99MG3 PRELIMINARY; PRT; 9 AA.  
 ID Q99MG3  
 AC Q99MG3  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE NRCAM protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP More M.I., Kirsch F.P., Rathjen F.G.;  
 RT "Targeted ablation of NRCAM and ankyrin-B results in disorganized lens fibres leading to cataract formation."  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF346472; AAK25814.1; -  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1039 MW; 32FCB721E3333327 CRC64;  
  
 Query Match 40.0%; Score 2; DB 11; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: November 25, 2003, 18:25:38  
Job time : 13.0979 secs

Qy 4 MP 5  
||  
Db 1 MP 2

## RESULT 74

O9QZA8 PRELIMINARY; PRT; 9 AA.  
AC Q9QZA8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE C-type lectin DCL1 (Fragment).  
GN DCL1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gorski K., Huang X., Tseng S.-Y., Rattis F., Pardoll D., Tsuchiya H.,  
RT "Dendritic cell regulation of DCL1 mRNA expression."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF192526; AAF04843.1; -.  
DR MGD; MGI:2136650; DCL1.  
KW Lectin.  
FT NON\_TER  
SQ SEQUENCE 9 AA; 994 MW; 342161ABI72EBAB7 CRC64;

Query Match 40.0%; Score 2; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MP 5  
||  
Db 1 MP 2

## RESULT 75

O83622 PRELIMINARY; PRT; 9 AA.  
AC O83622;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hypothetical 1.1 kDa protein (Fragment).  
OS Murray valley encephalitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Flavivirus.  
OX NCBI\_TaxID=11079;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88118912; PubMed=2828633;  
RA Hahn C.S., Hahn Y.S., Rice C.M., Lee E., Dalgarno L., Strauss E.G.,  
RA Strauss J.H.;  
RT "Conserved elements in the 3' untranslated region of flavivirus RNAs  
and potential cyclization sequences."  
RL J. Mol. Biol. 198; 33-41(1987).  
DR EMBL; M35172; AAA66627.1; -.  
KW Hypothetical protein.  
FT NON\_TER  
SQ SEQUENCE 9 AA; 1055 MW; FF36D40AAB05A2C1 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2  
||  
Db 4 SE 5

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 16.1968 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-15

Perfect score: 5

Sequence: 1 SEEMP 5

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	22	Colostrinin derive
2	5	100.0	5	22	Colostrinin peptid
3	5	100.0	5	22	Colostrinin peptid
4	5	100.0	5	22	Ewe colostrinin pe
5	5	100.0	5	23	Colostrinin consti
6	5	100.0	5	23	Colostrinin consti
7	5	100.0	5	23	Neural cell regula
8	5	100.0	9	22	Ewe colostrinin pe
9	5	100.0	18	16	Retinoblastoma bin

10	4	80.0	9	24	ABR20220	Human cancer-relat
11	4	80.0	9	24	ABR20832	Human cancer-relat
12	4	80.0	9	24	ABR21611	Human cancer-relat
13	4	80.0	9	24	ABR21660	Human cancer-relat
14	4	80.0	9	24	ABR22226	Human cancer-relat
15	4	80.0	9	24	ABR23023	Human cancer-relat
16	4	80.0	9	24	ABR23633	Human cancer-relat
17	4	80.0	10	20	AAW84091	TSG-6/falphi comp
18	4	80.0	10	22	AAE02365	TSG-6 related pept
19	4	80.0	10	23	ABG70874	Human lalphi (try
20	4	80.0	10	24	ABR07242	Human cancer-relat
21	4	80.0	10	24	ABR20268	Human cancer-relat
22	4	80.0	10	24	ABR20300	Human cancer-relat
23	4	80.0	10	24	ABR20312	Human cancer-relat
24	4	80.0	10	24	ABR21505	Human cancer-relat
25	4	80.0	10	24	ABR21668	Human cancer-relat
26	4	80.0	10	24	ABR21697	Human cancer-relat
27	4	80.0	10	24	ABR21706	Human cancer-relat
28	4	80.0	10	24	ABR22557	Human cancer-relat
29	4	80.0	10	24	ABR22897	Human cancer-relat
30	4	80.0	10	24	ABR23068	Human cancer-relat
31	4	80.0	10	24	ABR23099	Human cancer-relat
32	4	80.0	10	24	ABR23112	Human cancer-relat
33	4	80.0	10	24	ABR24311	Human cancer-relat
34	4	80.0	11	19	AAW78610	SH2 domain binding
35	4	80.0	13	15	AAE58755	Wild type T-antige
36	4	80.0	13	23	ABP54333	Human HGPAMY27 PK
37	4	80.0	14	23	AAE24501	Human RAT1ld6 case
38	4	80.0	15	24	ABR31680	Human cancer-relat
39	4	80.0	15	24	ABR31949	Human cancer-relat
40	4	80.0	15	24	ABR35147	Human cancer-relat
41	4	80.0	15	24	ABR35302	Human cancer-relat
42	4	80.0	15	24	ABR35636	Human cancer-relat
43	4	80.0	15	24	ABR35844	Human cancer-relat
44	4	80.0	15	24	ABR35895	Human cancer-relat
45	4	80.0	15	24	ABR36098	Human cancer-relat
46	4	80.0	15	24	ABR36234	Human cancer-relat
47	4	80.0	15	24	ABR36532	Human cancer-relat
48	4	80.0	15	24	ABR36715	Human cancer-relat
49	4	80.0	15	24	ABR36758	Human cancer-relat
50	4	80.0	15	24	ABR36986	Human cancer-relat
51	4	80.0	15	24	ABR37144	Human cancer-relat
52	4	80.0	15	24	ABR37484	Human cancer-relat
53	4	80.0	15	24	ABR37689	Human cancer-relat
54	4	80.0	15	24	ABR37742	Human cancer-relat
55	4	80.0	17	20	AAE25865	Human secreted pro
56	4	80.0	17	21	AAO21454	Diabetes specific
57	4	80.0	17	24	ABP82037	G protein-coupled
58	4	80.0	17	24	ABP82833	G protein-coupled
59	4	80.0	20	24	ABJ38221	Human cytomegalovi
60	4	80.0	20	24	ABJ38225	Human cytomegalovi
61	4	80.0	20	24	ABP82352	G protein-coupled
62	3	60.0	4	21	AAE27268	Murine confluency
63	3	60.0	4	22	AAE00020	Peptide #3 insert
64	3	60.0	4	23	AAE23664	Peptide #2 used to
65	3	60.0	5	14	AAE31242	Phosphopeptide 6.
66	3	60.0	5	15	AAE55746	Casein-kinase inhi
67	3	60.0	5	18	AAW22937	Low density lipopr
68	3	60.0	5	19	AAW66598	Phosphopeptide par
69	3	60.0	5	19	AAW66604	Phosphopeptide. S
70	3	60.0	5	19	AAW66608	Phosphopeptide. S
71	3	60.0	5	19	AAW66609	Phosphopeptide. S
72	3	60.0	5	21	AAE61293	Cadherin-6 cell ad
73	3	60.0	5	22	ABG99113	Peptide #1 associa
74	3	60.0	5	22	AAE05015	Cryptosporidium pa
75	3	60.0	5	22	AAE35189	Human Traf 6 aptam
76	3	60.0	5	23	AAE16284	Betaig-h3 fas-1 do
77	3	60.0	5	23	AAE15184	Human vav oncogene
78	3	60.0	5	24	ABB98699	Immunopotentiator
79	3	60.0	5	24	ABB98703	Immunopotentiator
80	3	60.0	6	10	AAE91564	Sequence of beta-D
81	3	60.0	6	15	AAE62207	CENP-B protein am
82	3	60.0	6	16	AAE67262	Ubiquitin peptide

83 3 60.0 6 19 AAW75322 Hexapeptide #15 bi  
 84 3 60.0 6 19 AAW75390 Hexapeptide #15 bi  
 85 3 60.0 6 19 AAW60847 HPV18 E7 B-cell ep  
 86 3 60.0 6 21 AAB36783 HRG-beta1 variant  
 87 3 60.0 6 21 AAB90359 MN protein proteog  
 88 3 60.0 6 21 AAY61296 Cadherin-6 cell ad  
 89 3 60.0 6 22 AAB70020 Murine CD4 D4 dona  
 90 3 60.0 6 22 AAB15582 Human SNAP-25 N-te  
 91 3 60.0 6 23 AB83403 Human herpesvirus  
 92 3 60.0 6 23 AAU80783 Casein kinase II r  
 93 3 60.0 6 24 ABU57804 HIV envelope prote  
 94 3 60.0 7 10 AAP91566 Sequence of beta-D  
 95 3 60.0 7 14 AAR32671 Peptide heptad. S  
 96 3 60.0 7 14 AAR32674 Peptide heptad. S  
 97 3 60.0 7 14 AAR32677 Peptide heptad. S  
 98 3 60.0 7 14 AAR32679 Peptide heptad. S  
 99 3 60.0 7 14 AAR32680 Peptide heptad. S  
 100 3 60.0 7 19 AAW57145 Measles virus mmo

## ALIGNMENTS

## RESULT 1

AAB72260  
 ID AAB72260 standard; peptide; 5 AA.

AC AAB72260;

XX 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 15.

XX Colostrinin; immune response; cytokine; blood cell proliferation;

KW central nervous system disorder; neurological disorder; mental disorder;

KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;

KW neurosis; infection.

XX Synthetic.

OS WO200111937-A2.

PN 22-FEB-2001.

PD 17-AUG-2000; 2000WO-US22818.

PF 17-AUG-1999; 99US-0149311.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

PI WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for

PT treating central nervous system diseases and bacterial and viral

PT infections, comprises administering colostrinin as an immunological

PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,

CC a proline rich polypeptide aggregate contained in colostrum. The

CC peptides have immune response modulatory activity, and are capable of

CC inducing cytokines. Colostrinin and its derived peptides are useful for

CC inducing cytokine production, for modulating an immunological response

CC and for inducing blood cell proliferation. The peptides are useful in the

CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,

CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic

CC disorders of the immune system, bacterial and viral infections and

CC acquired immunological deficiencies.

XX SQ Sequence 5 AA;  
 Query Match 100.0%; Score 5; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

OY 1 SEEMP 5

DB 1 SEEMP 5

DB 1 SEEMP 5

DB 1 SEEMP 5

DB 1 SEEMP 5

DB 1 SEEMP 5

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DB 1 SEEMP 5

DB 1 SEEMP 5

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DB 1 SEEMP 5

DB 1 SEEMP 5

DB 1 SEEMP 5

DB 1 SEEMP 5

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DB 1 SEEMP 5



DE Colostrinin peptide #14.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 KW  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX 17-AUG-1999; 99US-0149633.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 PI  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 CC  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 5; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEMP 5  
 Db |||||  
 1 SEEMP 5  
 XX  
 XX 18-JUN-2002 (first entry)  
 DT  
 XX Colostrinin constituent peptide #14.  
 DE  
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnary.  
 KW  
 XX Unidentified.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 5  
 FT /note= "Optionally C-terminal amide"  
 FT  
 XX WO200213850-A1.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2000; 2000WO-US22776.  
 PP  
 XX 17-AUG-2000; 2000WO-US22776.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 PI  
 XX WPI; 2002-269151/31.  
 DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 PT  
 XX Claim 6; Page 25; 51pp; English.  
 PS  
 XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

DE Colostrinin peptide #14.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 KW  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX 17-AUG-1999; 99US-0149633.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 PI  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 CC  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 5; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEMP 5  
 Db |||||  
 1 SEEMP 5  
 XX  
 XX 21-MAR-2001 (first entry)  
 DT  
 XX Ewe colostrinin peptide fragment B-3.  
 DE  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 KW  
 XX Ovis sp.  
 OS  
 XX WO200075173-A2.  
 PN  
 XX 14-DEC-2000.  
 PD  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REGG-) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI  
 XX WPI; 2001-071059/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidizing species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEMP 5  
 |||||  
 Db 1 SEEMP 5

#### RESULT 6

AAW51049  
 ID AAW51049 standard; Peptide; 5 AA.

XX AAW51049;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide.

XX Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; beta-casein; human.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FT Modified-site 5 /note= "optional C-terminal amidation"

PN W0200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. The peptide is  
 CC classified as having a beta-casein homologue precursor. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide.

XX Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEMP 5  
 |||||  
 Db 1 SEEMP 5

#### RESULT 7

AAO14591  
 ID AAO14591 standard; peptide; 5 AA.

XX AAO14591;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostrinin peptide 14.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers  
 FT Modified-site 5 /note= "Optional C-terminal amide"

PN W0200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

PS Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEMP 5

|||||

Db 1 SEEMP 5

RESULT 8

AAB59348

ID AAB59348 standard; Peptide; 9 AA.

XX

AC AAB59348;

XX

DT 21-MAR-2001 (first entry)

XX

Ewe colostrin peptide fragment derived sequence #8.

XX

Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder;

KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB02128.

XX

PR 02-JUN-1999; 99GB-0012852.

XX

PA (REGS-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

Peptides having an N-terminal amino acid sequence isolated from

PT colostrin for treating e.g. disorders of the central nervous system

PT and immune system, viral and bacterial infections, and diseases

PT characterized by amyloid plaques -

XX

PS Claim 8; Page 27; 63pp; English.

XX

The present invention provides the sequences of a number of peptides found in ewe's colostrin. Colostrin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques.

XX Sequence 9 AA;

Query Match 100.0%; Score 5; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEMP 5

|||||

Db 5 SEEMP 9

RESULT 9

AAR65234

ID AAR65234 standard; Protein; 18 AA.

XX

AC AAR65234;

XX

DT 25-MAR-2003 (updated)

DT 30-SEP-1995 (first entry)

XX

DE Retinoblastoma binding protein p48 T peptide.

XX

KW Retinoblastoma binding protein; RbAp48; tumour suppressor; cancer;

KW diagnosis; prognosis; T peptide; cloning; sequencing.

XX

OS Homo sapiens.

XX

PN WO9505392-A1.

XX

PD 23-FEB-1995.

XX

PF 11-AUG-1994; 94WO-US09170.

XX

PR 12-AUG-1993; 93US-0105454.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI Lee EYP, Qian Y;

XX

DR WPI; 1995-098718/13.

XX

PT p48 and p46 retinoblastoma binding proteins and corresponding DNA

PT bind to Rb competitively with the SV40 T antigen; for the

PT control, diagnosis and research of cancers.

XX

PS Example 1; Page 40; 102pp; English.

XX

The T peptide is used with K peptide (AAR65235) to isolate p48 protein from HeLa cell isolates by affinity chromatography, as part of a method for cloning the RbAp48 gene from a human HeLa cell cDNA library, followed by sequencing. p48 Supresses heat shock sensitive Ras mutations in yeast and is implicated as a retinoblastoma tumor suppressor. p46 May suppress the oncogene Ras p21 in human tumours. The protein binds to retinoblastoma competitively with the SV40 virus T antigen. DNA encoding p48 may be used as a probe or primer in research, as well as in the diagnosis or prognosis of certain cancers. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 5; DB 16; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.2;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEMP 5

|||||

Db 6 SEEMP 10

RESULT 10

ABR20220

ID ABR20220 standard; Peptide; 9 AA.

XX

AC ABR20220;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 185P2C9 HLA peptide #55.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.  
 XX XX  
 XX PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX XX  
 PA (AGEN-) AGENSYS INC.  
 XX XX  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX XX  
 DR WPI; 2003-075555/07.  
 XX XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX XX  
 XX Claim 13; Page 320; 1021pp; English.  
 XX XX  
 PS The present invention relates to novel human cancer-related genes and  
 PS proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX XX  
 SQ Sequence 9 AA;  
 Query Match 80.0%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 |||||  
 2 SEEM 5  
 DB  
 RESULT 11  
 ABR20832  
 ID ABR20832 standard; Peptide; 9 AA.  
 AC ABR20832;  
 XX XX  
 XX 19-MAY-2003 (first entry)  
 XX XX  
 DE Human cancer-related protein 185P2C9 HLA peptide #667.  
 XX XX  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX XX  
 OS Homo sapiens.  
 XX XX  
 PN WO200283921-A2.  
 XX XX  
 PD 24-OCT-2002.  
 XX XX  
 PF 10-APR-2002; 2002WO-US11654.  
 XX XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX XX  
 PA (AGEN-) AGENSYS INC.  
 XX XX  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;

PI Morrison K, Morrison RK, Raitano AB;  
 XX XX  
 DR WPI; 2003-075555/07.  
 XX XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX XX  
 XX Claim 13; Page 327; 1021pp; English.  
 XX XX  
 PS The present invention relates to novel human cancer-related genes and  
 PS proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX XX  
 SQ Sequence 9 AA;  
 Query Match 80.0%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 |||||  
 3 SEEM 6  
 DB  
 RESULT 12  
 ABR21611  
 ID ABR21611 standard; Peptide; 9 AA.  
 XX XX  
 AC ABR21611;  
 XX XX  
 XX 19-MAY-2003 (first entry)  
 XX XX  
 DE Human cancer-related protein 185P2C9 HLA peptide #1446.  
 XX XX  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX XX  
 OS Homo sapiens.  
 XX XX  
 PN WO200283921-A2.  
 XX XX  
 PD 24-OCT-2002.  
 XX XX  
 PF 10-APR-2002; 2002WO-US11654.  
 XX XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX XX  
 PA (AGEN-) AGENSYS INC.  
 XX XX  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX XX  
 DR WPI; 2003-075555/07.  
 XX XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX XX  
 XX Claim 13; Page 336; 1021pp; English.  
 PS

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
 ||||  
 Db 2 SEEM 5

RESULT 13

ID ABR21660 standard; Peptide; 9 AA.

XX ABR21660;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 185P2C9 HLA peptide #1495.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

XX 10-APR-2001; 2001US-283112P.

XX 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients

XX Claim 13; Page 337; 1021pp; English..

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
 ||||  
 Db 4 SEEM 7

RESULT 14

ID ABR22226 standard; Peptide; 9 AA.

XX ABR22226;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 185P2C9 HLA peptide #2061.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

XX 10-APR-2001; 2001US-283112P.

XX 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients

XX Claim 13; Page 343; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
DT ||||  
DB 3 SEEM 6

## RESULT 15

ABR23023  
ID ABR23023 standard; Peptide; 9 AA.

XX AC ABR23023;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 185P2C9 HLA peptide #2858.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX XX WPI; 2003-075555/07.

XX DT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response  
PT in cancer patients -

XX PS Claim 13; Page 353; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.

XX CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention.

XX SQ Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4

DT ||||

DB 2 SEEM 5

## RESULT 16

ABR23633

ID ABR23633 standard; Peptide; 9 AA.

XX AC ABR23633;

XX 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 185P2C9 HLA peptide #3468.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX XX WPI; 2003-075555/07.

XX DT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response  
PT in cancer patients -

XX PS Claim 13; Page 360; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.

XX CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention.

XX SQ Sequence 9 AA;

Query Match 80.0%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4

DT ||||

DB 3 SEEM 6

## RESULT 17

AAW84091

ID AAW84091 standard; peptide; 10 AA.

XX AC AAW84091;

XX DT 10-FEB-1999 (first entry)

XX DE TSG-6/1alpha complex N-terminal amino acid sequence Bikunin.

XX KW Tumour necrosis factor stimulated gene 6; TSG-6; recombinant; human;

XX KW diagnosis; cytokine; immune disorder; autoimmune disorder; infection;

XX KW inflammatory disease; neurodegenerative disease; cancer; hepatitis;

XX KW 1alpha; N-terminal.

OS Homo sapiens.  
 XX US5846763-A.  
 XX  
 XX 08-DEC-1998.  
 XX  
 XX 13-MAY-1994; 94US-0242097.  
 XX  
 XX 13-MAY-1994; 94US-0242097.  
 PR 14-JAN-1991; 91US-0642312.  
 PR 01-MAR-1993; 93US-0024868.  
 XX  
 XX (UUNY ) UNIV NEW YORK STATE.  
 XX  
 XX Lee TH, Vilcek J, Wisniewski H;  
 PI WPI; 1999-059056/05.  
 DR  
 XX DNA encoding tumour necrosis factor stimulated gene 6 protein -  
 PT useful for producing recombinant protein for diagnosis and therapy  
 PT of disease e.g. immune disorders or cancer  
 XX  
 XX Example 9; Columns 57-58; 65pp; English.  
 XX  
 CC This represents the N-terminal amino acid sequence of a human tumour  
 CC necrosis factor stimulated gene 6 (TSG-6) protein/lalpal complex  
 CC determined by microsequencing. A prokaryotic host cell transformed, or  
 CC a eukaryotic host cell transfected with expression vectors containing  
 CC the TSG-6 nucleic acid are used to produce recombinant human TSG-6  
 CC protein. TSG proteins, peptide fragments of TSG proteins or antibodies  
 CC to TSG proteins are useful for diagnosis or therapy of diseases mediated  
 CC by cytokine activity or inactivity, such as immune and autoimmune  
 CC disorders, infections, inflammatory diseases, neurodegenerative  
 CC diseases, cancer and alcohol-induced hepatitis.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 80.0%; Score 4; DB 20; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 Db |||||  
 6 SEEM 9  
 RESULT 18  
 AAE02365  
 ID AAE02365 standard; peptide; 10 AA.  
 XX  
 XX AAE02365;  
 XX  
 DT 30-AUG-2001 (first entry)  
 XX  
 DE TSG-6 related peptide #4.  
 XX  
 KW Tumour necrosis factor stimulated gene-6; TSG-6; antibacterial;  
 KW TNF; anti-inflammatory; antirheumatic; antiarthritic; autoimmune disease;  
 KW therapy; systemic lupus erythematosus; SLE; rheumatoid arthritis; sepsis;  
 KW infection; inflammatory disease; sarcoidosis; neurodegenerative disease;  
 KW atherosclerosis; Parkinson's disease; multiple sclerosis; leukaemia;  
 KW alcohol induced hepatitis; cancer.  
 XX  
 OS Unidentified.  
 XX  
 XX US6210905-B1.  
 XX  
 XX 03-APR-2001.  
 XX  
 XX 07-DEC-1998; 98US-0206695.  
 XX  
 XX 14-JAN-1991; 91US-0642312.  
 PR 13-MAY-1994; 94US-0242097.  
 PR

PR 01-MAR-1993; 93US-0024868.  
 XX  
 XX (UUNY ) UNIV NEW YORK STATE.  
 XX  
 XX Lee TH, Wisniewski H, Vilcek J;  
 PI WPI; 2001-280854/29.  
 XX  
 XX Tumor necrosis factor stimulated gene 6 (TSG-6) binding molecules,  
 PT useful for detecting TSG-6 expression in a biological sample, or for  
 PT disrupting TSG-6 action to prevent or treat diseases -  
 XX  
 XX Disclosure; Column 71; 65pp; English.  
 XX  
 XX The present sequence is a TSG-6 related peptide.  
 CC The present invention relates to TSG-6 antibodies which are  
 CC useful for detecting TSG-6 expression in a biological sample. They  
 CC are useful for measuring the induction of expression of TSG-6 in a  
 CC cell or for identifying a compound capable of inducing the expression  
 CC of TSG-6 in a cell. They are useful for disrupting the action of TSG-6,  
 CC preventing or treating diseases associated with overproduction, or  
 CC inappropriate production/action of TSG-6. They are used to prevent or  
 CC treat diseases such as acute and chronic immune and autoimmune diseases  
 CC (e.g. systemic lupus erythematosus (SLE), rheumatoid arthritis),  
 CC infections or sepsis, inflammatory diseases (e.g. sarcoidosis,  
 CC atherosclerosis), neurodegenerative diseases (e.g. Parkinson's disease,  
 CC multiple sclerosis), malignant pathologies involving TNF-secreting  
 CC tumours (e.g. leukaemia), alcohol induced hepatitis and as well as  
 CC conditions associated with tumour necrosis factor (TNF)-stimulated  
 CC leucocyte adhesion. They are also used to treat cancer.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 80.0%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 Db |||||  
 6 SEEM 9  
 RESULT 19  
 ABG70874  
 ID ABG70874 standard; Peptide; 10 AA.  
 XX  
 XX ABG70874;  
 AC  
 XX 29-NOV-2002 (first entry)  
 XX  
 XX Human lalpal (trypsin) heavy chain (HC2) N-terminal sequence #2.  
 DE  
 XX Human; tumour necrosis factor stimulated gene 6; TSG-6; HC2;  
 KW autoimmune pathology; inflammatory condition; sarcoidosis; thyroiditis;  
 KW chronic inflammatory bowel disease; ulcerative colitis; atherosclerosis;  
 KW Crohn's disease; malignant tumour; infection; AIDS; diabetes mellitus;  
 KW acquired immunodeficiency syndrome; rheumatoid arthritis;  
 KW systemic lupus erythematosus; graft versus host disease; Grave's disease;  
 KW neurodegenerative disease; multiple sclerosis; Huntington's Chorea;  
 KW Parkinson's disease; motor unit disorder; Alzheimer's disease; leukaemia;  
 KW lymphoma; alcohol-induced hepatitis; lalpal; trypsin; heavy chain.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US2002090708-A1.  
 PN  
 XX 11-JUL-2002.  
 PD  
 XX 06-MAR-2001; 2001US-0799118.  
 PF  
 XX 13-MAY-1994; 94US-0242097.  
 PR 07-DEC-1998; 98US-0206695.  
 PR 14-JAN-1991; 91US-0642312.  
 PR

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PR 01-MAR-1993; 93US-0024868.
XX
XX
XX (UNY ) UNIV NEW YORK STATE.
XX
XX Lee TH, Wisniewski HG, Vilcek J;
XX
XX WPI; 2002-690317/74.
XX
XX Novel tumor necrosis factor-induced protein or glycoprotein molecule
XX TSG-6 useful for preventing and treating rheumatoid arthritis, or other
XX inflammatory conditions, malignant tumors, and infections
XX
XX Example 14; Page 32; 68pp; English.
XX
XX The invention relates to an isolated tumor necrosis factor-induced
XX protein or glycoprotein molecule TSG-6, or its functional derivative,
XX where the molecule has a sequence which corresponds to at least 10 amino
XX acids of the human TSG-6 sequence appearing as ABG7070. TSG-6 protein is
XX useful for preventing and treating inflammatory conditions (e.g.
XX sarcoidosis, chronic inflammatory bowel disease, ulcerative
XX colitis, atherosclerosis and Crohn's disease), malignant tumors,
XX and infections (e.g. AIDS, acquired immunodeficiency syndrome).
XX Inflammatory conditions include autoimmune pathologies such as rheumatoid
XX arthritis, systemic lupus erythematosus, thyroiditis, graft versus host
XX disease, diabetes mellitus, Grave's disease, infections include
XX bacterial, viral, fungal infections, neurodegenerative diseases,
XX (e.g. multiple sclerosis, Huntington's Chorea and Parkinson's disease)
XX disorders of the motor unit (e.g. Alzheimer's disease), malignant
XX pathologies involving tumor necrosis factor (TNF)-secreting tumours
XX (e.g. leukaemia and lymphomas) and alcohol-induced hepatitis. Many other
XX diseases and disorders are given in the specification. The present
XX sequence represents human Ia1pha1 (trypsin) heavy chain (HC2) N-terminal
XX sequence. Ia1pha1 trypsin was shown to be a binding partner of TSG-6.
XX
XX SQ Sequence 10 AA;
XX
XX Query Match 80.0%; Score 4; DB 23; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 93;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SEEM: 4
XX ||||
XX 6 SEEM 9
XX
XX Db
XX
XX RESULT 20
XX ABR07242
XX ID ABR07242 standard; Peptide; 10 AA.
XX
XX AC ABR07242;
XX
XX DT 19-MAY-2003 (first entry)
XX
XX DE Human cancer-related protein 109P1D4 HLA peptide #1177.
XX
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX OS Homo sapiens.
XX
XX PN WO200283921-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 10-APR-2002; 2002WO-US11654.
XX
XX PR 10-APR-2001; 2001US-282739P.
XX
XX PR 10-APR-2001; 2001US-283112P.
XX
XX PR 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients
XX
XX Claim 13; Page 321; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
XX SQ Sequence 10 AA;
XX
XX Query Match 80.0%; Score 4; DB 24; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 93;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 EEMP 5
XX ||||
XX 4 EEMP 7
XX
XX Db
XX
XX RESULT 21
XX ABR20268
XX ID ABR20268 standard; Peptide; 10 AA.
XX
XX AC ABR20268;
XX
XX DT 19-MAY-2003 (first entry)
XX
XX DE Human cancer-related protein 185P2C9 HLA peptide #103.
XX
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX OS Homo sapiens.
XX
XX PN WO200283921-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 10-APR-2002; 2002WO-US11654.
XX
XX PR 10-APR-2001; 2001US-282739P.
XX
XX PR 10-APR-2001; 2001US-283112P.
XX
XX PR 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients
XX
XX Claim 13; Page 321; 1021pp; English.
XX
XX PS

```



XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX Sequence 10 AA;  
 SQ  
 Query Match 80.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
 ||||  
 Db 4 SEEM 7

RESULT 22  
 ABR20300  
 ID ABR20300 standard; Peptide; 10 AA.  
 AC ABR20300;  
 XX  
 XX 19-MAY-2003 (first entry)  
 DT  
 XX Human cancer-related protein 185P2C9 HLA peptide #135.  
 DE  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX Homo sapiens.  
 OS  
 XX WO200283921-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 10-APR-2001; 2001US-282739P.  
 PR  
 XX 10-APR-2001; 2001US-283112P.  
 PR  
 XX 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 PI  
 XX WPI; 2003-075555/07.  
 XX  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 PT  
 XX Claim 13; Page 321; 1021pp; English.  
 PS  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX Sequence 10 AA;  
 SQ  
 Query Match 80.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
 ||||  
 Db 6 SEEM 9

RESULT 23  
 ABR20312  
 ID ABR20312 standard; Peptide; 10 AA.  
 AC ABR20312;  
 XX  
 XX 19-MAY-2003 (first entry)  
 DT  
 XX Human cancer-related protein 185P2C9 HLA peptide #147.  
 DE  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX Homo sapiens.  
 OS  
 XX WO200283921-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 10-APR-2002; 2002WO-US11654.  
 PF  
 XX 10-APR-2001; 2001US-282739P.  
 PR  
 XX 10-APR-2001; 2001US-283112P.  
 PR  
 XX 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 PI  
 XX WPI; 2003-075555/07.  
 XX  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 PT  
 XX Claim 13; Page 321; 1021pp; English.  
 PS  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX Sequence 10 AA;  
 SQ  
 Query Match 80.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
 ||||  
 Db 2 SEEM 5

## RESULT 24

ABR21505  
 ID ABR21505 standard; Peptide; 10 AA.

XX ABR21505;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 185P2C9 HLA peptide #1340.

DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients

XX Claim 13; Page 335; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX Sequence 10 AA;

Query Match 80.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
 ||||  
 Db 7 SEEM 10

## RESULT 25

ABR21668  
 ID ABR21668 standard; Peptide; 10 AA.

XX ABR21668;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 185P2C9 HLA peptide #1503.

DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients

XX Claim 13; Page 337; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX Sequence 10 AA;

Query Match 80.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
 ||||  
 Db 4 SEEM 7

## RESULT 26

ABR21697  
 ID ABR21697 standard; Peptide; 10 AA.

XX ABR21697;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 185P2C9 HLA peptide #1532.

DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX Homo sapiens.

PN WO200283921-A2.  
 XX 24-OCT-2002.  
 XX 10-APR-2002; 2002WO-US11654.  
 XX 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 337; 1021pp; English.  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of the protein, as tools for modulating or  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX SQ Sequence 10 AA;  
 Query Match 80.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 Db |||||  
 6 SEEM 9  
 RESULT 27  
 ABR21706  
 ID ABR21706 standard; Peptide; 10 AA.  
 XX ABR21706;  
 AC ABR21706;  
 XX 19-MAY-2003 (first entry)  
 DT Human cancer-related protein 185P2C9 HLA peptide #1541.  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX Homo sapiens.  
 OS WO200283921-A2.  
 PN 24-OCT-2002.  
 XX 10-APR-2002; 2002WO-US11654.  
 XX 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 337; 1021pp; English.  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of the protein, as tools for modulating or  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX SQ Sequence 10 AA;  
 Query Match 80.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 Db |||||  
 6 SEEM 9  
 RESULT 28  
 ABR22557  
 ID ABR22557 standard; Peptide; 10 AA.  
 XX ABR22557;  
 AC ABR22557;  
 XX 19-MAY-2003 (first entry)  
 DT Human cancer-related protein 185P2C9 HLA peptide #2392.  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX Homo sapiens.  
 OS WO200283921-A2.  
 PN 24-OCT-2002.  
 XX 10-APR-2002; 2002WO-US11654.  
 XX 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -

PA (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 337; 1021pp; English.  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of the protein, as tools for modulating or  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX SQ Sequence 10 AA;  
 Query Match 80.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 Db |||||  
 2 SEEM 5  
 RESULT 28  
 ABR22557  
 ID ABR22557 standard; Peptide; 10 AA.  
 XX ABR22557;  
 AC ABR22557;  
 XX 19-MAY-2003 (first entry)  
 DT Human cancer-related protein 185P2C9 HLA peptide #2392.  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX Homo sapiens.  
 OS WO200283921-A2.  
 PN 24-OCT-2002.  
 XX 10-APR-2002; 2002WO-US11654.  
 XX 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -

PT in cancer patients -  
XX  
PS Claim 13; Page 347; 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as CC therapeutic, prognostic and diagnostic reagents for cancer. The present CC sequence is a human leukocyte antigen (HLA) peptide, used in an example CC from the invention.  
XX  
SQ Sequence 10 AA;  
Query Match 80.0%; Score 4; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SEEM 4  
DB 6 SEEM 9  
|||||  
RESULT 29  
ABR22897  
ID ABR22897 standard; Peptide; 10 AA.  
XX  
AC ABR22897;  
XX  
DT 19-MAY-2003 (first entry)  
DE Human cancer-related protein 185P2C9 HLA peptide #2732.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
PR 10-APR-2001; 2001US-283112P.  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response PT in cancer patients -  
XX  
PS Claim 13; Page 351; 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as CC therapeutic, prognostic and diagnostic reagents for cancer. The present CC sequence is a human leukocyte antigen (HLA) peptide, used in an example CC from the invention.  
XX  
SQ Sequence 10 AA;  
Query Match 80.0%; Score 4; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SEEM 4  
DB 7 SEEM 10  
|||||  
RESULT 30  
ABR23068  
ID ABR23068 standard; Peptide; 10 AA.  
XX  
AC ABR23068;  
XX  
DT 19-MAY-2003 (first entry)  
DE Human cancer-related protein 185P2C9 HLA peptide #2903.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US11654.  
XX  
PR 10-APR-2001; 2001US-282739P.  
PR 10-APR-2001; 2001US-283112P.  
PR 25-APR-2001; 2001US-286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response PT in cancer patients -  
XX  
PS Claim 13; Page 353; 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as CC therapeutic, prognostic and diagnostic reagents for cancer. The present CC sequence is a human leukocyte antigen (HLA) peptide, used in an example CC from the invention.  
XX  
SQ Sequence 10 AA;  
Query Match 80.0%; Score 4; DB 24; Length 10;

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Best Local Similarity 100.0%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4
DB 4 SEEM 7

RESULT 31
ABR23099
ID ABR23099 standard; Peptide; 10 AA.
XX AC ABR23099;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 185P2C9 HLA peptide #2934.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients
XX PS Claim 13; Page 354; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 10 AA;
XX Query Match 80.0%; Score 4; DB 24; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 93;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4
DB 6 SEEM 9

RESULT 32
ABR23112
ID ABR23112 standard; Peptide; 10 AA.
XX AC ABR23112;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 185P2C9 HLA peptide #2947.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients
XX PS Claim 13; Page 354; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 10 AA;
XX Query Match 80.0%; Score 4; DB 24; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 93;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4
DB 2 SEEM 5

RESULT 33
ABR24311
ID ABR24311 standard; Peptide; 10 AA.
XX AC ABR24311;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 185P2C9 HLA peptide #4146.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.

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XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD
XX PF 24-OCT-2002.
XX PD
XX PF 10-APR-2002; 2002WO-US11654.
XX PR
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX PI WPI; 2003-075555/07.
XX DR
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients.
XX PT
XX PS Claim 13; Page 368; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 10 AA;

Query Match 80.0%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4
Db |||||
7 SEEM 10

RESULT 34
AAW78610
ID AAW78610 standard; peptide; 11 AA.
XX AC
XX AC AAW78610;
XX DT
XX DT 04-NOV-1998 (first entry)
XX DE
XX DE SH2 domain binding inhibiting peptide SEQ ID NO:99.
XX KW
XX KW SH2 domain; binding; inhibition; interaction; site specific;
XX KW signal transduction; protein tyrosine kinase; phosphotyrosine;
XX KW growth factor receptor; oncogene; cellular growth; cell proliferation;
XX KW metabolic control; diabetes; PTK; proto-oncogene; insulin receptor.
XX OS
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT Misc-difference 4
XX FT /note= "unspecified"
XX PN US5801149-A.

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XX PD
XX PD 01-SEP-1998.
XX PF
XX PF 21-MAR-1995; 95US-0408604.
XX PR
XX PR 21-MAR-1995; 95US-0408604.
XX PR 19-JUN-1991; 91US-0722359.
XX PR 09-OCT-1992; 92US-0959949.
XX PR 08-OCT-1993; 93US-0134558.
XX PA (JOSL-) JOSLIN DIABETES CENT INC.
XX PI
XX PI Shoelson S;
XX PI WPI; 1998-494822/42.
XX PT Inhibiting site-specific SH2 domain interaction - with peptide
XX PT containing phosphotyrosine or phosphotyrosine mimic
XX PS
XX PS Disclosure; Column 71; 70pp; English.
XX CC A method has been developed of inhibiting a site-specific interaction
XX CC between a first molecule having an SH2 domain and a second molecule that
XX CC interacts with the SH2 domain. The method comprises contacting the first
XX CC molecule with a 4- to 30-mer peptide containing a sequence of formula:
XX CC R1-Met-R3-Met (I), where R1 = phosphotyrosine (pTyr) or a
XX CC phosphotyrosine analogue having a hydrolysis-resistant phosphorous
XX CC moiety, and R3 = any amino acid. AAW78501 to AAW78523 represent
XX CC specifically claimed examples of the peptides described. The peptides are
XX CC useful for modulating both cellular growth to control unwanted cell
XX CC proliferation in e.g. selected malignancies and for metabolic control in
XX CC e.g. diabetes, by inhibiting signal transduction molecules such as
XX CC protein tyrosine kinases (PTKs) which include growth factor receptors,
XX CC proto-oncogene and oncogene products and the insulin receptor. The
XX CC peptides are also useful for treating and for studying the enzymatic
XX CC mechanisms of PTPase activity and the metabolic and biochemical roles of
XX CC PTPases. AAW78524 to AAW78702 represent other peptides given in the
XX CC present invention, but which are not specifically claimed.
XX SQ Sequence 11 AA;

Query Match 80.0%; Score 4; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEMP 5
Db |||||
5 EEMP 8

RESULT 35
AAR58755
ID AAR58755 standard; peptide; 13 AA.
XX AC
XX AC AAR58755;
XX DT
XX DT 25-MAR-2003 (updated)
XX DT 30-MAR-1995 (first entry)
XX DE
XX DE Wild type T-antigen peptide contg. amino acids 102-114.
XX KW
XX KW retinoblastoma protein; PRB; p107; MYOD; MEF2; MASH; pocket protein;
XX KW transcription factor; tumour suppressor; decrease cell proliferation;
XX KW identification; agent; treatment; tissue regeneration; T-antigen;
XX KW SV40; simian virus.
XX OS
XX OS Simian virus 40.
XX PN WO9418239-A1.
XX PD
XX PD 18-AUG-1994.
XX PF
XX PF 14-FEB-1994; 94WO-US01499.

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XX PR 11-FEB-1993; 93US-0021538.  
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.  
 XX PI Gu W, Mahdavi V, Nadal-ginard B, Schneider JW;  
 XX PS WPI; 1994-279691/34.  
 XX DR  
 XX PT Identifying agents useful for decreasing undesired cell  
 XX PT proliferation - e.g. to treat a neoplasm, or useful for inducing  
 XX PT replication of cells in a terminally differentiated state  
 XX PS  
 XX PS Example 8; Page 50; 106pp; English.  
 XX CC AAR58755 is a wild type T-antigen peptide contg. amino acids 102-114,  
 XX CC which has been show to bind PRB (retinoblastoma protein). This peptide  
 XX CC competed effectively with PRB binding to MyoD, whereas AAR58757, an  
 XX CC equivalent peptide contg. a single substitution has no binding with  
 XX CC PRB. MyoD does not however contain the highly conserved PRB-binding  
 XX CC motif (AAR58756) that is essential for PRB-binding of large T, E1A and  
 XX CC E7 proteins. It is concluded that MyoD interacts with PRB in a specific  
 XX CC manner that is competed by T-antigen, and that involves the bHLH and  
 XX CC pocket domains respectively, of these two molecules. MyoD effects on  
 XX CC the cell cycle and PRB on the myogenic pathway result from direct  
 XX CC binding of the 2 molecules with each other. The method can be used for  
 XX CC the regeneration of tissue, eg. muscle tissue, in eg. mammals.  
 XX CC (See also AAR58756-8 and AAO67372).  
 XX CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 13 AA;  
 Query Match 80.0%; Score 4; DB 15; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 Db |||||  
 5 SEEM 8  
 RESULT 36  
 ID ABP54333 standard; Peptide; 13 AA.  
 AC ABP54333;  
 XX DT 16-JAN-2003 (first entry)  
 DE Human HGPRBMY27 PKC phosphorylation site peptide 7 SEQ ID NO:27.  
 XX Human; G protein coupled receptor; GPCR; HGPRBMY27; antiinflammatory;  
 KW antiinfertility; pulmonary; cytotstatic; nephrotropic; hormonal;  
 KW circulatory; gene therapy; inflammatory disorder; reproductive disorder;  
 KW pulmonary disorder; cancer; renal disorder; connective tissue disorder;  
 KW endocrine disorder.  
 XX OS Homo sapiens.  
 XX WO200272755-A2.  
 XX PD 19-SEP-2002.  
 XX PF 06-MAR-2002; 2002WO-US06796.  
 XX PR 07-MAR-2001; 2001US-273808P.  
 XX PR 27-MAR-2001; 2001US-278983P.  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX PI Ramanathan C, Feder J, Mintier G, Cacace A, Barber L;  
 XX WPI; 2002-657945/70.  
 XX DR

XX PT New polynucleotide encoding a human G-protein coupled receptor for  
 XX PT preventing, treating, or ameliorating e.g. an inflammatory,  
 XX PT reproductive, pulmonary, renal connective tissue, or endocrine disorder  
 XX PS  
 XX PS Disclosure; Page 43; 356pp; English.  
 XX CC The present invention describes a human G protein coupled receptor  
 XX CC (GPCR), designated HGPRBMY27 (I). (I) has antiinflammatory,  
 XX CC antiinfertility, pulmonary, cytotstatic, nephrotropic, hormonal and  
 XX CC circulatory activities, and can be used in gene therapy. (I) or the  
 XX CC protein encoded by it can be used to prevent, treat, or ameliorate a  
 XX CC medical condition, such as inflammatory disorders, reproductive a  
 XX CC disorders, pulmonary disorders, cancer, renal disorders, connective  
 XX CC tissue disorders, endocrine disorders, or disorders involving  
 XX CC aberrations in tubular tissues. They can also be used to diagnose a  
 XX CC pathological condition or a susceptibility to (I). The protein can  
 XX CC be used to screen for candidate compounds capable of modulating activity  
 XX CC of a GPCR polypeptide. The present sequence represents a PKC  
 XX CC phosphorylation site peptide from human HGPRBMY27, which is given in the  
 XX CC exemplification of the present invention.  
 XX SQ Sequence 13 AA;  
 Query Match 80.0%; Score 4; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EEMP 5  
 Db |||||  
 10 EEMP 13  
 RESULT 37  
 ID AAE24501 standard; peptide; 14 AA.  
 XX AC AAE24501;  
 XX DT 04-OCT-2002 (first entry)  
 DE Human RATLid6 casein kinase II phosphorylation site #3.  
 XX Human; ubiquitin conjugating enzyme; UBC; RATLid6; immune disorder;  
 KW regulated in activated T-lymphocyte Id6; neuronal disorder; cancer;  
 KW tumour; lymphoproliferative; cancer; adenocarcinoma; leukaemia; myeloma;  
 KW sarcoma; neurodegenerative; inflammatory; rheumatoid arthritis; asthma;  
 KW multiple sclerosis; psoriasis; neuronal; Alzheimer's disease; dementia;  
 KW depression; epilepsy; acquired immuno deficiency syndrome; allergy;  
 KW AIDS; anaemia; atopic dermatitis; diabetes mellitus; dermatological;  
 KW myocardial infarction; renal tubular acidosis; gonadal dysgenesis;  
 KW dysplasia; cataract; cytotstatic; neuroprotective; nootropic; anti-HIV;  
 KW anticonvulsant; antiinflammatory; Cushing's syndrome; cardiant;  
 KW ophthalmological; casein kinase II.  
 XX OS Homo sapiens.  
 XX WO200236741-A2.  
 XX PD 10-MAY-2002.  
 XX PF 29-OCT-2001; 2001WO-US46559.  
 XX PR 30-OCT-2000; 2000US-244688P.  
 XX PR 30-JUL-2001; 2001US-308706P.  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX PI Bowen MA, Wu Y, Yang W, Finger JN;  
 XX WPI; 2002-479758/51.  
 XX DR

PT Novel ubiquitin conjugating enzyme polypeptide isolated from activated  
PT human T cell, for screening modulators useful for treating cancer,  
PT immune disorder, lymphoproliferative disorder, neurodegenerative  
PT disorder -  
XX  
PS Disclosure; Page 90; 169pp; English.  
XX  
XX The invention relates to a novel ubiquitin conjugating enzyme (UBC)  
CC homologue, RAU1d6 (regulated in activated T-lymphocytes 1d6) and its  
CC corresponding nucleic acid. The invention also relates to methods for  
CC treating, diagnosing, preventing and screening for disorders related  
CC to the expression of RAU1d6. UBC is useful for screening for candidate  
CC compounds capable of binding to and/or modulating its activity. UBC is  
CC useful for treating an immune or neuronal disorder in a mammal. The  
CC method is useful for treating a cancer or tumour. It is useful for  
CC suppressing the immune response in a subject requiring the suppression.  
CC It is also useful for treating lymphoproliferative disorder, cancer e.g.  
CC adenocarcinoma, leukaemia, myeloma, sarcoma, etc, neurodegenerative  
CC disorder, inflammatory disorders e.g. rheumatoid arthritis, asthma,  
CC multiple sclerosis, psoriasis, etc, neuronal disorders e.g. Alzheimer's  
CC disease, dementia, depression, epilepsy, etc, immune disorder or immune  
CC related disorders such as acquired immuno deficiency syndrome (AIDS),  
CC allergy, anaemia, atopic dermatitis, diabetes mellitus, myocardial  
CC infarction, etc, developmental disorders e.g. Cushing's syndrome, renal  
CC tubular acidosis, gonadal dysgenesis, dysplasia, cataract, etc. The  
CC present sequence is human RAU1d6 casein kinase II phosphorylation  
CC site.  
XX  
SQ Sequence 14 AA;

Query Match 80.0%; Score 4; DB 23; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EEMP 5  
|||  
Db 11 EEMP 14

RESULT 38  
ABR31680  
ID ABR31680 standard; Peptide; 15 AA.  
XX  
AC ABR31680;  
XX  
XX 19-MAY-2003 (first entry)  
XX  
XX Human cancer-related protein 109P1D4 HLA peptide #1452.  
XX  
XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX human leukocyte antigen.  
XX  
XX Homo sapiens.  
XX WO200283921-A2.  
XX  
XX 24-OCT-2002.  
XX  
XX 10-APR-2002; 2002WO-US11654.  
XX  
XX 10-APR-2001; 2001US-282739P.  
XX 10-APR-2001; 2001US-283112P.  
XX 25-APR-2001; 2001US-286630P.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX Morrison K, Morrison RK, Raitano AB;  
XX  
XX WPI; 2003-075555/07.  
XX  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and

PT diagnostic reagents for eliciting cellular or humoral immune response  
PT in cancer patients -  
XX  
XX Claim 13; Page 497; 1021pp; English.  
XX  
XX The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention.  
XX  
SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 24; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EEMP 5  
|||  
Db 6 EEMP 9

RESULT 39  
ABR31949  
ID ABR31949 standard; Peptide; 15 AA.  
XX  
AC ABR31949;  
XX  
XX 19-MAY-2003 (first entry)  
XX  
XX Human cancer-related protein 109P1D4 HLA peptide #1721.  
XX  
XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
XX human leukocyte antigen.  
XX  
XX Homo sapiens.  
XX WO200283921-A2.  
XX  
XX 24-OCT-2002.  
XX  
XX 10-APR-2002; 2002WO-US11654.  
XX  
XX 10-APR-2001; 2001US-282739P.  
XX 10-APR-2001; 2001US-283112P.  
XX 25-APR-2001; 2001US-286630P.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
XX Morrison K, Morrison RK, Raitano AB;  
XX  
XX WPI; 2003-075555/07.  
XX  
XX New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response  
XX in cancer patients -  
XX  
XX Claim 13; Page 502; 1021pp; English.  
XX  
XX The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the



CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention.

XX SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 24; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEMP 5  
|||  
Db 6 EEMP 9

RESULT 40

ABR35147  
ID ABR35147 standard; Peptide; 15 AA.

XX AC ABR35147;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 185P2C9 HLA peptide #4403.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response  
XX in cancer patients -

XX PS Claim 13; Page 561; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and  
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
XX proteins are useful for eliciting a humoral or cellular immune response.  
XX The genes are useful as probes and primers for the amplification and/or  
XX detection of genes, mRNAs or their fragments, as reagents for the  
XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
XX directing the expression of the protein, as tools for modulating or  
XX inhibiting the expression of genes and/or translation of transcripts, and  
XX as therapeutic agents. The proteins and peptides are useful as  
XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.

XX SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 24; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
|||  
Db 2 SEEM 5

RESULT 41

ABR35302  
ID ABR35302 standard; Peptide; 15 AA.

XX AC ABR35302;

XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 185P2C9 HLA peptide #4558.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;

XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US11654.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 10-APR-2001; 2001US-283112P.

XX PR 25-APR-2001; 2001US-286630P.

XX PA (AGEN-) AGENSYS INC.

XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX PT New composition comprising a substance that modulates the structure of  
XX proteins and polynucleotides, useful for therapeutic, prognostic and  
XX diagnostic reagents for eliciting cellular or humoral immune response  
XX in cancer patients -

XX PS Claim 13; Page 563; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and  
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
XX proteins are useful for eliciting a humoral or cellular immune response.  
XX The genes are useful as probes and primers for the amplification and/or  
XX detection of genes, mRNAs or their fragments, as reagents for the  
XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
XX directing the expression of the protein, as tools for modulating or  
XX inhibiting the expression of genes and/or translation of transcripts, and  
XX as therapeutic agents. The proteins and peptides are useful as  
XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.

XX SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 24; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
|||  
Db 8 SEEM 11

RESULT 42

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ABR35636
ID ABR35636 standard; Peptide; 15 AA.
XX
AC ABR35636;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 185P2C9 HLA peptide #4892.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
XX WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
PR 10-APR-2001; 2001US-283112P.
PR 25-APR-2001; 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients
XX
PS Claim 13; Page 569; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 80.0%; Score 4; DB 24; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEEM 4
DB 10 SEEM 13
|||||
19-MAY-2003 (first entry)
Human cancer-related protein 185P2C9 HLA peptide #5100.
Human; cytostatic; vaccine; cancer; immune response; HLA;
Human leukocyte antigen.
Homo sapiens.
WO200283921-A2.
24-OCT-2002.
19-MAY-2003 (first entry)
Human cancer-related protein 185P2C9 HLA peptide #5151.
Human; cytostatic; vaccine; cancer; immune response; HLA;
human leukocyte antigen.
Homo sapiens.
WO200283921-A2.
24-OCT-2002.
10-APR-2002; 2002WO-US11654.
XX
XX

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PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 DR  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 PS Claim 13; Page 574; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 80.0%; Score 4; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 DB |||||  
 1 SEEM 4  
 RESULT 45  
 ABR36098  
 ID ABR36098 standard; Peptide; 15 AA.  
 AC ABR36098;  
 XX  
 XX 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 185P2C9 HLA peptide #5354.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US11654.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 DR

XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 XX Claim 13; Page 577; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 80.0%; Score 4; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 DB |||||  
 2 SEEM 5  
 RESULT 46  
 ABR36234  
 ID ABR36234 standard; Peptide; 15 AA.  
 XX  
 AC ABR36234;  
 XX  
 XX 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 185P2C9 HLA peptide #5490.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US11654.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 DR  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 XX Claim 13; Page 580; 1021pp; English.  
 PS  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC diagnostic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEEM 4  
 ||||  
 8 SEEM 11

Db

#### RESULT 47

ID ABR36532 standard; Peptide; 15 AA.

XX ABR36532;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 185P2C9 HLA peptide #5788.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

XX human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

XX 10-APR-2001; 2001US-283112P.

XX 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients

PS Claim 13; Page 585; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC diagnostic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEEM 4  
 ||||  
 10 SEEM 13

Db

#### RESULT 48

ABR36715

ID ABR36715 standard; Peptide; 15 AA.

XX ABR36715;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 185P2C9 HLA peptide #5971.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

XX human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

XX 10-APR-2001; 2001US-283112P.

XX 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients

PS Claim 13; Page 588; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC diagnostic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX SQ Sequence 15 AA;

Query Match 80.0%; Score 4; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEEM 4  
 ||||  
 3 SEEM 6

Db



XX 10-APR-2002; 2002WO-US11654.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 PS Claim 13; Page 596; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 80.0%; Score 4; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 DB 8 SEEM 11  
 XX  
 RESULT 52  
 ABR37484  
 ID ABR37484 standard; Peptide; 15 AA.  
 XX  
 AC ABR37484;  
 XX  
 DT 19-MAY-2003 (first entry)  
 DE Human cancer-related protein 185P2C9 HLA peptide #6740.  
 XX  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US11654.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 PS Claim 13; Page 605; 1021pp; English.

PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 PS Claim 13; Page 602; 1021pp; English.  
 XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 80.0%; Score 4; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 DB 10 SEEM 13  
 XX  
 RESULT 53  
 ABR37689  
 ID ABR37689 standard; Peptide; 15 AA.  
 XX  
 AC ABR37689;  
 XX  
 DT 19-MAY-2003 (first entry)  
 DE Human cancer-related protein 185P2C9 HLA peptide #6945.  
 XX  
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US11654.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 PS Claim 13; Page 605; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX SQ Sequence 15 AA;  
 CC Query Match 80.0%; Score 4; DB 24; Length 15;  
 CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 DB |||||  
 3 SEEM 6

RESULT 54  
 ABR37742  
 ID ABR37742 standard; Peptide; 15 AA.  
 XX AC ABR37742;  
 XX DT 19-MAY-2003 (first entry)  
 XX DE Human cancer-related protein 185P2C9 HLA peptide #6998.  
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.  
 XX PF 10-APR-2002; 2002WO-US11654.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 10-APR-2001; 2001US-283112P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 606; 1021pp; English.  
 XX CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX SQ Sequence 15 AA;  
 CC Query Match 80.0%; Score 4; DB 24; Length 15;  
 CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEEM 4  
 DB |||||  
 1 SEEM 4

RESULT 55  
 AAY25865  
 ID AAY25865 standard; Protein; 17 AA.  
 XX AC AAY25865;  
 XX DT 04-OCT-1999 (first entry)  
 XX DE Human secreted protein fragment encoded from gene 55.  
 XX KW Secreted protein; human; treatment; diagnosis; therapy; cancer; tumour;  
 KW neurodegenerative disorder; developmental abnormality; blood disorder;  
 KW fetal deficiency; blood disorder; leukemia; immune system; inflammation;  
 KW autoimmune disease; hepatic disease; renal disease; allergy; resclerosis;  
 KW ischaemic shock; Alzheimer's disease; cognitive disorder; schizophrenia;  
 KW cardiovascular disorder; wound healing; stroke; arthritis; obesity;  
 KW asthma; sepsis; acne; psoriasis; transplant rejection; infection; AIDS;  
 KW metabolic disorder.  
 XX OS Homo sapiens.  
 XX PN WO9938881-A1.  
 XX PD 05-AUG-1999.  
 XX PF 27-JAN-1999; 99WO-US01621.  
 XX PR 30-JAN-1998; 98US-0073170.  
 XX PR 30-JAN-1998; 98US-0073159.  
 XX PR 30-JAN-1998; 98US-0073160.  
 XX PR 30-JAN-1998; 98US-0073161.  
 XX PR 30-JAN-1998; 98US-0073162.  
 XX PR 30-JAN-1998; 98US-0073164.  
 XX PR 30-JAN-1998; 98US-0073165.  
 XX PR 30-JAN-1998; 98US-0073167.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Carter KC, Endress GA, Feng P, Ferrie AM, Florence C;  
 PI Florence KA, Janat F, Ni J, Rosen CA, Ruben SM;  
 PI Soppet DR, Young P, Yu G;  
 XX WPI; 1999-469315/39.  
 XX DR N-PSDB; AA200464.  
 XX PT New isolated human genes and the secreted polypeptides they encode  
 XX useful in, e.g. treatment of Alzheimer's  
 XX Disclosure; Page 370; 393pp; English.  
 XX CC This invention describes novel human genes (see AA200410-200477) and the  
 CC secreted proteins (see AAY25711-Y25778) and fragments (see  
 CC AAY25779-Y25907) they encode. The polynucleotides and their corresponding  
 CC secreted polypeptides are useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. Also pathological  
 CC conditions can be diagnosed by determining the amount of the new  
 CC polypeptides in a sample or by determining the presence of mutations in  
 CC the new polynucleotides. Specific uses are described for each of the 67

CC polynucleotides of the invention, based on which tissues they are most  
 CC highly expressed in, and include developing products for the diagnosis  
 CC or treatment of cancer, tumours, neurodegenerative disorders,  
 CC developmental abnormalities and fetal deficiencies, blood disorders,  
 CC leukemias, diseases of the immune system, autoimmune diseases, hepatic  
 CC and renal disease, inflammation, allergies, ischaemic shock, Alzheimer's  
 CC and cognitive disorders, schizophrenia, restenosis, cardiovascular  
 CC disorders, wound healing, stroke, arthritis, obesity, asthma, sepsis,  
 CC acne, psoriasis, transplant rejection, metabolic disorders, infections  
 CC and AIDS. The polypeptides are also useful for identifying their binding  
 CC partners.

XX Sequence 17 AA;

Query Match 80.0%; Score 4; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEMP 5

Db 8 EEMP 11

RESULT 56

AAO21454

ID AAO21454 standard; Peptide; 17 AA.

XX

AC AAO21454;

XX

06-AUG-2002 (first entry)

XX

Diabetes specific endogenous retroviral-9 related peptide #19.

DE

XX

Diabetes specific endogenous retroviral-9.

KW

XX

Unidentified.

OS

XX

PN KR99075721-A.

XX

PD 15-OCT-1999.

XX

PF 24-MAR-1998; 98KR-0010108.

XX

PR 24-MAR-1998; 98KR-0010108.

XX

PA (GREG ) KOREA GREEN CROSS CORP.

XX

PI Yoon JW, Jeon HS, Park HJ, Ahn JS, Hah YJ, Chung SI;

XX

WT; 2000-58522/55.

XX

DR

XX

PT Gene of diabetes specific endogenous retroviral-9 and amino acid

XX

sequences -

XX

PS Disclosure; Page 4; 13pp; Korean.

XX

XX

CC The invention relates to the gene of diabetes specific endogenous

CC retroviral-9 and amino acid sequences. This sequence represents a peptide

CC relating to the diabetes specific endogenous retroviral-9 amino acids of

CC the invention.

XX

XX

SQ Sequence 17 AA;

Query Match 80.0%; Score 4; DB 21; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4

Db 3 SEEM 6

RESULT 57

ABP82037

ID ABP82037 standard; Peptide; 17 AA.

XX

AC ABP82037;

XX

04-MAR-2003 (first entry)

XX

G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:710.

DE

XX

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KW ulcer.

XX

OS Homo sapiens.

XX

WO200261087-A2.

XX

08-AUG-2002.

XX

19-DEC-2001; 2001WO-US50107.

XX

19-DEC-2000; 2000US-357144P.

XX

(LIFE-) LIFESPAN BIOSCIENCES INC.

PA

XX

PI Burmer GC, Roush CL, Brown JP;

XX

WPI; 2003-046718/04.

XX

DR

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors

XX

(GPCR), useful for diagnosing and designing drugs for treating

XX

conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,

XX

cancer or autoimmune diseases -

XX

Claim 1; Fig 2; 523pp; English.

XX

CC

The present invention describes antigenic peptides (I) comprising:

XX

(a) any one of 1601 sequences (see ABP82037 to ABP83619) of 12-24 amino

XX

acids. Also described: (1) an assay for the detection of a particular

XX

G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;

XX

and (2) an isolated antibody having high specificity and high affinity

XX

or avidity for a particular GPCR. (I) can be used as GPCR modulators and

XX

in gene therapy. The antigenic peptides for GPCRs are useful in detecting

XX

an antibody against a particular GPCR, and in the production of specific

XX

antibodies. The peptides and antibodies are also useful for detecting the

XX

presence or absence of corresponding GPCRs. The antigenic peptides for

XX

GPCRs and antibodies are useful for diagnosing and designing drugs for

XX

treating immune-related diseases, growth-related diseases, cell

regeneration-related disease, immunological-related cell proliferative

XX

diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,

XX

atherosclerosis, bacterial, fungal, protozoan or viral infections,

XX

osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute

XX

inflammation, allergies, Crohn's disease, diabetes, graft versus host

XX

disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,

XX

anxiety, depression, schizophrenia, dementia, mental retardation, memory

XX

loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or

XX

hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or

XX

any other disorder in which GPCRs are involved. The antibodies may be

XX

used in immunoassays and immunodiagnoses. AB242523 to AB242869 encode

XX

GPCR proteins given in ABP81675 to ABP82018, which are used in the

XX

exemplification of the present invention.

XX

SQ Sequence 17 AA;

Query Match 80.0%; Score 4; DB 24; Length 17;





```

Db          17 SEEM 20
|||||
RESULT 60
ABJ38225
ID ABJ38225 standard; Peptide; 20 AA.
XX
AC ABJ38225;
XX
DT 22-MAY-2003 (first entry)
XX
XX Human cytomegalovirus CTL epitope peptide SEQ ID NO 283.
XX
XX Virucide; immunostimulant; cytotoxic T-lymphocyte; CTL; epitope; antigen;
KW human cytomegalovirus; HCMV; pp28; pp50; pp65; pp71; pp150; gB; gH; IE-1;
KW IE-2; US2; US3; US6; US11; UL18; cytomegalovirus infection; pregnancy;
KW transplantation.
XX
XX Human cytomegalovirus.
OS
XX WO2003000720-A1.
PN
XX 03-JAN-2003.
XX
XX 26-JUN-2002; 2002WO-AU00829.
PF
XX 26-JUN-2001; 2001AU-0005931.
PR
XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA
XX Khanna R, Elkington RA, Walker SJ;
PI
XX WPI; 2003-300379/29.
DR
XX
XX New human cytomegalovirus (CMV) cytotoxic T-cell epitope peptide,
PT useful for diagnosing, preventing or treating CMV infection, comprises
PT pp28, pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US11
PT or UL18.
XX
XX Claim 70; Page 124; 308pp; English.
PS
XX
XX The invention relates to a novel isolated peptide comprising one or more
CC cytotoxic T-lymphocyte (CTL) epitope(s) of the same or different antigen
CC of a human cytomegalovirus (HCMV). The HCMV antigens can comprise pp28,
CC pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US11 or UL18.
CC The peptide comprises a sequence of about 9-20 contiguous amino acids of
CC the antigen. The peptide epitopes are useful in diagnosing, preventing or
CC treating cytomegalovirus infection in humans, and in monitoring immune
CC responses in various clinical settings (e.g. transplantation or
CC pregnancy). This sequence represents a human cytomegalovirus CTL epitope
CC peptide of the invention.
XX
XX Sequence 20 AA;
SQ
Query Match 80.0%; Score 4; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEEM 4
|||||
Db 7 SEEM 10

RESULT 61
ABP82352
ID ABP82352 standard; Peptide; 20 AA.
XX
AC ABP82352;
XX
DT 04-MAR-2003 (first entry)
XX
XX G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1025.

```

```

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor; modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
XX Homo sapiens.
OS
XX WO200261087-A2.
PN
XX 08-AUG-2002.
XX
XX 19-DEC-2001; 2001WO-US50107.
PF
XX 19-DEC-2000; 2000US-257144P.
PR
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX Burmer GC, Roush CL, Brown JP;
PI
XX WPI; 2003-046718/04.
DR
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases.
XX
XX Claim 1; Fig 2; 523pp; English.
PS
XX
XX The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.
XX
XX Sequence 20 AA;
SQ
Query Match 80.0%; Score 4; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EEMP 5
|||||
Db 12 EEMP 15

```

RESULT 62  
 AAB27268  
 ID AAB27268 standard; peptide; 4 AA.  
 AC AAB27268;  
 DT 23-FEB-2001 (first entry)  
 DE Murine confluency regulated adhesion molecule CRAM-1 CK2 motif #1.  
 KW Immunoglobulin superfamily; Ig Sf; C2 domain; vascular adhesion molecule;  
 KW inflammation; cancer; wound; angiogenesis; mouse;  
 KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200053749-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 13-MAR-2000; 2000WO-EP02219.  
 XX  
 PR 11-MAR-1999; 99EP-0200746.  
 XX  
 PA (RMFD-) RMF DICTAGENE SA.  
 XX  
 PI Imhof BA, Aurrand-Lions M;  
 XX  
 DR WPI; 2000-587436/55.  
 XX  
 PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or  
 CRAM-2) polypeptide, useful for treatment of tumors, inflammation  
 reactions and modulating vascular permeability -  
 XX  
 PS Example; Page 23; 59pp; English.  
 XX  
 CC The present sequence comprises one of the two CK2 motifs found in the  
 murine confluency regulated adhesion molecule 1 (CRAM-1, also known as  
 JAM-2). CRAM-1 is a member of the immunoglobulin superfamily (Ig Sf).  
 CC The CRAM-1 protein and coding sequence can be used in the treatment of  
 cancer, inflammation, to modulate cell-cell interactions and  
 angiogenesis, and in the modulation of wound healing.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 21; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEE 3  
 DB 2 SEE 4  
 RESULT 63  
 AAE00020  
 ID AAE00020 standard; peptide; 4 AA.  
 AC AAE00020;  
 DT 31-MAY-2001 (first entry)  
 DE Peptide #3 insert used to construct BLC RP-II protease variant.  
 XX  
 KW Residual protease II; RP-II; additive; cleaning composition; detergent.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200116285-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 31-AUG-2000; 2000WO-DK00476.  
 XX

XX  
 PR 31-AUG-1999; 99DK-0001212.  
 PR 20-OCT-1999; 99DK-0001500.  
 XX  
 PA (NOVO ) NOVOZYMES AS.  
 XX  
 XX Norregaard-madsen M, Rahbek Ostergaard P, Voge Christensen CB;  
 PI Flønsted Lassen S;  
 XX  
 DR WPI; 2001-226680/23.  
 XX  
 XX Novel RP-II type protease and its variants useful as constituents in  
 PT detergent compositions, additives and cleaning compositions -  
 XX  
 PS Disclosure; Page 14; 132pp; English.  
 XX  
 CC The present sequence is a peptide insert used to construct  
 CC Bacillus licheniformis (BLC) RP-II (Residual protease II) variant.  
 CC RP-II protease is useful as a constituent in additives,  
 CC detergent compositions and other cleaning compositions, optionally in  
 CC combination with other enzymes such as proteases, lipases, cellulases,  
 CC amylases, peroxidases or oxidases. The variants of RP-II have improved  
 CC properties such as substrate specificities, catalytic rate, stability,  
 CC especially towards the action of proteolytic enzymes and improved  
 CC resistance towards peroxidase.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 60.0%; Score 3; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEE 3  
 DB 1 SEE 3  
 RESULT 64  
 AAE23664  
 ID AAE23664 standard; peptide; 4 AA.  
 XX  
 AC AAE23664;  
 XX  
 DT 10-SEP-2002 (first entry)  
 XX  
 DE Peptide #2 used to generate kringle fusion protein.  
 XX  
 KW Kringle peptide; angiogenesis-associated disease; psoriasis; cancer;  
 KW arthritis; macular degeneration; endothelial cell proliferation;  
 KW diabetic retinopathy; cytostatic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200226782-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 27-SEP-2001; 2001WO-US42423.  
 XX  
 PR 29-SEP-2000; 2000US-0675226.  
 PR 31-AUG-2001; 2001US-0942704.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 PI Henkin J, Davidson DJ;  
 XX  
 DR WPI; 2002-452273/48.  
 XX  
 PT Using kringle peptides conjugated to functionalized polymers, e.g.  
 PT ethoxypolyethylene, polyethylene glycol or methoxypolyethylene glycol,  
 PT to treat angiogenic disorders e.g. cancer, macular degeneration and  
 PT arthritis -  
 XX

PS Example 1; Page 16; 34pp; English.

XX The present invention relates to conjugated kringle peptide fragments  
 CC consisting of a functionalised kringle peptide fragment chemically  
 CC coupled to a functionalised polymer. The conjugated kringle peptides  
 CC may be administered to a patient for treating angiogenesis-associated  
 CC diseases such as psoriasis, cancer, arthritis, macular degeneration,  
 CC diabetic retinopathy and for inhibiting endothelial cell proliferation.  
 CC The present DNA sequence is a peptide used to generate kringle fusion  
 CC proteins comprising a kringle 5 peptide fragment. This peptide is used  
 CC to construct PET32-kan-EK-SLPD-K5, PET32-kan-EK-SEED-K5, PET32-kan-Tev-  
 CC SEED-K5 in the exemplification of the invention.

XX Sequence 4 AA;

Query Match 60.0%; Score 3; DB 23; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 DB 1 SEE 3

RESULT 65  
 AAR31242  
 ID AAR31242 standard; peptide; 5 AA.

XX AAR31242;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 18-MAY-1993 (first entry)  
 DT  
 XX Phosphopeptide 6.

XX Phosphopeptide; active agent; oral; composition; anionic; polymyxic;  
 KW stabiliser; carboxylate; polymer; sulfonate; destabilisation;  
 KW fluoride; caries; gingivitis.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 1 /label= Phosphoserine  
 FT Modified-site 2 /label= Phosphoserine  
 FT Modified-site 3 /label= Phosphoserine  
 FT Modified-site 3 /label= Phosphoserine

XX EF523776-A2.

XX 20-JAN-1993.

XX 03-JUL-1992; 92EP-0202023.

XX 17-JUL-1991; 91US-0731592.

XX (UNIL ) UNILEVER NV.  
 XX (UNIL ) UNILEVER PLC.

XX Burger AR, Elliott DL, Schick LA;  
 XX WPI; 1993-019802/03.

XX Oral compens. contg. a phosphopeptide - with addn. of an anionic  
 CC polymeric stabiliser to inhibit destabilisation in the oral  
 CC environment

XX Claim 6; Page 17-18; 18pp; English.

XX The sequences given in AAR31237-42 represent phosphopeptides which  
 CC were used as the active agents in an oral composition. These  
 CC peptides were stabilised by an anionic polymeric stabiliser. The

CC anionic polymers were chosen from a group consisting of carboxylate  
 CC polymers, sulfonate polymers, polymers having both a carboxylate and  
 CC a sulfonate moiety, and other such mixtures. The anionic polymeric  
 CC stabiliser inhibits destabilisation of the phosphopeptide in the oral  
 CC environment. These oral compositions, pref. containing a fluoride  
 CC source may be used for inhibiting caries and gingivitis.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 5 AA;

Query Match 60.0%; Score 3; DB 14; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
 DB 3 SEE 5

RESULT 66  
 AAR55746  
 ID AAR55746 standard; peptide; 5 AA.

XX AAR55746;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 16-NOV-1994 (first entry)  
 DT  
 XX Casein-kinase inhibitor.

XX Casein-kinase inhibitor; fatty acyl-peptide; conjugate;  
 KW antiproliferative; tumor; psoriasis; docosahexaenoic acid; DHA;  
 KW eicosapentaenoic acid; EPA; antitumor; protein-kinase inhibitor  
 KW human papilloma virus; phosphorylation; consensus sequence.

XX Synthetic.

XX WO9412530-A1.

XX 09-JUN-1994.

XX 29-NOV-1993; 93WO-HU00065.

XX 30-NOV-1992; 92US-0984293.

XX (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.  
 XX (SYNT-) SYNTHETIC PEPTIDES INC.

XX Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;  
 XX Szederkenyi F, Vadasz Z;  
 XX WPI; 1994-200194/24.

XX New fatty acyl-peptide conjugates for inhibiting cell  
 CC proliferation - more active than free peptide, partic. for  
 CC treating tumours, virus-infected cells, psoriasis, etc.

XX Disclosure; Fig. 1; 45pp; English.

XX The peptides given in AAR55718-48 can each be conjugated through an  
 CC amide linkage with a polyunsaturated fatty acid moiety, such as  
 CC docosahexaenoic acid or eicosapentaenoic acid, to improve  
 CC antiproliferative activity. The human papilloma virus  
 CC casein-kinase II phosphorylation consensus sequence given in  
 CC AAR55746 can be used to modulate casein-kinase activity associated  
 CC with cell proliferation.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 5 AA;

Query Match 60.0%; Score 3; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

## RESULT 67

AAW22937  
ID AAW22937 standard; peptide; 5 AA.

AC AAW22937;

DT 02-OCT-1997 (first entry)

DE Low density lipoprotein binding peptide.

KW Low density; lipoprotein; LDL; binding; absorbent; removal;  
body fluid; reagent.

OS Synthetic.

Key Location/Qualifiers

FT Modified-site 5

FT /note= "amidated"

PN W09700889-A1.

XX 09-JAN-1997.

PF 21-JUN-1996; 96WO-JP01734.

PR 21-JUN-1995; 95JP-0176904.

PA (ASAH ) ASAHI KASEI KOGYO KK.

PA (ASAH ) ASAHI MEDICAL CO LTD.

PI Aritomi M, Hatanaka Y;

XX WPI; 1997-087320/08.

XX Peptide binding to low density lipoprotein - useful in removing LDL  
from body fluids and as carrier peptide(s) for drugs

PS Example 11; Page 50; 61pp; Japanese.

XX The present low density lipoprotein (LDL) binding peptide can be  
used as an absorbent to remove LDL from body fluids, or as a  
LDL binding reagent. The peptide can be prepared easily and at low  
cost, and has excellent stability and preservability. It  
specifically binds LDL, and does not cause bradykinin production,  
white blood cell activation or blood agglutination.

XX Sequence 5 AA;

Query Match 60.0%; Score 3; DB 18; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 2 EEM 4

## RESULT 68

AAW66598  
ID AAW66598 standard; peptide; 5 AA.

AC AAW66598;

DT 27-NOV-1998 (first entry)

XX Phosphopeptide partial sequence.

XX

KW casein; calcium phosphate complex; amorphous calcium phosphate; ACP;  
phosphopeptide; delivery vehicle; calcium fluoride; calcium deficiency;  
osteoporosis; osteomalacia; tooth; bone disease.

OS Synthetic.  
OS Bos taurus.

Key Location/Qualifiers

FT Modified-site 1

FT /note= "Ser(P)"

FT Modified-site 2

FT /note= "Ser(P)"

FT Modified-site 3

FT /note= "Ser(P)"

XX W09840406-A1.

XX 17-SEP-1998.

XX 13-MAR-1998; 98WO-AU00160.

XX 13-MAR-1997; 97AU-0005662.

XX (UYME ) UNIV MELBOURNE.

XX (VICT-) VICTORIAN DAIRY IND AUTHORITY.

XX Reynolds EC;

XX WPI; 1998-520803/44.

XX Stable calcium phosphate complex including phosphopeptide

PT stabilised amorphous calcium phosphate - useful for treatment of

PT dental caries, calcium malabsorption and bone diseases such as

PT osteoporosis and osteomalacia.

XX Claim 1; Page 35; 43pp; English.

XX The invention relates to a stable calcium phosphate complex including

CC phosphopeptide stabilised amorphous calcium phosphate (ACP) or its

CC derivative, where the phosphopeptide includes the present amino acid

CC sequence: Ser(P)-Ser(P)-Ser(P)-Glu-Glu. The amorphous phases stabilised

CC by the phosphopeptides are a delivery vehicle for co-localisation of Ca,

CC P and phosphate at the tooth surface in a slow-release amorphous form

CC producing superior anticaries efficacy over prior art. The amorphous

CC phases stabilised by the phosphopeptides are also useful as dietary

CC supplements to increase calcium bioavailability and to help prevent

CC diseases associated with calcium deficiencies. They are particularly

CC useful for treatment or prevention of dental caries, calcium

CC malabsorption and bone diseases such as osteoporosis and osteomalacia.

CC The compositions are useful in humans and in veterinary medicine in

CC domestic animals such as cattle, sheep, horses and companion animals e.g.

CC cats and dogs as well as zoo animals.

XX Sequence 5 AA;

Query Match 60.0%; Score 3; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 3 SEE 5

## RESULT 69

AAW66604

ID AAW66604 standard; peptide; 5 AA.

XX AAW66604;

XX 27-NOV-1998 (first entry)

XX Phosphopeptide.

XX casein; calcium phosphate complex; amorphous calcium phosphate; ACP;  
 KW phosphopeptide; delivery vehicle; calcium fluoride; calcium deficiency;  
 KW osteoporosis; osteomalacia; tooth; bone disease.  
 XX Synthetic.  
 OS Bos taurus.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "Ser(P)"  
 FT Modified-site 2 /note= "Ser(P)"  
 FT Modified-site 3 /note= "Ser(P)"  
 FT  
 XX WO9840406-A1.  
 PN 17-SEP-1998.  
 XX 13-MAR-1998; 98WO-AU00160.  
 XX 13-MAR-1997; 97AU-0005662.  
 XX (UYME ) UNIV MELBOURNE.  
 PA (VICT-) VICTORIAN DAIRY IND AUTHORITY.  
 XX Reynolds EC;  
 XX WPI; 1998-520803/44.  
 XX Stable calcium phosphate complex including phospho:peptide  
 PT stabilised amorphous calcium phosphate - useful for treatment of  
 PT dental caries, calcium malabsorption and bone diseases such as  
 PT osteoporosis and osteomalacia.  
 XX Example 3; Page 19; 43pp; English.  
 XX The invention relates to a stable calcium phosphate complex including  
 CC phosphopeptide stabilised amorphous calcium phosphate (ACP) or its  
 CC derivative, where the phosphopeptide includes the amino acid sequence:  
 CC Ser(P)-Ser(P)-Glu-Glu. The amorphous phases stabilised by the  
 CC phosphopeptides are a delivery vehicle for co-localisation of Ca,  
 CC P and phosphate at the tooth surface in a slow-release amorphous form  
 CC producing superior anticaries efficacy over prior art. The amorphous  
 CC phases stabilised by the phosphopeptides are also useful as dietary  
 CC supplements to increase calcium bioavailability and to help prevent  
 CC diseases associated with calcium deficiencies. They are particularly  
 CC useful for treatment or prevention of dental caries, calcium  
 CC malabsorption and bone diseases such as osteoporosis and osteomalacia.  
 CC The compositions are useful in humans and in veterinary medicine in  
 CC domestic animals such as cattle, sheep, horses and companion animals  
 CC e.g. cats and dogs as well as zoo animals. The adsorption of  
 CC phosphopeptides AAW66603-W66609 onto hydroxyapatite was investigated. The  
 CC results confirm that the Ser(P) cluster sequence is the major determinant  
 CC for high affinity binding and that all three contiguous Ser(P) residues  
 CC are essential as loss of any one, even when substituted with Glu or Asp,  
 CC resulted in a considerably lower affinity constant K.  
 XX Sequence 5 AA;  
 Query Match 60.0%; Score 3; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEE 3  
 Db 3 SEE 5  
 RESULT 70  
 AAW66608  
 ID AAW66608 standard; peptide; 5 AA.

XX AAW66608;  
 AC 27-NOV-1998 (first entry)  
 DT Phosphopeptide.  
 XX casein; calcium phosphate complex; amorphous calcium phosphate; ACP;  
 KW phosphopeptide; delivery vehicle; calcium fluoride; calcium deficiency;  
 KW osteoporosis; osteomalacia; tooth; bone disease.  
 XX Synthetic.  
 OS Bos taurus.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 2 /note= "Ser(P)"  
 FT Modified-site 3 /note= "Ser(P)"  
 FT  
 XX WO9840406-A1.  
 PN 17-SEP-1998.  
 XX 13-MAR-1998; 98WO-AU00160.  
 XX 13-MAR-1997; 97AU-0005662.  
 XX (UYME ) UNIV MELBOURNE.  
 PA (VICT-) VICTORIAN DAIRY IND AUTHORITY.  
 XX Reynolds EC;  
 XX WPI; 1998-520803/44.  
 XX Stable calcium phosphate complex including phospho:peptide  
 PT stabilised amorphous calcium phosphate - useful for treatment of  
 PT dental caries, calcium malabsorption and bone diseases such as  
 PT osteoporosis and osteomalacia.  
 XX Example 3; Page 19; 43pp; English.  
 XX The invention relates to a stable calcium phosphate complex including  
 CC phosphopeptide stabilised amorphous calcium phosphate (ACP) or its  
 CC derivative, where the phosphopeptide includes the amino acid sequence:  
 CC Ser(P)-Ser(P)-Glu-Glu. The amorphous phases stabilised by the  
 CC phosphopeptides are a delivery vehicle for co-localisation of Ca,  
 CC P and phosphate at the tooth surface in a slow-release amorphous form  
 CC producing superior anticaries efficacy over prior art. The amorphous  
 CC phases stabilised by the phosphopeptides are also useful as dietary  
 CC supplements to increase calcium bioavailability and to help prevent  
 CC diseases associated with calcium deficiencies. They are particularly  
 CC useful for treatment or prevention of dental caries, calcium  
 CC malabsorption and bone diseases such as osteoporosis and osteomalacia.  
 CC The compositions are useful in humans and in veterinary medicine in  
 CC domestic animals such as cattle, sheep, horses and companion animals  
 CC e.g. cats and dogs as well as zoo animals. The adsorption of  
 CC phosphopeptides AAW66603-W66609 onto hydroxyapatite was investigated. The  
 CC results confirm that the Ser(P) cluster sequence is the major determinant  
 CC for high affinity binding and that all three contiguous Ser(P) residues  
 CC are essential as loss of any one, even when substituted with Glu or Asp,  
 CC resulted in a considerably lower affinity constant K.  
 XX Sequence 5 AA;  
 Query Match 60.0%; Score 3; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEE 3  
 Db 3 SEE 5



CC in a mammal. They can also be used for treating e.g. psoriasis.  
 CC arthritis, age-related macular degeneration, multiple sclerosis and  
 CC diabetes. The products can also be used for detection and diagnosis and  
 CC in bioreactors. AAY60592 to AAY64572 represent specifically claimed  
 CC peptides, and AAY64573 to AAY64643 and AA233183 to AA233186 represent  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 60.0%; Score 3; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEE 3  
 DB 3 SEE 5  
 RESULT 73  
 ABG99113  
 ID ABG99113 standard; peptide; 5 AA.  
 XX AC ABG99113;  
 DT 14-JAN-2003 (first entry)  
 XX Peptide #1 associated with intein catalysed cyclisation of GFP.  
 DE  
 XX Intein; intein-catalysed cyclic peptide library; cancer; tumour cell;  
 KW cardiovascular disease; obesity; neurological disorder; apoptosis;  
 KW cell death; cell division; cell growth; arrhythmia potential;  
 KW cardiomyocyte; heart failure; sarcolemmal calcium cycling; stroke;  
 KW cell proliferation; atherosclerosis; metabolism; skin disorder;  
 KW bone morphogenetic protein; endocrinology; infectious disease;  
 KW viral infection; bacterial infection; diabetic ulcer; wound healing;  
 KW keloid formation; skin connective tissue cell; antibiotic transport;  
 KW drug resistance; cytostatic; anorectic; neuroprotective; cardiant;  
 KW haemostatic; GFP.  
 XX  
 OS Unidentified.  
 XX WO200166565-A2.  
 PN  
 XX 13-SEP-2001.  
 PD  
 XX 06-MAR-2001; 2001WO-US07162.  
 PF  
 XX 06-MAR-2000; 2000US-187130P.  
 PR  
 XX (RIGE-) RIGEL PHARM INC.  
 PA  
 XX Kinsella TM;  
 PI  
 XX WPI; 2001-589926/66.  
 DR  
 XX Fusion polypeptide for generating libraries of cyclic peptides in vivo,  
 PT comprises terminal intein motifs and a random peptide -  
 XX Disclosure; Fig 12C-1; 115pp; English.  
 PS  
 XX The present invention relates to methods and compositions utilising  
 CC inteins to generate libraries of cyclic peptides in vivo. The  
 CC compositions of the invention are useful for making cyclic peptides  
 CC in vivo. Libraries of cells can be transformed with libraries of  
 CC fusion nucleic acids. Intein-catalysed cyclic peptide libraries are  
 CC useful for screening for an altered phenotype and identifying target  
 CC molecules. The library is introduced into a cell, screened for an  
 CC altered phenotype and target molecules that bind to the cyclic peptide  
 CC are isolated. The method is useful for making cyclic peptides which  
 CC retain biological activity, and for screening for cyclic peptides  
 CC capable of altering the phenotype of a cell. The cyclic peptides are  
 CC useful for altering cellular phenotypes and/or physiology, in screening  
 CC assays to identify target molecules associated with changes in cellular

CC phenotype or physiology and as drugs to treat a number of disease  
 CC state, such as cancer, cardiovascular diseases, obesity and  
 CC neurological disorders. The bioactive cyclic peptide is useful as the  
 CC starting point for designing/synthesising derivative molecules with  
 CC similar or more favourable properties for use as a drug and to pull out  
 CC target molecules. By introducing random libraries into any tumour cell,  
 CC peptides which induce apoptosis, cell death, loss of cell division or  
 CC decreased cell growth can be identified and this method is useful in  
 CC cancer applications. The methods are also useful in cardiovascular  
 CC applications, to screen for diminished arrhythmia potential in  
 CC cardiomyocytes, for enhanced contractile properties of cardiomyocytes  
 CC and diminish heart failure potential and to identify agents that  
 CC regulate the intracellular and sarcolemmal calcium cycling in  
 CC cardiomyocytes to prevent arrhythmias and agents that diminish embolic  
 CC phenomena in arteries and arterioles leading to stroke. Candidate  
 CC bioactive peptide libraries are inserted into these cell types and  
 CC their proliferation in response to specific stimuli is monitored.  
 CC Furthermore, the methods are also useful in screening for decreases in  
 CC atherosclerosis, in screens to regulate obesity by controlling food  
 CC intake mechanisms or reducing the responses of the receptor signalling  
 CC pathways that regulate metabolism, in neurobiology applications, to  
 CC screen for agonists of bone morphogenetic proteins, in skin biology  
 CC applications, including viral and bacterial infection, to screen for  
 CC cyclic peptides which block HIV-1 infection, regulation or inhibition  
 CC of keloid formation and wound healing for diabetic ulcers. Candidate  
 CC libraries are inserted into skin connective tissue cells and bioactive  
 CC peptides which promote the growth of these cells are isolated.  
 CC Further applications include screening for bioactive peptides that  
 CC block antibiotic transport mechanisms, drug toxicities and drug  
 CC resistance, improving the performance of existing or developmental  
 CC drugs, and in biotechnology. The present sequence represents a  
 CC peptide associated with intein catalysed cyclisation of inverted  
 CC loop 3 of GFP.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 60.0%; Score 3; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEE 3  
 DB 1 SEE 3  
 RESULT 74  
 AAE05015  
 ID AAE05015 standard; peptide; 5 AA.  
 XX AC AAE05015;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX  
 DE Cryptosporidium parvum N-terminal S15 glycoprotein fragment #1.  
 XX S60 antigen; protozoacide; vaccine; intestinal infection; diarrhoea;  
 KW AIDS; Acquired Immune Deficiency Syndrome; cancer; S15 glycoprotein.  
 XX  
 OS Cryptosporidium parvum.  
 XX WO200140248-A1.  
 PN  
 XX 07-JUN-2001.  
 PD  
 XX 01-DEC-2000; 2000WO-AU01492.  
 PF  
 XX 01-DEC-1999; 99AU-0004400.  
 PR  
 XX (MACQ-) MACQUARIE RES LTD.  
 PA  
 XX Winter G, Slade MB, Williams KL, Gooley AA;  
 PI  
 XX



DR WPI; 2001-408274/43.

XX Novel nucleic acids encoding antigenic polypeptides of Cryptosporidium  
PT useful in antigenic preparations for immunizing animals against  
PT Cryptosporidium -

XX Example; Page 25; 72pp; English.

PS The invention relates to Cryptosporidium parvum S60 potential vaccine  
XX antigen and its corresponding DNA molecule. S60 antigens are used in  
CC vaccine preparations for immunizing animals, preferably human, against  
CC Cryptosporidium. The S60 protein is processed into two glycoproteins  
CC S15 and S45. This S45 and S15 glycoproteins behave as a single membrane  
CC glycoprotein S60. S60 vaccine antigen is used for treating intestinal  
CC infections such as diarrhoea in immunosuppressed patients e.g., AIDS  
CC (Acquired Immune Deficiency Syndrome), cancer patients and recipients  
CC of transplants. The present sequence is Cryptosporidium parvum N-terminal  
CC S15 glycoprotein fragment related to the invention.

XX Sequence 5 AA;

Query Match 60.0%; Score 3; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3

Db 1 SEE 3

#### RESULT 75

AAB35189

ID AAB35189 standard; Peptide; 5 AA.

XX AAB35189;

DT 09-APR-2001 (first entry)

XX Human Traf 6 aptamer clone peptide SEQ ID NO: 40.

XX Human; protein degradation; siah-mediated degradation protein; SMDP;  
KW SCF-complex protein; SCP; siah-1alpha; siah-1 interacting protein; SIP;  
KW Skp1-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division;  
XX Skp1-associated destruction-box protein; inflammatory disease.

OS Homo sapiens.

XX WO200077207-A2.

XX 21-DEC-2000.

XX 09-JUN-2000; 2000WO-US15873.

XX 11-JUN-1999; 99US-0330517.

XX (BURN-) BURNHAM INST.

XX Reed JC, Matsuzawa S;

XX WPI; 2001-071273/08.

XX Siah-Mediated Degradation Protein, useful for drug screening, for  
PT therapeutic applications and for functional genomics -

XX Example 15; Page 71; 121pp; English.

XX The present invention provides the protein and coding sequences of  
CC several siah-mediated degradation proteins and SCF-complex proteins.  
CC These are designated siah-1alpha, siah-1 interacting protein (SIP), which  
CC encodes two proteins due to alternative splicing (Sip-L and Sip-S),  
CC Skp1-associated F-box protein-lalpha and beta and -2 (SAF-lalpha,  
CC SAF-lbeta and SAF-2) and Skp1-associated destruction-box protein (SAD).  
CC The proteins and their coding sequences are useful in the diagnosis and

CC treatment of cancers, disorders where too little cell division occurs  
CC such as bone marrow aplasias, immunodeficiencies and inflammatory  
CC diseases including sepsis, fibrosis, arthritis and graft versus host  
CC disease.

XX SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4

Db 3 EEM 5

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Title: US-09-641-801-15

Perfect score: 5

Sequence: 1 SEEMP 5

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Database : Published Applications AA:

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10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	15	US-10-281-652-15
2	4	80.0	10	9	US-09-799-118-10
3	4	80.0	13	15	US-10-092-135-27
4	4	80.0	14	12	US-10-005-549-24
5	4	80.0	17	11	US-09-813-153-250
6	4	80.0	17	15	US-10-225-567A-710
7	4	80.0	17	15	US-10-225-567A-1506
8	4	80.0	20	15	US-10-225-567A-1025
9	3	60.0	4	11	US-09-834-765-727
10	3	60.0	4	9	US-09-882-291-19
11	3	60.0	5	10	US-09-850-715-15
12	3	60.0	5	11	US-09-885-593B-1
13	3	60.0	5	11	US-09-885-593B-2
14	3	60.0	5	12	US-09-992-124A-13
15	3	60.0	5	12	US-10-276-601-4
					Sequence 15, Appl
					Sequence 10, Appl
					Sequence 27, Appl
					Sequence 24, Appl
					Sequence 250, Appl
					Sequence 710, Appl
					Sequence 1506, Ap
					Sequence 1505, Ap
					Sequence 727, App
					Sequence 19, Appl
					Sequence 15, Appl
					Sequence 1, Appl
					Sequence 2, Appl
					Sequence 13, Appl
					Sequence 4, Appl

5	12	US-10-148-687-11	3	60.0	Sequence 11, Appl
5	15	US-10-006-869-1239	3	60.0	Sequence 1239, Ap
5	15	US-10-206-699-144	3	60.0	Sequence 144, App
6	10	US-09-872-349-6	3	60.0	Sequence 6, Appl
6	10	US-09-929-924-18	3	60.0	Sequence 18, Appl
6	11	US-09-882-291-18	3	60.0	Sequence 18, Appl
6	12	US-10-315-964A-393	3	60.0	Sequence 393, App
6	12	US-10-315-964A-396	3	60.0	Sequence 396, App
6	12	US-10-317-251A-393	3	60.0	Sequence 393, App
6	12	US-10-317-251A-396	3	60.0	Sequence 393, App
6	12	US-10-317-252A-393	3	60.0	Sequence 393, App
6	12	US-10-317-252A-396	3	60.0	Sequence 396, App
6	14	US-10-156-820-96	3	60.0	Sequence 96, Appl
6	15	US-10-006-869-1242	3	60.0	Sequence 1242, Ap
6	16	US-10-082-747A-83	3	60.0	Sequence 83, Appl
7	9	US-09-206-576-5	3	60.0	Sequence 5, Appl
7	9	US-09-962-055-41	3	60.0	Sequence 41, Appl
7	10	US-09-971-127-2	3	60.0	Sequence 2, Appl
7	10	US-09-989-903-32	3	60.0	Sequence 32, Appl
7	10	US-09-971-142A-2	3	60.0	Sequence 2, Appl
7	10	US-09-884-767A-65	3	60.0	Sequence 65, Appl
7	10	US-09-884-767A-96	3	60.0	Sequence 96, Appl
7	10	US-09-884-767A-137	3	60.0	Sequence 137, App
7	10	US-09-884-767A-138	3	60.0	Sequence 138, App
7	10	US-09-884-767A-141	3	60.0	Sequence 141, App
7	10	US-09-884-767A-160	3	60.0	Sequence 160, App
7	10	US-09-976-740-41	3	60.0	Sequence 41, Appl
7	11	US-09-882-291-17	3	60.0	Sequence 17, Appl
7	11	US-09-922-226-46	3	60.0	Sequence 46, Appl
7	12	US-10-376-383-5	3	60.0	Sequence 5, Appl
7	12	US-09-970-641-2	3	60.0	Sequence 2, Appl
7	12	US-10-148-687-15	3	60.0	Sequence 15, Appl
7	14	US-10-023-529-41	3	60.0	Sequence 41, Appl
7	14	US-10-023-523-41	3	60.0	Sequence 41, Appl
7	15	US-10-068-564-32	3	60.0	Sequence 32, Appl
7	15	US-10-006-869-1245	3	60.0	Sequence 1245, Ap
7	15	US-10-194-985-23	3	60.0	Sequence 23, Appl
8	9	US-09-374-671-66	3	60.0	Sequence 66, Appl
8	9	US-09-876-187-9	3	60.0	Sequence 9, Appl
8	10	US-09-883-835-4	3	60.0	Sequence 4, Appl
8	11	US-09-882-291-16	3	60.0	Sequence 16, Appl
8	12	US-10-339-351-25	3	60.0	Sequence 25, Appl
8	12	US-09-315-355-39	3	60.0	Sequence 39, Appl
8	12	US-10-100-303A-117	3	60.0	Sequence 117, App
8	15	US-10-196-107A-66	3	60.0	Sequence 66, Appl
8	15	US-10-006-869-1248	3	60.0	Sequence 1248, Ap
8	15	US-10-193-788-32	3	60.0	Sequence 32, Appl
9	7	US-08-344-824-123	3	60.0	Sequence 123, App
9	9	US-09-790-399-26	3	60.0	Sequence 26, Appl
9	9	US-09-834-765-21	3	60.0	Sequence 21, Appl
9	9	US-09-834-765-134	3	60.0	Sequence 134, App
9	9	US-09-834-765-225	3	60.0	Sequence 225, App
9	9	US-09-834-765-641	3	60.0	Sequence 641, App
9	9	US-09-817-647-20	3	60.0	Sequence 20, Appl
9	10	US-09-824-053-8	3	60.0	Sequence 8, Appl
9	10	US-09-824-053-15	3	60.0	Sequence 15, Appl
9	10	US-09-919-048-65	3	60.0	Sequence 65, Appl
9	10	US-09-919-048-68	3	60.0	Sequence 68, Appl
9	10	US-09-919-048-78	3	60.0	Sequence 78, Appl
9	10	US-09-919-048-85	3	60.0	Sequence 85, Appl
9	10	US-09-919-048-167	3	60.0	Sequence 167, App
9	10	US-09-919-048-169	3	60.0	Sequence 169, App
9	10	US-09-919-048-174	3	60.0	Sequence 174, App
9	10	US-09-919-048-184	3	60.0	Sequence 184, App
9	10	US-09-779-308-87	3	60.0	Sequence 87, Appl
9	10	US-09-779-308-93	3	60.0	Sequence 93, Appl
9	10	US-09-779-308-132	3	60.0	Sequence 132, App
9	10	US-09-779-308-512	3	60.0	Sequence 512, App
9	10	US-09-779-308-516	3	60.0	Sequence 516, App
9	10	US-09-814-661A-27	3	60.0	Sequence 27, Appl
9	10	US-09-877-665-20	3	60.0	Sequence 20, Appl
9	11	US-09-791-383-69	3	60.0	Sequence 69, Appl
9	11	US-09-791-389-69	3	60.0	Sequence 69, Appl

Sequence 7, Appli  
Sequence 51, Appl  
Sequence 53, Appl  
Sequence 16, Appl  
Sequence 607, Appl  
Sequence 821, Appl  
Sequence 1188, Appl  
Sequence 1192, Appl  
Sequence 28, Appl  
Sequence 240, Appl  
Sequence 325, Appl  
Sequence 419, Appl

89 3 60.0 9 11 US-09-824-584-7  
90 3 60.0 9 11 US-09-852-370-51  
91 3 60.0 9 11 US-09-852-370-53  
92 3 60.0 9 12 US-09-932-165-16  
93 3 60.0 9 12 US-09-932-165-607  
94 3 60.0 9 12 US-09-932-165-821  
95 3 60.0 9 12 US-09-932-165-1188  
96 3 60.0 9 12 US-09-932-165-1192  
97 3 60.0 9 12 US-09-793-451-28  
98 3 60.0 9 12 US-09-793-451-240  
99 3 60.0 9 12 US-09-793-451-325  
100 3 60.0 9 12 US-09-793-451-419

## ALIGNMENTS

## RESULT 1

US-10-281-652-15  
; Sequence 15, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: BOLDGOCH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281.652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-15

Query Match 100.0%; Score 5; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEMP 5  
Db 1 SEEMP 5

## RESULT 2

US-09-799-118-10  
; Sequence 10, Application US/09799118  
; Patent No. US20020090708A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Tae Ho  
; APPLICANT: Wisniewski, Hans Georg  
; APPLICANT: Vilcek, Jan  
; TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding  
; Therefor and Uses Thereof  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/799,118  
FILING DATE: 06-Mar-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/242,097  
FILING DATE: 13-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: LEE26/VILCEK-1B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-628-5197  
TELEFAX: 212-737-3528

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-799-118-10

Query Match 80.0%; Score 4; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
Db 6 SEEM 9

## RESULT 3

US-10-092-135-27  
; Sequence 27, Application US/10092135  
; Publication No. US20030054374A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
; FILE REFERENCE: D0134.NP  
; CURRENT APPLICATION NUMBER: US/10/092,135  
; CURRENT FILING DATE: 2002-03-06  
; PRIOR APPLICATION NUMBER: US 60/273,808  
; PRIOR FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US 60/278,983  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-092-135-27

Query Match 80.0%; Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEMP 5  
Db 10 EEMP 13

## RESULT 4

US-10-005-549-24  
; Sequence 24, Application US/10005549  
; Publication No. US20030190613A1  
; GENERAL INFORMATION:

APPLICANT: BOWEN, MICHAEL A.  
APPLICANT: WU, YULI  
APPLICANT: YANG, WEN-PIN  
APPLICANT: FINGER, JOSHUA  
APPLICANT: NADLER, STEVEN  
APPLICANT: CARROLL, PAMELA  
APPLICANT: FEDER, JOHN  
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING AN ACTIVATED HUMAN  
TITLE OF INVENTION: T-LYMPHOCYTE-DERIVED PROTEIN RELATED TO UBIQUITIN  
TITLE OF INVENTION: CONJUGATING ENZYME  
FILE REFERENCE: D00340P  
CURRENT APPLICATION NUMBER: US/10/005,549  
CURRENT FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: 60/308,706  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/244,688  
PRIOR FILING DATE: 2000-10-30  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-005-549-24

Query Match 80.0%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEMP 5  
Db 11 EEMP 14

## RESULT 5

US-09-813-153-250  
Sequence 250, Application US/09813153  
Publication No. US20030045459A1  
GENERAL INFORMATION:  
APPLICANT: ROSEN ET AL.  
TITLE OF INVENTION: 67 Human secreted proteins  
FILE REFERENCE: P2023  
CURRENT APPLICATION NUMBER: US/09/813,153  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: US/09/363,044  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: 60/073,160  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/073,159  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/073,165  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/073,164  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/073,167  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/073,162  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/073,161  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/073,170  
PRIOR FILING DATE: 1998-01-30  
NUMBER OF SEQ ID NOS: 298  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 250  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-813-153-250

Query Match 80.0%; Score 4; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEMP 5  
Db 8 EEMP 11

## RESULT 6

US-10-225-567A-710  
Sequence 710, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: LifeSpan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 710  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-225-567A-710

Query Match 80.0%; Score 4; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
Db 6 SEEM 9

## RESULT 7

US-10-225-567A-1506  
Sequence 1506, Application US/10225567A  
Publication No. US20030113798A1  
GENERAL INFORMATION:  
APPLICANT: LifeSpan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burner, Glenna C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/257,144  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1506  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-225-567A-1506

Query Match 80.0%; Score 4; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEMP 5  
Db 13 EEMP 16

## RESULT 8

US-10-225-567A-1025  
Sequence 1025, Application US/10225567A

Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenn C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1025  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-1025

Query Match 80.0%; Score 4; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEMP 5  
Db 12 EEMP 15

RESULT 9  
US-09-834-765-727  
; Sequence 727, Application US/09834765  
; Patent No. US20020055478A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
; FILE REFERENCE: 129.6USU1  
; CURRENT APPLICATION NUMBER: US/09/834,765  
; CURRENT FILING DATE: 2001-09-31  
; PRIOR APPLICATION NUMBER: 60/197,647  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 770  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 727  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-765-727

Query Match 60.0%; Score 3; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 1 SEE 3

RESULT 10  
US-09-882-291-19  
; Sequence 19, Application US/09882291  
; Publication No. US20030040472A1  
; GENERAL INFORMATION:  
; APPLICANT: Zealand Pharmaceuticals A/S  
; TITLE OF INVENTION: No. US20030040472A1el Peptide Conjugates  
; FILE REFERENCE: 007-2001  
; CURRENT APPLICATION NUMBER: US/09/882,291

; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence  
US-09-882-291-19

Query Match 60.0%; Score 3; DB 11; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 1 SEE 3

RESULT 11  
US-09-850-715-15  
; Sequence 15, Application US/09850715  
; Patent No. US20020102656A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Douglas T.  
; APPLICANT: Dempsey, Paul W.  
; TITLE OF INVENTION: Modulating the Immune Response  
; FILE REFERENCE: A-64962/WH/D/DAV  
; CURRENT APPLICATION NUMBER: US/09/850,715  
; CURRENT FILING DATE: 2001-05-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/849,488  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9424631.1  
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-12-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptides  
; OTHER INFORMATION: encoded by genetically engineered nucleic acids  
US-09-850-715-15

Query Match 60.0%; Score 3; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 2 SEE 4

RESULT 12  
US-09-885-593B-1  
; Sequence 1, Application US/09885593B  
; Publication No. US20030096741A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles W. Slattery  
; APPLICANT: John Leonora  
; TITLE OF INVENTION: ENHANCED MINERAL DELIVERY  
; FILE REFERENCE: SLATT.002A  
; CURRENT APPLICATION NUMBER: US/09/885,593B  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 60/214,606  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT

; ORGANISM: Homo sapiens and Bos taurus  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)...(3)  
; OTHER INFORMATION: PHOSPHORYLATION of Ser  
US-09-885-593B-1

Query Match 60.0%; Score 3; DB 11; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
DB 3 SEE 5

RESULT 13  
US-09-885-593B-2  
; Sequence 2, Application US/09885593B  
; Publication No. US20030096741A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles W. Slattery  
; APPLICANT: John Leonora  
; TITLE OF INVENTION: ENHANCED MINERAL DELIVERY  
; FILE REFERENCE: SLATT.002A  
; CURRENT APPLICATION NUMBER: US/09/885,593B  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 60/214,606  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Mineral Target Binding Sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (2)...(3)  
; OTHER INFORMATION: PHOSPHORYLATION of Ser  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(5)  
; OTHER INFORMATION: Xaa = Any Amino Acid other than serine or  
; OTHER INFORMATION: phosphoserine  
US-09-885-593B-2

Query Match 60.0%; Score 3; DB 11; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
DB 3 SEE 5

RESULT 14  
US-09-992-124A-13  
; Sequence 13, Application US/09992124A  
; Publication No. US20030162289A1  
; GENERAL INFORMATION:  
; APPLICANT: Heidaran, Mohammad A.  
; APPLICANT: Haaland, Perry D.  
; APPLICANT: Wilkins, Jamie H.  
; APPLICANT: Spargo, Catherine A.  
; APPLICANT: Campbell, Robert L.  
; TITLE OF INVENTION: Peptides Promoting Cell Adherence, Growth and Secretion  
; FILE REFERENCE: 102-410  
; CURRENT APPLICATION NUMBER: US/09/992,124A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide selected for biological activity  
US-09-992-124A-13

Query Match 60.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
DB 2 EEM 4

RESULT 15  
US-10-276-601-4  
; Sequence 4, Application US/10276601  
; Publication No. US20030175885A1  
; GENERAL INFORMATION:  
; APPLICANT: REGEN BIOTECH, INC.  
; APPLICANT: Kim, In-San  
; APPLICANT: Kim, Jung-Eun  
; TITLE OF INVENTION: Peptides and Derivatives Thereof Showing Cell Attachment, Spread  
; TITLE OF INVENTION: Detachment Activity  
; FILE REFERENCE: 58049-00009  
; CURRENT APPLICATION NUMBER: US/10/276,601  
; CURRENT FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-276-601-4

Query Match 60.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5  
|||  
DB 2 EMP 4

RESULT 16  
US-10-148-687-11  
; Sequence 11, Application US/10148687  
; Publication No. US20030185836A1  
; GENERAL INFORMATION:  
; APPLICANT: WINTER, Gerhard  
; APPLICANT: SLADE, Martin Basil  
; APPLICANT: WILLIAMS, Keith Leslie  
; APPLICANT: GOOLEY, Andrew Arthur  
; APPLICANT: Macquarie Research Ltd  
; TITLE OF INVENTION: Cryptosporidium sporozoite antigens  
; FILE REFERENCE: 047763-5019-US  
; CURRENT APPLICATION NUMBER: US/10/148,687  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: PCT/AU00/01492  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: AU PQ4400  
; PRIOR FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Cryptosporidium parvum  
US-10-148-687-11

Query Match 60.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 1 SEE 3

## RESULT 17

US-10-006-869-1239  
; Sequence 1239, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1239  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-10-006-869-1239

Query Match 60.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 3 SEE 5

## RESULT 18

US-10-206-699-144  
; Sequence 144, Application US/10206699  
; Publication No. US20030100510A1  
; GENERAL INFORMATION:  
; APPLICANT: Sundaramoorthy, M.  
; APPLICANT: Hudson, B.  
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer  
; FILE REFERENCE: MBHB 01-1017  
; CURRENT APPLICATION NUMBER: US/10/206,699  
; CURRENT FILING DATE: 2002-07-26  
; PRIOR APPLICATION NUMBER: US 60/308,523  
; PRIOR FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: US 60/351,289  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: US 60/366,854  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: US 60/385,362  
; PRIOR FILING DATE: 2002-06-03  
; NUMBER OF SEQ ID NOS: 307  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 144  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-206-699-144

Query Match 60.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

## RESULT 19

US-09-872-349-6  
; Sequence 6, Application US/09872349  
; Patent No. US20020132980A1  
; GENERAL INFORMATION:  
; APPLICANT: Sidney Pestka  
; TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO  
; FILE REFERENCE: PBLI-P01-007  
; CURRENT APPLICATION NUMBER: US/09/872,349  
; CURRENT FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/208,240  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 60/255,296  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: phosphorylated  
; OTHER INFORMATION: peptide  
US-09-872-349-6

Query Match 60.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 1 SEE 3

## RESULT 20

US-09-929-924-18  
; Sequence 18, Application US/09929924  
; Patent No. US20020147151A1  
; GENERAL INFORMATION:  
; APPLICANT: Center, David M.  
; APPLICANT: Cruickshank, William W.  
; APPLICANT: Kornfeld, Hardy  
; TITLE OF INVENTION: IL-16 ANTAGONISTS  
; FILE REFERENCE: Research Corporation Tech., Inc.  
; CURRENT APPLICATION NUMBER: US/09/929,924  
; CURRENT FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 09/368,632  
; PRIOR FILING DATE: 1999-08-05  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: IL-16 antagonist peptide  
US-09-929-924-18

Query Match 60.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

## RESULT 21



US-09-882-291-18  
; Sequence 18, Application US/09882291  
; Publication No. US20030040472A1  
; GENERAL INFORMATION:  
; APPLICANT: Zealand Pharmaceuticals A/S  
; TITLE OF INVENTION: No. US00030040472A1el Peptide Conjugates  
; FILE REFERENCE: 007-2001  
; CURRENT APPLICATION NUMBER: US/09/882,291  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence  
US-09-882-291-18

Query Match 60.0%; Score 3; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 1 SEE 3

RESULT 22  
US-10-315-964A-393  
; Sequence 393, Application US/10315964A  
; Publication No. US20030148956A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M3  
; CURRENT APPLICATION NUMBER: US/10/315,964A  
; CURRENT FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 393  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-315-964A-393

Query Match 60.0%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 1 SEE 3

RESULT 23  
US-10-315-964A-396  
; Sequence 396, Application US/10315964A  
; Publication No. US20030148956A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company

; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A.  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M3  
; CURRENT APPLICATION NUMBER: US/10/315,964A  
; CURRENT FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 396  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-315-964A-396

Query Match 60.0%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 1 SEE 3

RESULT 24  
US-10-317-251A-393  
; Sequence 393, Application US/10317251A  
; Publication No. US20030148957A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M2  
; CURRENT APPLICATION NUMBER: US/10/317,251A  
; CURRENT FILING DATE: 2002-12-11  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 393  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-317-251A-393

Query Match 60.0%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 1 SEE 3

RESULT 25

US-10-317-251A-396  
; Sequence 396, Application US/10317251A  
; Publication No. US20030148957A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M2  
; CURRENT APPLICATION NUMBER: US/10/317,251A  
; CURRENT FILING DATE: 2002-12-11  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 396  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-317-251A-396  
  
Query Match 60.0%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SEE 3  
Db 1 SEE 3  
  
RESULT 26  
US-10-317-252A-393  
; Sequence 393, Application US/10317252A  
; Publication No. US20030148958A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M  
; CURRENT APPLICATION NUMBER: US/10/317,252A  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 393  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-317-252A-393  
  
Query Match 60.0%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY .1 SEE 3

Db 1 SEE 3  
|||  
RESULT 27  
US-10-317-252A-396  
; Sequence 396, Application US/10317252A  
; Publication No. US20030148958A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Isfort, Robert J  
; APPLICANT: Mazur, Wieslaw A  
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists  
; FILE REFERENCE: 8847M  
; CURRENT APPLICATION NUMBER: US/10/317,252A  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/349,117  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: US 60/376,337  
; PRIOR FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: US 60/388,895  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/411,988  
; PRIOR FILING DATE: 2002-09-19  
; NUMBER OF SEQ ID NOS: 530  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 396  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized artificial peptide  
US-10-317-252A-396  
  
Query Match 60.0%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SEE 3  
Db 1 SEE 3  
|||  
RESULT 28  
US-10-156-820-96  
; Sequence 96, Application US/10156820  
; Publication No. US20020150558A1  
; GENERAL INFORMATION:  
; APPLICANT: Boulanger, Pierre  
; APPLICANT: Hong, Saw See  
; APPLICANT: Karayan, Lucie  
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses  
; FILE REFERENCE: 032751-036  
; CURRENT APPLICATION NUMBER: US/10/156,820  
; CURRENT FILING DATE: 2002-06-30  
; PRIOR APPLICATION NUMBER: PCT/FR98/00184  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: FR 97/01005  
; PRIOR FILING DATE: 1997-01-30  
; PRIOR APPLICATION NUMBER: FR 97/11166  
; PRIOR FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSeq for Windows version 4.0  
; SEQ ID NO 96  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Phagotome  
US-10-156-820-96  
  
Query Match 60.0%; Score 3; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

## RESULT 29

US-10-006-869-1242  
; Sequence 1242, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1242  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-10-006-869-1242

Query Match 60.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 4 SEE 6

## RESULT 30

US-10-082-747A-83  
; Sequence 83, Application US/10082747A  
; Publication No. US20030129688A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ballinger, Marcus D.  
; APPLICANT: Jones, Jennifer T.  
; APPLICANT: Fairbrother, Wayne J.  
; APPLICANT: Sliwkowski, Mark X.  
; APPLICANT: Wells, James A.  
; TITLE OF INVENTION: HERGULIN VARIANTS  
; FILE REFERENCE: 402E-476112US  
; CURRENT APPLICATION NUMBER: US/10/082,747A  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/101,544  
; PRIOR FILING DATE: 1998-07-17  
; PRIOR APPLICATION NUMBER: PCT/US/98/01579  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 08/799,054  
; PRIOR FILING DATE: 1997-02-10  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 83  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence at human heregulin-beta1  
; OTHER INFORMATION: residue 211-216  
US-10-082-747A-83

Query Match 60.0%; Score 3; DB 16; Length 6;

Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 3 SEE 5

## RESULT 31

US-09-206-576-5  
; Sequence 5, Application US/09206576  
; Patent No. US20020032157A1  
; GENERAL INFORMATION:  
; APPLICANT: Giachelli, Cecilia M.  
; APPLICANT: Steitz, Susie  
; TITLE OF INVENTION: Methods of Inhibiting Ectopic Calcification  
; FILE REFERENCE: P-UW 3244  
; CURRENT APPLICATION NUMBER: US/09/206,576  
; CURRENT FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-206-576-5

Query Match 60.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 4 SEE 6

## RESULT 32

US-09-962-055-41  
; Sequence 41, Application US/09962055  
; Patent No. US20020052033A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; Lees, Robert S.  
; Law, Simon W.  
; Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
; BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
; TREATING ATHEROSCLEROSIS  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/962,055  
; FILING DATE: 24-Sep-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/979,608  
; FILING DATE: 26-NOV-1997  
; APPLICATION NUMBER: US 60/031,930  
; FILING DATE: 27-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Louis  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-09-362-055-41

Query Match 60.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 4 SEE 6

## RESULT 33

US-09-971-127-2  
; Sequence 2, Application US/09971127  
; Patent No. US20020110901A1  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Chin-Shiou  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SURFACE  
; FILE REFERENCE: 10231-0004-999  
; CURRENT APPLICATION NUMBER: US/09/971,127  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 09/507,299  
; PRIOR FILING DATE: 2000-02-18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-09-971-127-2

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 5 SEE 7

## RESULT 34

US-09-989-903-32  
; Sequence 32, Application US/09989903  
; Patent No. US20020146804A1  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandez-Alnemri, Teresa  
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
; FILE REFERENCE: 480140.434D1  
; CURRENT APPLICATION NUMBER: US/09/989,903  
; CURRENT FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-989-903-32

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 3 EEM 5

## RESULT 35

US-09-971-142A-2  
; Sequence 2, Application US/09971142A  
; Patent No. US20020164643A1  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Chin-Shiou  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SURFACE  
; FILE REFERENCE: 10231-0024-999  
; CURRENT APPLICATION NUMBER: US/09/971,142A  
; CURRENT FILING DATE: 2001-10-03  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows, Version 4.0  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-09-971-142A-2

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 5 SEE 7

## RESULT 36

US-09-884-767A-65  
; Sequence 65, Application US/09884767A  
; Publication No. US20020192789A1  
; GENERAL INFORMATION:  
; APPLICANT: DYAX Corp.  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Luneau, Christopher J.  
; APPLICANT: Ladner, Robert C  
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES  
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
; CURRENT APPLICATION NUMBER: US/09/884,767A  
; CURRENT FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 09/597,321  
; PRIOR FILING DATE: 2000-06-19  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 65  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic enterokinase cleavage sequence  
US-09-884-767A-65

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

```
RESULT 37
US-09-884-767A-96
; Sequence 96, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-96

Query Match          60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db 2 SEE 4

RESULT 38
US-09-884-767A-137
; Sequence 137, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-137

Query Match          60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db 2 SEE 4

RESULT 39
US-09-884-767A-138
; Sequence 138, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-138

Query Match          60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db 2 SEE 4
```

```
US-09-884-767A-138
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-138

Query Match          60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db 2 SEE 4

RESULT 40
US-09-884-767A-141
; Sequence 141, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 141
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-141

Query Match          60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db 2 SEE 4

RESULT 41
US-09-884-767A-160
; Sequence 160, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 160
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-160

Query Match          60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
Db 2 SEE 4
```

; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
; CURRENT APPLICATION NUMBER: US/09/884,767A  
; CURRENT FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 09/597,321  
; PRIOR FILING DATE: 2000-06-19  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 160  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic enterokinase cleavage sequence  
US-09-884-767A-160

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

RESULT 42  
US-09-976-740-41  
; Sequence 41, Application US/09976740  
; Publication No. US20020194633A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ATHEROSCLEROSIS  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/09/976,740  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 09/616,289  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-976-740-41

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 4 SEE 6

RESULT 43  
US-09-882-291-17  
; Sequence 17, Application US/09882291  
; Publication No. US20030040472A1  
; GENERAL INFORMATION:  
; APPLICANT: Zealand Pharmaceuticals A/S  
; TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates  
; FILE REFERENCE: 007-2001  
; CURRENT APPLICATION NUMBER: US/09/882,291

; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence  
US-09-882-291-17

Query Match 60.0%; Score 3; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 1 SEE 3

RESULT 44  
US-09-922-226-46  
; Sequence 46, Application US/09922226  
; Publication No. US20030077664A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Yi  
; APPLICANT: Thatcher, Scott M.  
; APPLICANT: Xiao, Jia-Hao  
; APPLICANT: Kusari, Jyotirmoy  
; APPLICANT: Chandraratna, Roshantha A.  
; TITLE OF INVENTION: Methods of Screening For Compounds That  
; TITLE OF INVENTION: Modulate Hormone Receptor Activity  
; FILE REFERENCE: P-AP 4681  
; CURRENT APPLICATION NUMBER: US/09/922,226  
; CURRENT FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: US 60/284,797  
; PRIOR FILING DATE: 2001-04-18  
; NUMBER OF SEQ ID NOS: 191  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 46  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-922-226-46

Query Match 60.0%; Score 3; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 4 SEE 6

RESULT 45  
US-10-376-383-5  
; Sequence 5, Application US/10376383  
; Publication No. US20030158113A1  
; GENERAL INFORMATION:  
; APPLICANT: Giachelli, Cecilia M.  
; APPLICANT: Steitz, Susie  
; TITLE OF INVENTION: Methods of Inhibiting Ectopic Calcification  
; FILE REFERENCE: P-UW 3244  
; CURRENT APPLICATION NUMBER: US/10/376,383  
; CURRENT FILING DATE: 2003-02-26  
; PRIOR APPLICATION NUMBER: US/09/206,576  
; PRIOR FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 7

;  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-376-383-5

Query Match 60.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 4 SEE 6

## RESULT 46

US-09-970-641-2  
; Sequence 2, Application US/09970641  
; Publication No. US20030165987A1  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Chin-Shiou  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SURFACE  
; TITLE OF INVENTION: IMPRINTING  
; FILE REFERENCE: 10231-0004-999  
; CURRENT APPLICATION NUMBER: US/09/970,641  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: US/09/507,299  
; PRIOR FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-09-970-641-2

Query Match 60.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 5 SEE 7

## RESULT 47

US-10-148-687-15  
; Sequence 15, Application US/10148687  
; Publication No. US20030185836A1  
; GENERAL INFORMATION:  
; APPLICANT: WINTER, Gerhard  
; APPLICANT: SLADE, Martin Basil  
; APPLICANT: WILLIAMS, Keith Leslie  
; APPLICANT: GOOLEY, Andrew Arthur  
; APPLICANT: Macquarie Research Ltd  
; TITLE OF INVENTION: Cryptosporidium sporozoite antigens  
; FILE REFERENCE: 047763-5019-US  
; CURRENT APPLICATION NUMBER: US/10/148,687  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: PCT/AU00/01492  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: AU PQ4400  
; PRIOR FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Cryptosporidium parvum  
US-10-148-687-15

Query Match 60.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 1 SEE 3

## RESULT 48

US-10-023-529-41  
; Sequence 41, Application US/10023529  
; Publication No. US20020129388A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/10/023,529  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 09/616,289  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/517,849  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-023-529-41

Query Match 60.0%; Score 3; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 4 SEE 6

## RESULT 49

US-10-023-523-41  
; Sequence 41, Application US/10023523  
; Publication No. US20020152485A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/10/023,523  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: US/09/616,289  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/517,849  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547

;; PRIOR FILING DATE: 1997-06-03  
;; NUMBER OF SEQ ID NOS: 53  
;; SOFTWARE: FastSEQ for Windows Version 4.0  
;; SEQ ID NO 41  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-023-523-41

Query Match 60.0%; Score 3; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEE 3  
Db 4 SEE 6

RESULT 50  
US-10-068-564-32  
; Sequence 32, Application US/10068564  
; Publication No. US20030040096A1.  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandez-Alnemri, Teresa  
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING  
; TITLE OF INVENTION: AND METHODS OF USE  
; FILE REFERENCE: 480140.434C2  
; CURRENT APPLICATION NUMBER: US/10/068,564  
; CURRENT FILING DATE: 2002-02-05  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-068-564-32

Query Match 60.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEM 4  
Db 3 EEM 5

RESULT 51  
US-10-006-869-1245  
; Sequence 1245, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1245  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-10-006-869-1245

Query Match 60.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SEE 3  
Db 5 SEE 7

RESULT 52  
US-10-194-985-23  
; Sequence 23, Application US/10194985  
; Publication No. US20030105287A1  
; GENERAL INFORMATION:  
; APPLICANT: Schaeffer, Michael  
; APPLICANT: Schneiderbauer, Michaela  
; APPLICANT: Weidner, Sascha  
; APPLICANT: Hallek, Michael  
; TITLE OF INVENTION: GSF Forschungszentrum fuer Umwelt und Gesundheit GmbH  
; TITLE OF INVENTION: Inhibition of the Proliferation of Cells of the  
; TITLE OF INVENTION: Multiple Myeloma  
; FILE REFERENCE: 080345-000100US  
; CURRENT APPLICATION NUMBER: US/10/194,985  
; CURRENT FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: DE 19941897.7  
; PRIOR FILING DATE: 1999-09-02  
; PRIOR APPLICATION NUMBER: US 09/625,225  
; PRIOR FILING DATE: 2000-07-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: region of  
; OTHER INFORMATION: Interest within acidic putative Hck binding domain  
US-10-194-985-23

Query Match 60.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEE 3  
Db 1 SEE 3

RESULT 53  
US-09-374-671-66  
; Sequence 66, Application US/09374671  
; Patent No. US20020012963A1  
; GENERAL INFORMATION:  
; APPLICANT: Morgenstern, Jay P.  
; APPLICANT: Kanieczny, Andrzej  
; APPLICANT: Bizindaukas, Christine B.  
; APPLICANT: Brauer, Andrew W.  
; TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
; TITLE OF INVENTION: Dander and Uses Therefor  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/374,671  
; FILING DATE:



```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/491,861
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-374-671-66

Query Match 60.0%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
DB 5 SEE 7

RESULT 54
US-09-876-187-9
; Sequence 9, Application US/09876187
; Patent No. US20020090603A1
; GENERAL INFORMATION:
; APPLICANT: Lipton, Stuart A.
; APPLICANT: Okamoto, Shu-ichi
; TITLE OF INVENTION: Methods of Differentiating and
; TITLE OF INVENTION: Protecting Cells By Modulating the P38/MEF2 Pathway
; FILE REFERENCE: P-LJ 4714
; CURRENT APPLICATION NUMBER: US/09/876,187
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/209,539
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-876-187-9

Query Match 60.0%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
DB 1 SEE 3

RESULT 55
US-09-883-825-4
; Sequence 4, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:

Query Match 60.0%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-883-825-4

Query Match 60.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4
DB 4 EEM 6

RESULT 56
US-09-882-291-16
; Sequence 16, Application US/09882291
; Publication NO. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1el Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
US-09-882-291-16

Query Match 60.0%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 SEE 3  
Db 1 SEE 3

## RESULT 57

US-10-339-351-25  
; Sequence 25, Application US/10339351  
; Publication No. US20030148417A1

## GENERAL INFORMATION:

; APPLICANT: Societe des Produits Nestle S.A.  
; TITLE OF INVENTION: No. US20030148417A1e1 cacao endoproteinases and their use in the  
; TITLE OF INVENTION: production of cocoa flavour  
; FILE REFERENCE: 80265-6707  
; CURRENT APPLICATION NUMBER: US/10/339,351  
; PRIOR FILING DATE: 2003-02-11  
; PRIOR FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patentin Ver. 3.1  
; SEQ ID NO 25  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Theobroma cacao  
US-10-339-351-25

## Query Match

Best Local Similarity 60.0%; Score 3; DB 12; Length 8;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 2 SEE 4

## RESULT 58

US-09-315-355-39  
; Sequence 39, Application US/09315355  
; Publication No. US20030157482A1

## GENERAL INFORMATION:

; APPLICANT: KEESEE, SUSAN  
; APPLICANT: OBAR, ROBERT  
; APPLICANT: WU, YING-YE  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
; TITLE OF INVENTION: DETECTION OF CERVICAL CANCER  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Teeta, Hurwitz & Thibeault  
; STREET: 125 High St.  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/315,355  
FILING DATE:

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: GREENHALGH, DUNCAN A  
REGISTRATION NUMBER: 38,678  
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids

; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-315-355-39

Query Match 60.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 4 SEE 6

## RESULT 59

US-10-100-303A-117  
; Sequence 117, Application US/10100303A  
; Publication No. US20030202980A1

## GENERAL INFORMATION:

; APPLICANT: Caplan, et al.  
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction  
; TITLE OF INVENTION: to Allergy  
; FILE REFERENCE: 2002834-0166  
; CURRENT APPLICATION NUMBER: US/10/100,303A  
; CURRENT FILING DATE: 2002-03-18  
; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 117  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Juglans nigra  
US-10-100-303A-117

## Query Match

Best Local Similarity 60.0%; Score 3; DB 12; Length 8;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
Db 3 EEM 5

## RESULT 60

US-10-196-107A-66  
; Sequence 66, Application US/10196107A  
; Publication No. US20030049691A1

## GENERAL INFORMATION:

; APPLICANT: Moigenstern, Jay P.  
; ADDRESSEE: Konieczny, Andrzej  
; ADDRESSEE: Bizindaukas, Christine B.  
; ADDRESSEE: Brauer, Andrew W.

TITLE OF INVENTION: Allergenic Protein and Peptides from Dog  
Dander and Uses Therefor

## NUMBER OF SEQUENCES: 109

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive & Cockfield, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/196,107A  
FILING DATE: 16-Jul-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/374,671  
FILING DATE: 1999-AUG-16

APPLICATION NUMBER: US 08/491,861  
FILING DATE: 1995-OCT-27  
APPLICATION NUMBER: PCT/US93/12468  
FILING DATE: 1993-DEC-30  
APPLICATION NUMBER: US 08/156,549  
FILING DATE: 1993-NOV-22  
APPLICATION NUMBER: US 07/999,712  
FILING DATE: 1992-DEC-31  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiorgio, Jeanne M.  
REGISTRATION NUMBER: 41,710  
REFERENCE/DOCKET NUMBER: IMI-026C2CNCPADV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 66:  
US-10-196-107A-66

Query Match 60.0%; Score 3; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
DB 5 SEE 7

RESULT 61  
US-10-006-869-1248  
Sequence 1248, Application US/10006869  
Publication No. US20030082166A1  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Symonds, James Matthew  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
FILE REFERENCE: 100086.407C7  
CURRENT APPLICATION NUMBER: US/10/006,869  
CURRENT FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 4052  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1248  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Representative cyclic modulating agent based on  
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-10-006-869-1248

Query Match 60.0%; Score 3; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
DB 6 SEE 8

RESULT 62  
US-10-193-768-32  
Sequence 32, Application US/10193768  
Publication No. US20030109423A1  
GENERAL INFORMATION:  
APPLICANT: Lu, Jun Ping

APPLICANT: Cantley, Lewis C.  
APPLICANT: Yaffe, Michael  
APPLICANT: Fischer, Gunter  
TITLE OF INVENTION: INHIBITORS OF PHOSPHOSERINE AND  
TITLE OF INVENTION: PHOSPHOTHREONINE-PROLINE-SPECIFIC ISOMERASES  
FILE REFERENCE: BIDMC97-03pa  
CURRENT APPLICATION NUMBER: US/10/193,768  
CURRENT FILING DATE: 2002-07-10  
PRIOR APPLICATION NUMBER: US/08/988,842  
PRIOR FILING DATE: 1997-12-11  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32  
LENGTH: 8  
TYPE: PRT  
ORGANISM: synthetic nucleotide  
US-10-193-768-32

Query Match 60.0%; Score 3; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5  
DB 1 EMP 3

RESULT 63  
US-08-344-824-123  
Sequence 123, Application US/08344824  
Publication No. US20030152580A1  
GENERAL INFORMATION:  
APPLICANT: SETTE, Alessandro  
APPLICANT: SIDNEY, John  
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
NUMBER OF SEQUENCES: 399  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Street Tower, 20th  
STREET: Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,824  
FILING DATE: 23-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,634  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-80-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-344-824-123

Query Match 60.0%; Score 3; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05; DB 9; Length 9;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 7 EEM 9

## RESULT 64

US-09-790-399-26  
; Sequence 26, Application US/09790399  
; Patent No. US20020038000A1  
; GENERAL INFORMATION:  
; APPLICANT: Gold, Larry  
; APPLICANT: Tuerk, Craig  
; APPLICANT: Pribnow, David  
; APPLICANT: Smith, Jonathan D.  
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation  
; FILE REFERENCE: NEX02/C1-CON2  
; CURRENT APPLICATION NUMBER: US/09/790,399  
; CURRENT FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 09/197,649  
; PRIOR FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: 07/829,461  
; PRIOR FILING DATE: 1992-01-31  
; PRIOR APPLICATION NUMBER: 07/739,055  
; PRIOR FILING DATE: 1991-08-01  
; PRIOR APPLICATION NUMBER: 07/561,968  
; PRIOR FILING DATE: 1990-08-02  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-790-399-26

Query Match 60.0%; Score 3; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; DB 9; Length 9;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 5 SEE 7

## RESULT 65

US-09-834-765-21  
; Sequence 21, Application US/09834765  
; Patent No. US20020055478A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
; FILE REFERENCE: 129.6USU1  
; CURRENT APPLICATION NUMBER: US/09/834,765  
; CURRENT FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/197,647  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 770  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-765-21

Query Match 60.0%; Score 3; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05; DB 9; Length 9;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 4 EEM 6

## RESULT 66

US-09-834-765-134  
; Sequence 134, Application US/09834765  
; Patent No. US20020055478A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
; FILE REFERENCE: 129.6USU1  
; CURRENT APPLICATION NUMBER: US/09/834,765  
; CURRENT FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/197,647  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 770  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 134  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-765-134

Query Match 60.0%; Score 3; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; DB 9; Length 9;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 7 EEM 9

## RESULT 67

US-09-834-765-225  
; Sequence 225, Application US/09834765  
; Patent No. US20020055478A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
; FILE REFERENCE: 129.6USU1  
; CURRENT APPLICATION NUMBER: US/09/834,765  
; CURRENT FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/197,647  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 770  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 225  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-765-225

Query Match 60.0%; Score 3; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; DB 9; Length 9;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEM 4  
|||  
Db 4 EEM 6

## RESULT 68

US-09-834-765-641  
; Sequence 641, Application US/09834765  
; Patent No. US20020055478A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Paris  
; APPLICANT: Pia M. Challita-Bid  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Ava Jakobovits  
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
; TITLE OF INVENTION: AND DETECTION OF CANCER  
; FILE REFERENCE: 129.6USU1  
; CURRENT APPLICATION NUMBER: US/09/834,765  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR FILING DATE: 60/197,647  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 770  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 641  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-765-641

Query Match 60.0%; Score 3; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEM 4  
|||  
Db 7 EEM 9

## RESULT 69

US-09-817-647-20  
; Sequence 20, Application US/09817647  
; Patent No. US20020082229A1  
; GENERAL INFORMATION:  
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao  
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related  
; ; Ligands and Uses Therefor  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS: 23  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/817,647  
; FILING DATE: 26-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/107,979  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Conley, Deirdre L.  
; REGISTRATION NUMBER: 36,487  
; REFERENCE/DOCKET NUMBER: P1084R1-2  
; TELECOMMUNICATION INFORMATION:

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 EEM 4  
Db 7 EEM 9

## RESULT 71

US-09-824-053-15  
; Sequence 15, Application US/09824053  
; Patent No. US20020106725A1  
; GENERAL INFORMATION:  
; APPLICANT: Peter Stougaard  
; Ole Cai Hansen  
; TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A  
; METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hulton & Williams  
; STREET: 1900 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006-1109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/824,053  
; FILING DATE: 03-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/669,304  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stanislaus Akeman  
; REGISTRATION NUMBER: 28,562  
; REFERENCE/DOCKET NUMBER: <Unknown>  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 955-1926  
; TELEFAX: (202) 778-2201  
; TELEX: NO. US20020106725A1e  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-824-053-15

Query Match 60.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEM 4  
Db 7 EEM 9

## RESULT 72

US-09-919-048-65  
; Sequence 65, Application US/09919048  
; Patent No. US20020150908A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Cannon, Martin J.  
; APPLICANT: Santin, Alessandro  
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer  
; FILE REFERENCE: D6223CIP/A/D/CIP

; CURRENT APPLICATION NUMBER: US/09/919,048  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 09/861,966  
; PRIOR FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 188  
; SEQ ID NO 65  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Residues 88-96 of the hepsin protein  
US-09-919-048-65

Query Match 60.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEM 4  
Db 4 EEM 6

## RESULT 73

US-09-919-048-68  
; Sequence 68, Application US/09919048  
; Patent No. US20020150908A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Cannon, Martin J.  
; APPLICANT: Santin, Alessandro  
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer  
; FILE REFERENCE: D6223CIP/A/D/CIP  
; CURRENT APPLICATION NUMBER: US/09/919,048  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 09/861,966  
; PRIOR FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 188  
; SEQ ID NO 68  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Residues 89-97 of the hepsin protein  
US-09-919-048-68

Query Match 60.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEM 4  
Db 3 EEM 5

## RESULT 74

US-09-919-048-78  
; Sequence 78, Application US/09919048  
; Patent No. US20020150908A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Cannon, Martin J.  
; APPLICANT: Santin, Alessandro  
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer  
; FILE REFERENCE: D6223CIP/A/D/CIP  
; CURRENT APPLICATION NUMBER: US/09/919,048  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 09/861,966  
; PRIOR FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 188  
; SEQ ID NO 78  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens

; FEATURE:  
; OTHER INFORMATION: Residues 250-258 of the hepsin protein  
US-09-919-048-78  
Query Match 60.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

RESULT 75  
US-09-919-048-85  
; Sequence 85, Application US/09919048  
; Patent No. US20020150908A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Cannon, Martin J.  
; APPLICANT: Santin, Alessandro  
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer  
; FILE REFERENCE: D6223CIP/A/D/CIP  
; CURRENT APPLICATION NUMBER: US/09/919,048  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 09/861,966  
; PRIOR FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 188  
; SEQ ID NO 85  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Residues 87-95 of the hepsin protein  
US-09-919-048-85

Query Match 60.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 5 EEM 7

Search completed: November 25, 2003, 20:25:41  
Job time : 10.9468 secs

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# OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 5.45213 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-15

Perfect score: 5

Sequence: 1 SEEMP 5

## Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

## Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCRUS\_COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfileel.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	4	US-09-641-803-15
2	5	100.0	18	3	US-08-105-454-3
3	4	80.0	10	2	US-08-242-097-10
4	4	80.0	10	3	US-09-206-695-10
5	4	80.0	10	4	US-09-000-179-5
6	4	80.0	10	4	US-09-799-118-10
7	4	80.0	10	5	PCT-US96-11995-5
8	4	80.0	11	1	US-08-408-604A-99
9	4	80.0	13	5	PCT-US94-01499-1
10	4	80.0	17	4	US-09-120-653D-26
11	3	60.0	5	1	US-07-729-099-8
12	3	60.0	5	1	US-08-257-392-8
13	3	60.0	5	3	US-08-770-035-8
14	3	60.0	5	3	US-08-981-122-80
15	3	60.0	5	3	US-08-981-122-90
16	3	60.0	5	3	US-08-849-488-15
17	3	60.0	5	4	US-09-236-160-4
18	3	60.0	5	4	US-09-236-160-29
19	3	60.0	5	4	US-09-187-859-1239
20	3	60.0	5	4	US-09-800-170-50
21	3	60.0	5	4	US-09-839-542B-1239
22	3	60.0	6	1	US-07-791-935B-1
23	3	60.0	6	1	US-07-671-757-26
24	3	60.0	6	1	US-08-704-170-115
25	3	60.0	6	3	US-09-020-880-83
26	3	60.0	6	3	US-08-075-541D-17
27	3	60.0	6	4	US-09-187-859-1242

28	3	60.0	6	4	US-09-101-544-83	Sequence 83, Appl
29	3	60.0	6	4	US-08-432-483A-5	Sequence 5, Appl
30	3	60.0	6	4	US-09-155-613A-96	Sequence 96, Appl
31	3	60.0	6	4	US-09-839-542B-1242	Sequence 1242, Ap
32	3	60.0	6	5	PCT-US94-02631-115	Sequence 115, App
33	3	60.0	7	1	US-07-638-492-13	Sequence 13, Appl
34	3	60.0	7	1	US-08-182-175A-71	Sequence 71, Appl
35	3	60.0	7	1	US-08-182-175A-74	Sequence 74, Appl
36	3	60.0	7	1	US-08-182-175A-77	Sequence 77, Appl
37	3	60.0	7	1	US-08-182-175A-79	Sequence 79, Appl
38	3	60.0	7	1	US-08-182-175A-80	Sequence 80, Appl
39	3	60.0	7	1	US-08-486-721A-7	Sequence 7, Appl
40	3	60.0	7	3	US-09-024-020B-25	Sequence 25, Appl
41	3	60.0	7	3	US-08-931-858E-91	Sequence 91, Appl
42	3	60.0	7	3	US-08-981-739-91	Sequence 91, Appl
43	3	60.0	7	4	US-09-425-043-25	Sequence 25, Appl
44	3	60.0	7	4	US-09-187-789-32	Sequence 32, Appl
45	3	60.0	7	4	US-08-979-608A-41	Sequence 41, Appl
46	3	60.0	7	4	US-09-187-859-1245	Sequence 1245, Ap
47	3	60.0	7	4	US-09-139-600-27	Sequence 27, Appl
48	3	60.0	7	4	US-09-206-576-5	Sequence 5, Appl
49	3	60.0	7	4	US-09-839-542B-1245	Sequence 1245, Ap
50	3	60.0	7	5	PCT-US92-06412-71	Sequence 71, Appl
51	3	60.0	7	5	PCT-US92-06412-74	Sequence 74, Appl
52	3	60.0	7	5	PCT-US92-06412-77	Sequence 77, Appl
53	3	60.0	7	5	PCT-US92-06412-79	Sequence 79, Appl
54	3	60.0	7	5	PCT-US92-06412-80	Sequence 80, Appl
55	3	60.0	7	6	5472855-31	Sequence 80, Appl
56	3	60.0	8	1	US-07-872-644-4	Patent No. 5472855
57	3	60.0	8	1	US-08-045-264A-24	Sequence 4, Appl
58	3	60.0	8	1	US-08-014-426-56	Sequence 24, Appl
59	3	60.0	8	1	US-08-297-494-4	Sequence 56, Appl
60	3	60.0	8	1	US-08-297-510-4	Sequence 4, Appl
61	3	60.0	8	1	US-08-066-325-154	Sequence 4, Appl
62	3	60.0	8	1	US-08-066-325-155	Sequence 154, App
63	3	60.0	8	1	US-08-467-264-15	Sequence 155, App
64	3	60.0	8	1	US-08-479-532-4	Sequence 15, Appl
65	3	60.0	8	1	US-08-455-526-4	Sequence 4, Appl
66	3	60.0	8	1	US-08-455-525-4	Sequence 4, Appl
67	3	60.0	8	2	US-08-467-603-66	Sequence 4, Appl
68	3	60.0	8	2	US-08-705-660-39	Sequence 66, Appl
69	3	60.0	8	2	US-08-466-793-66	Sequence 39, Appl
70	3	60.0	8	2	US-08-491-861A-66	Sequence 66, Appl
71	3	60.0	8	3	US-09-139-491-4	Sequence 4, Appl
72	3	60.0	8	3	US-08-989-045-39	Sequence 39, Appl
73	3	60.0	8	3	US-09-258-754-233	Sequence 233, App
74	3	60.0	8	3	US-09-042-107-233	Sequence 233, App
75	3	60.0	8	4	US-09-187-859-1248	Sequence 1248, Ap
76	3	60.0	8	4	US-08-988-842-32	Sequence 32, Appl
77	3	60.0	8	4	US-09-374-671A-66	Sequence 66, Appl
78	3	60.0	8	4	US-09-839-542B-1248	Sequence 1248, Ap
79	3	60.0	8	5	PCT-US92-03222-4	Sequence 4, Appl
80	3	60.0	8	5	PCT-US94-01319-56	Sequence 56, Appl
81	3	60.0	9	1	US-08-467-083-24	Sequence 24, Appl
82	3	60.0	9	1	US-08-615-181-77	Sequence 77, Appl
83	3	60.0	9	1	US-08-616-368A-6	Sequence 6, Appl
84	3	60.0	9	1	US-08-594-447-40	Sequence 40, Appl
85	3	60.0	9	1	US-08-541-964-39	Sequence 39, Appl
86	3	60.0	9	1	US-08-414-417B-24	Sequence 24, Appl
87	3	60.0	9	2	US-07-829-461A-1	Sequence 1, Appl
88	3	60.0	9	2	US-08-486-348A-24	Sequence 24, Appl
89	3	60.0	9	2	US-08-468-545B-24	Sequence 24, Appl
90	3	60.0	9	2	US-08-665-647-54	Sequence 54, Appl
91	3	60.0	9	2	US-08-986-234-40	Sequence 40, Appl
92	3	60.0	9	2	US-08-466-680B-24	Sequence 24, Appl
93	3	60.0	9	3	US-08-899-437-20	Sequence 20, Appl
94	3	60.0	9	3	US-09-054-298-6	Sequence 6, Appl
95	3	60.0	9	3	US-09-197-649-26	Sequence 26, Appl
96	3	60.0	9	3	US-08-669-304-8	Sequence 8, Appl
97	3	60.0	9	3	US-08-669-304-15	Sequence 15, Appl
98	3	60.0	9	3	US-09-126-121-20	Sequence 20, Appl
99	3	60.0	9	3	US-08-818-655-6	Sequence 6, Appl
100	3	60.0	9	3		

## ALIGNMENTS

RESULT 1  
US-09-641-803-15  
; Sequence 15, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOCH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641.803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-15

Query Match 100.0%; Score 5; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEMP 5  
|||||  
Db 1 SEEMP 5

RESULT 2  
US-08-105-454-3  
; Sequence 3, Application US/08105454  
; Patent No. 6071715  
; GENERAL INFORMATION:  
; APPLICANT: Qian, Yue-Wei  
; APPLICANT: Lee, Eva Y.-H. P.  
; TITLE OF INVENTION: No. 6071715el Proteins Which Bind to  
; TITLE OF INVENTION: Retinoblastoma Proteins and Their  
; TITLE OF INVENTION: Encoding DNA Sequences  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 2300 One American Center  
; CITY: Austin  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 78701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/105.454  
; FILING DATE: Concurrently herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: UTSK:196/KIT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512-320-7200

; TELEFAX: 512-474-7577  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-105-454-3

Query Match 100.0%; Score 5; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEMP 5  
|||||  
Db 6 SEEMP 10

RESULT 3  
US-08-242-097-10  
; Sequence 10, Application US/08242097  
; Patent No. 5846763  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Tae Ho  
; APPLICANT: Wisniewski, Hans Georg  
; APPLICANT: Vilcek, Jan  
; TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding  
; TITLE OF INVENTION: Therefor and Uses Thereof  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Broadway and Neimark  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/242,097  
; FILING DATE: 13-MAY-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-628-5197  
; TELEFAX: 212-737-3528  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-242-097-10

Query Match 80.0%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
|||||  
Db 6 SEEM 9

RESULT 4  
US-09-206-695-10  
; Sequence 10, Application US/09206695

Patent No. 6210905  
GENERAL INFORMATION:  
APPLICANT: Lee, Tae Ho  
APPLICANT: Wisniewski, Hans Georg  
APPLICANT: Vilcek, Jan  
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding  
TITLE OF INVENTION: Therefor and Uses Thereof  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/206,695  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/242,097  
FILING DATE: 13-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B  
TELEPHONE: 212-628-5197  
TELEFAX: 212-737-3528  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-206-695-10

Query Match 80.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEEM 4  
Db 6 SEEM 9

RESULT 5  
US-09-000-179-5  
Sequence 5, Application US/09000179  
Patent No. 6313091  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: A Pharmaceutical Composition  
Containing TSG-6 Protein for Treating Inflammatory Diseases and  
TITLE OF INVENTION: Cancer-Related Pathologies and Methods of Using same  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/000,179  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/001,311  
FILING DATE: 20-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WISNIEWSKI=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-628-5197  
TELEFAX: 212-737-3528  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-000-179-5

Query Match 80.0%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEEM 4  
Db 6 SEEM 9

RESULT 6  
US-09-799-118-10  
Sequence 10, Application US/09799118  
Patent No. 6518401  
GENERAL INFORMATION:  
APPLICANT: Lee, Tae Ho  
Wisniewski, Hans Georg  
Vilcek, Jan  
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding  
Therefor and Uses Thereof  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/799,118  
FILING DATE: 06-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/242,097  
FILING DATE: 13-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-628-5197  
TELEFAX: 212-737-3528  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 10;  
US-09-799-118-10

Query Match 80.0%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEEM 4  
Db 6 SEEM 9

RESULT 7  
PCT-US96-11995-5  
; Sequence 5, Application PC/TUS9611995  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: A Pharmaceutical Composition Containing TSG-6  
; TITLE OF INVENTION: Protein for Treating Inflammatory Diseases and Cancer-Related  
; TITLE OF INVENTION: Methods of Using same  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/11995  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,311  
; FILING DATE: 20-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WISNIEWSKI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-628-5197  
; TELEFAX: 212-737-3528  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US96-11995-5

Query Match 80.0%; Score 4; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEEM 4  
Db 6 SEEM 9

RESULT 8  
US-08-408-604A-99  
; Sequence 99, Application US/08408604A  
; Patent No. 5801149  
; GENERAL INFORMATION:  
; APPLICANT: Shoelson, Steven  
; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES  
; NUMBER OF SEQUENCES: 211

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 10;  
US-09-799-118-10

Query Match 80.0%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEEM 4  
Db 6 SEEM 9

RESULT 9  
PCT-US94-01499-1  
; Sequence 1, Application PC/TUS9401499  
; GENERAL INFORMATION:  
; APPLICANT: Bernardo Nadal-Ginard et al.  
; TITLE OF INVENTION: Control of Cell  
; TITLE OF INVENTION: Proliferation  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/01499  
; FILING DATE:

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 10;  
US-09-799-118-10

Query Match 80.0%; Score 4; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEMP 5  
Db 5 EEMP 8

RESULT 9  
PCT-US94-01499-1  
; Sequence 1, Application PC/TUS9401499  
; GENERAL INFORMATION:  
; APPLICANT: Bernardo Nadal-Ginard et al.  
; TITLE OF INVENTION: Control of Cell  
; TITLE OF INVENTION: Proliferation  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/01499  
; FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: John W. Freeman  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00108/099001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13  
TYPE: amino acid  
STRANDEDNESS: N/A  
TOPOLOGY: N/A  
PCT-US94-01499-1

Query Match 80.0%; Score 4; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
DB 5 SEEM 8

## RESULT 10

US-09-120-653D-26  
Sequence 26, Application US/09120653D  
Patent No. 6365727  
GENERAL INFORMATION:  
APPLICANT: YOON, JI-WON  
APPLICANT: JUN, HEE-SOOK  
APPLICANT: PARK, HAE-JOON  
APPLICANT: AHN, JONG-SEONG  
APPLICANT: HA, YOUNG-JU  
APPLICANT: CHUNG, SOO-IL  
TITLE OF INVENTION: DNA and peptides of a diabetes-specific endogenous retrovirus  
FILE REFERENCE: 98-338  
CURRENT APPLICATION NUMBER: US/09/120,653D  
CURRENT FILING DATE: 1998-07-22  
PRIOR APPLICATION NUMBER: KR 98-10108  
PRIOR FILING DATE: 1998-03-24  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Kopatentin 1.71  
SEQ ID NO 26  
TYPE: PRT  
LENGTH: 17  
ORGANISM: DIABETES-SPECIFIC RETROVIRUS ENDOGENOUS ERV-9  
US-09-120-653D-26

Query Match 80.0%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEM 4  
DB 3 SEEM 6

## RESULT 11

US-07-729-099-8  
Sequence 8, Application US/07729099  
Patent No. 5403581  
GENERAL INFORMATION:  
APPLICANT: Binger, Mary-Helen  
APPLICANT: Pasamontes, Luis  
TITLE OF INVENTION: Coccidiosis Vaccines  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/729,099  
FILING DATE: 19910712  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Roseman, Catherine R  
REGISTRATION NUMBER: 34,240  
REFERENCE/DOCKET NUMBER: 8514  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-6208  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Eimeria tenella  
US-07-729-099-8

Query Match 60.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
DB 3 SEE 5

## RESULT 12

US-08-257-392-8  
Sequence 8, Application US/08257392  
Patent No. 5688513  
GENERAL INFORMATION:  
APPLICANT: Binger, Mary-Helen  
APPLICANT: Pasamontes, Luis  
TITLE OF INVENTION: Coccidiosis Vaccines  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/257,392  
FILING DATE: 09-JUN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/729,099  
FILING DATE: 12-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Roseman, Catherine R

Query Match 60.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
DB 3 SEE 5

REGISTRATION NUMBER: 34,240  
REFERENCE/DOCKET NUMBER: 8514  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-6208  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Eimeria tenella  
US-08-257-392-8

Query Match 60.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 3 SEE 5

RESULT 13  
US-08-770-035-8  
Sequence 8, Application US/08770035  
Patent No. 6008342  
GENERAL INFORMATION:  
APPLICANT: Binger, Mary-Helen  
APPLICANT: Pasamontes, Luis  
TITLE OF INVENTION: Coccidiosis Vaccines  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,035  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/729,099  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Roseman, Catherine R  
REGISTRATION NUMBER: 34,240  
REFERENCE/DOCKET NUMBER: 8514  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-6208  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Eimeria tenella  
US-08-770-035-8

Query Match 60.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 3 SEE 5

RESULT 14  
US-08-981-122-80  
Sequence 80, Application US/08981122B  
Patent No. 6127339  
GENERAL INFORMATION:  
APPLICANT: Hatanaka, Yoshihiro  
APPLICANT: Arimoto, Masaharu  
TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/08/981,122B  
CURRENT FILING DATE: 1997-12-18  
PRIOR APPLICATION NUMBER: JP 7-176904  
PRIOR FILING DATE: 1995-06-21  
PRIOR APPLICATION NUMBER: PCT/JP96/01734  
PRIOR FILING DATE: 1996-06-21  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 80  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Sequence of peptides synthesized in Comparative Example 2  
Patent No. 6127339  
OTHER INFORMATION: from L-form F-moc amino acids by solid phase method using a  
OTHER INFORMATION: multipetide synthesizing system (RAMPS) or an automatic peptide  
OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)  
US-08-981-122-80

Query Match 60.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 2 EEM 4

RESULT 15  
US-08-981-122-90  
Sequence 90, Application US/08981122B  
Patent No. 6127339  
GENERAL INFORMATION:  
APPLICANT: Hatanaka, Yoshihiro  
APPLICANT: Arimoto, Masaharu  
TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/08/981,122B  
CURRENT FILING DATE: 1997-12-18  
PRIOR APPLICATION NUMBER: JP 7-176904  
PRIOR FILING DATE: 1995-06-21  
PRIOR APPLICATION NUMBER: PCT/JP96/01734  
PRIOR FILING DATE: 1996-06-21  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 90  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: AMIDATION  
LOCATION: 5  
OTHER INFORMATION: Sequence of peptides synthesized in Comparative Examples 8 and 9  
Patent No. 6127339

; OTHER INFORMATION: from L-form F-moc amino acids by solid phase method using an  
; OTHER INFORMATION: automatic peptide synthesizer (9050 plus peptide synthesizer)  
US-08-981-122-90

Query Match 60.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 2 EEM 4

## RESULT 16

US-08-849-488-15  
; Sequence 15, Application US/08849488  
; Patent No. 6238670  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Douglas T.  
; TITLE OF INVENTION: Modulating the Immune Response  
; FILE REFERENCE: A-64962/WHO/DAV  
; CURRENT APPLICATION NUMBER: US/08/849,488  
; EARLIER FILING DATE: 1997-10-21  
; EARLIER APPLICATION NUMBER: PCT/GB95/02851  
; EARLIER FILING DATE: 1995-12-06  
; EARLIER APPLICATION NUMBER: GB 9424631.1  
; EARLIER FILING DATE: 1994-12-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptides  
; OTHER INFORMATION: encoded by genetically engineered nucleic acids  
US-08-849-488-15

Query Match 60.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

## RESULT 17

US-09-236-160-4  
; Sequence 4, Application US/09236160A  
; Patent No. 6307090  
; GENERAL INFORMATION:  
; APPLICANT: BURKE JR., Terrence R.  
; TITLE OF INVENTION: ACYLATED OLIGOPEPTIDE DERIVATIVES HAVING CELL SIGNAL  
; FILE REFERENCE: 175895  
; CURRENT APPLICATION NUMBER: US/09/236,160A  
; CURRENT FILING DATE: 1999-01-22  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: mammalian  
US-09-236-160-4

Query Match 60.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||

Db 1 EEM 3  
RESULT 18  
US-09-236-160-29  
; Sequence 29, Application US/09236160A  
; Patent No. 6307090  
; GENERAL INFORMATION:  
; APPLICANT: BURKE JR., Terrence R.  
; TITLE OF INVENTION: ACYLATED OLIGOPEPTIDE DERIVATIVES HAVING CELL SIGNAL  
; TITLE OF INVENTION: INHIBITING ACTIVITY  
; FILE REFERENCE: 175895  
; CURRENT APPLICATION NUMBER: US/09/236,160A  
; CURRENT FILING DATE: 1999-01-22  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: mammalian  
US-09-236-160-29

Query Match 60.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 1 EEM 3

## RESULT 19

US-09-187-859-1239  
; Sequence 1239, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1239  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-09-187-859-1239

Query Match 60.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 3 SEE 5

## RESULT 20

US-09-800-170-50  
; Sequence 50, Application US/098000170  
; Patent No. 6481667  
; GENERAL INFORMATION:  
; APPLICANT: Kinsella, Todd  
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES  
; FILE REFERENCE: A-68614-1/DJB/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/09/800,170  
; CURRENT FILING DATE: 2001-08-28

; PRIOR APPLICATION NUMBER: US 60/187,130  
; PRIOR FILING DATE: 2000-03-06  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 50  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: fragment of myc epitope  
US-09-800-170-50

Query Match 60.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 1 SEE 3

RESULT 21  
US-09-839-542B-1239  
; Sequence 1239, Application US/09839542B  
; Patent No. 6569996

; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086 407D1  
; CURRENT APPLICATION NUMBER: US/09/839,542B  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 1239  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-09-839-542B-1239

Query Match 60.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 3 SEE 5

RESULT 22  
US-07-791-935B-1  
; Sequence 1, Application US/07791935B  
; Patent No. 5366871

; GENERAL INFORMATION:  
; APPLICANT: RECHSTEINER, MARTIN C.  
; APPLICANT: YOO, YUNG JOON  
; TITLE OF INVENTION: UBICUITIN-PEPTIDE EXTENSIONS AS  
; TITLE OF INVENTION: ENZYME SUBSTRATES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Thorpe, No. 5366871th & Western  
; STREET: 9035 South 700 East, Suite 200  
; CITY: Sandy  
; STATE: Utah  
; COUNTRY: USA  
; ZIP: 84070  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage

; COMPUTER: compaq LTE/286  
; OPERATING SYSTEM: DOS 4.01  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/791,935B  
; FILING DATE: 19911113  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: none  
; FILING DATE: na  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Western, M. Wayne  
; REGISTRATION NUMBER: 22,788  
; REFERENCE/DOCKET NUMBER: T310  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (801) 566-6633  
; TELEFAX: (801) 566-0750  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acid residues  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
US-07-791-935B-1

Query Match 60.0%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 1 SEE 3

RESULT 23  
US-07-671-757-26

; Sequence 26, Application US/07671757  
; Patent No. 5484770  
; GENERAL INFORMATION:  
; APPLICANT: LAERUM, Ole D  
; TITLE OF INVENTION: PEPTIDE COMPOUNDS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States of America  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/671,757  
; FILING DATE: 19910408  
; CLASSIFICATION: 530  
; CLASSIFICATION: A 61 K 37/02  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8821785.6  
; FILING DATE: 16-SEP-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FICHTER, Richard E  
; REGISTRATION NUMBER: 26,382  
; REFERENCE/DOCKET NUMBER: REP/Laerum/757  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 683-0500  
; TELEFAX: (703) 683-1080  
; TELEX: 89-9124 BATO ACTN  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: AMINO ACID



; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-07-671-757-26

Query Match 60.0%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SEE 3  
|||  
Db 1 SEE 3  
|||

RESULT 24  
US-08-704-170-115  
; Sequence 115, Application US/08704170  
; Patent No. 5707626  
; GENERAL INFORMATION:  
; APPLICANT: Douvas, Angeline  
; APPLICANT: Takehana, Yoshi  
; APPLICANT: Ehresmann, Glenn  
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR  
; TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Robbins, Berliner & Carson  
; STREET: 201 No. 5707626th Figueroa Street, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/704,170  
; FILING DATE: 11-MAR-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/029,850  
; FILING DATE: 11-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitala, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-331  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-704-170-115

Query Match 60.0%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SEE 3  
|||  
Db 3 SEE 5  
|||

RESULT 25  
US-09-020-880-83  
; Sequence 83, Application US/09020880A  
; Patent No. 6136558  
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Ballinger, Marcus D.  
; APPLICANT: Jones, Jennifer T.  
; APPLICANT: Fairbrother, Wayne J.  
; APPLICANT: Sliwkowski, Mark X.  
; APPLICANT: Wells, James A.  
; TITLE OF INVENTION: HEREGULIN VARIANTS  
; FILE REFERENCE: 14918-720CON1  
; CURRENT APPLICATION NUMBER: US/09/020,880A  
; CURRENT FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: US 60/037,581  
; EARLIER FILING DATE: 1997-02-10  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 83  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: No. 6136558 relevant (recombinant)  
US-09-020-880-83  
  
Query Match 60.0%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SEE 3  
|||  
Db 3 SEE 5  
|||

RESULT 26  
US-08-075-541D-17  
; Sequence 17, Application US/08075541D  
; Patent No. 6183745  
; GENERAL INFORMATION:  
; APPLICANT: TINDLE, ROBERT  
; APPLICANT: FERNANDO, GERMAIN  
; APPLICANT: FRAZER, IAN  
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND  
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: 1601 MARKET STREET, 36TH FLOOR  
; CITY: PHILADELPHIA  
; STATE: PENNSYLVANIA  
; COUNTRY: USA  
; ZIP: 19103-2398  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/075,541D  
; FILING DATE: 10-JUN-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU pk 3876  
; FILING DATE: 12-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: pct/au91/00575  
; FILING DATE: 12-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NADEL, ALAN S  
; REGISTRATION NUMBER: 27,363  
; REFERENCE/DOCKET NUMBER: 8795-4  
; TELEPHONE: 215-567-2020  
; TELEFAX: 215-567-2991  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-075-541D-17

Query Match 60.0%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 1 SEE 3

## RESULT 27

US-09-187-859-1242  
; Sequence 1242, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1242  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-09-187-859-1242

Query Match 60.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 4 SEE 6

## RESULT 28

US-09-101-544-83  
; Sequence 83, Application US/09101544  
; Patent No. 6387638  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ballinger, Marcus D.  
; APPLICANT: Jones, Jennifer T.  
; APPLICANT: Fairbrother, Wayne J.  
; APPLICANT: Slikowski, Mark X.  
; APPLICANT: Wells, James A.  
; TITLE OF INVENTION: HERGULIN VARIANTS  
; FILE REFERENCE: 14918-720CON2  
; CURRENT APPLICATION NUMBER: US/09/101,544  
; CURRENT FILING DATE: 1998-07-17  
; PRIOR APPLICATION NUMBER: US 09/020,880  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: US 60/037,581  
; PRIOR FILING DATE: 1997-02-10  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 83  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: No. 6387638 relevant (recombinant)  
US-09-101-544-83

Query Match 60.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 3 SEE 5

## RESULT 29

US-08-432-483A-5  
; Sequence 5, Application US/08432483A  
; Patent No. 6410022  
; GENERAL INFORMATION:  
; APPLICANT: Rittershaus, Charles W.  
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER  
; TITLE OF INVENTION: TRANSFER PROTEIN (CTEP) ACTIVITY  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: Ten South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-7407  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/432,483A  
; FILING DATE: 1-May-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Leon R. Yankwich  
; REGISTRATION NUMBER: 30,237  
; REFERENCE/DOCKET NUMBER: 95,179 (TCS-95179)  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FEATURE:  
; NAME/KEY: 6 amino acids of lipophilic peptide  
; NAME/KEY: adjuvant Pam3-Cys-Ser-Glu4.  
; LOCATION:  
; US-08-432-483A-5

Query Match 60.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 2 SEE 4

## RESULT 30

US-09-155-613A-96  
; Sequence 96, Application US/09155613A  
; Patent No. 6420120  
; GENERAL INFORMATION:  
; APPLICANT: Boulanger, Pierre  
; APPLICANT: Hong, Saw See  
; APPLICANT: Karayan, Lucie  
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses

FILE REFERENCE: 032751-036  
CURRENT APPLICATION NUMBER: US/09/155,613A  
CURRENT FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: PCT/FR98/00184  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: FR 97/01005  
PRIOR FILING DATE: 1997-01-30  
PRIOR APPLICATION NUMBER: FR 97/11166  
PRIOR FILING DATE: 1997-09-09  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 96  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Phagotopoe  
US-09-155-613A-96

Query Match 60.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
DB 2 SEE 4

RESULT 31  
US-09-839-542B-1242  
Sequence 1242, Application US/09839542B  
Patent No. 6569996  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Symonds, James Matthew  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
FILE REFERENCE: 100086.407D1  
CURRENT APPLICATION NUMBER: US/09/839,542B  
CURRENT FILING DATE: 2001-04-20  
NUMBER OF SEQ ID NOS: 4052  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1242  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Representative cyclic modulating agent based on  
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-09-839-542B-1242

Query Match 60.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
DB 4 SEE 6

RESULT 32  
PCT-US94-02631-115  
Sequence 115, Application PC/TUS9402631  
GENERAL INFORMATION:  
APPLICANT: Douvas, Angeline  
APPLICANT: Takehana, Yoshi  
APPLICANT: Ehresmann, Glenn  
TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR  
TITLE OF INVENTION: IMMUNOINFECTIVE CLUSTER VIRUS INFECTIONS  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Robbins, Berliner & Carson

STREET: 201 North Figueroa Street, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90012  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02631  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/029,850  
FILING DATE: 11-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Spitals, John P.  
REGISTRATION NUMBER: 29,215  
REFERENCE/DOCKET NUMBER: 1920-331  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 115:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US94-02631-115

Query Match 60.0%; Score 3; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
DB 3 SEE 5

RESULT 33  
US-07-638-492-13  
Sequence 13, Application US/07638492  
Patent No. 5494672  
GENERAL INFORMATION:  
APPLICANT: Hodges, Robert S.  
APPLICANT: Paranchych, William  
APPLICANT: Irvin, Randall T.  
APPLICANT: Lee, Kok K.  
APPLICANT: Parimi, Sastry A.  
APPLICANT: Zoutman, Dick E.  
APPLICANT: Dolg, Peter C.  
APPLICANT: Wong, Wah Y.  
TITLE OF INVENTION: Pseudomonas Peptide Composition and  
TITLE OF INVENTION: Method  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/638,492  
FILING DATE: 04-JAN-1991  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: Sholtz, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 8900-0002.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: peptide 13

US-07-638-492-13

Query Match 60.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
Db 1 EEM 3

RESULT 34

US-08-182-175A-71

Sequence 71, Application US/08182175A  
Patent No. 5559223  
GENERAL INFORMATION:  
APPLICANT: Saverio Carl Falco  
APPLICANT: Sharon J. Keeler  
APPLICANT: Janet A. Rice  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E.I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,175A

FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743,006

FILING DATE: 9 August 1991

ATTORNEY/AGENT INFORMATION:

NAME: Linda Axamethy Floyd

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: BB-1031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 992-4929

TELEFAX: (302) 892-7949

TELEX: 835420

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-182-175A-71

Query Match 60.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
Db 3 EEM 5

RESULT 35

US-08-182-175A-74

Sequence 74, Application US/08182175A  
Patent No. 5559223  
GENERAL INFORMATION:  
APPLICANT: Saverio Carl Falco  
APPLICANT: Sharon J. Keeler  
APPLICANT: Janet A. Rice  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E.I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,175A

FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743,006

FILING DATE: 9 August 1991

ATTORNEY/AGENT INFORMATION:

NAME: Linda Axamethy Floyd

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: BB-1031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 992-4929

TELEFAX: (302) 892-7949

TELEX: 835420

INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-182-175A-74

Query Match 60.0%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
Db 3 EEM 5

RESULT 36

US-08-182-175A-77

Sequence 77, Application US/08182175A  
Patent No. 5559223  
GENERAL INFORMATION:  
APPLICANT: Saverio Carl Falco  
APPLICANT: Sharon J. Keeler

```
/ APPLICANT: Janet A. Rice
/ TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing B
/ NUMBER OF SEQUENCES: 113
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E.I. du Pont de Nemours and Company
/ STREET: 1007 Market Street
/ CITY: Wilmington
/ STATE: Delaware
/ COUNTRY: USA
/ ZIP: 19898
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: Macintosh
/ OPERATING SYSTEM: Macintosh System, 6.0
/ SOFTWARE: Microsoft Word, 4.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/182,175A
/ FILING DATE:
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/743,006
/ FILING DATE: 9 August 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Linda Axamethy Floyd
/ REGISTRATION NUMBER: 33,692
/ REFERENCE/DOCKET NUMBER: BB-1031
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (302) 992-4929
/ TELEFAX: (302) 892-7949
/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 77:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: protein
/ MOLECULE TYPE: protein
/ US-08-182-175A-77

Query Match 60.0%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4
Db 3 EEM 5

RESULT 37
US-08-182-175A-79
/ Sequence 79, Application US/08182175A
/ Patent No. 5559223
/ GENERAL INFORMATION:
/ APPLICANT: Saverio Carl Falco
/ APPLICANT: Sharon J. Keeler
/ TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing B
/ NUMBER OF SEQUENCES: 113
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E.I. du Pont de Nemours and Company
/ STREET: 1007 Market Street
/ CITY: Wilmington
/ STATE: Delaware
/ COUNTRY: USA
/ ZIP: 19898
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: Macintosh
/ OPERATING SYSTEM: Macintosh System, 6.0
/ SOFTWARE: Microsoft Word, 4.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/182,175A
/ FILING DATE:
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/743,006
/ FILING DATE: 9 August 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Linda Axamethy Floyd
/ REGISTRATION NUMBER: 33,692
/ REFERENCE/DOCKET NUMBER: BB-1031
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (302) 992-4929
/ TELEFAX: (302) 892-7949
/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 80:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ FILING DATE:
```

```
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/743,006
/ FILING DATE: 9 August 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Linda Axamethy Floyd
/ REGISTRATION NUMBER: 33,692
/ REFERENCE/DOCKET NUMBER: BB-1031
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (302) 992-4929
/ TELEFAX: (302) 892-7949
/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 79:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: protein
/ MOLECULE TYPE: protein
/ US-08-182-175A-79

Query Match 60.0%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4
Db 3 EEM 5

RESULT 38
US-08-182-175A-80
/ Sequence 80, Application US/08182175A
/ Patent No. 5559223
/ GENERAL INFORMATION:
/ APPLICANT: Saverio Carl Falco
/ APPLICANT: Sharon J. Keeler
/ TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
/ NUMBER OF SEQUENCES: 113
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E.I. du Pont de Nemours and Company
/ STREET: 1007 Market Street
/ CITY: Wilmington
/ STATE: Delaware
/ COUNTRY: USA
/ ZIP: 19898
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: Macintosh
/ OPERATING SYSTEM: Macintosh System, 6.0
/ SOFTWARE: Microsoft Word, 4.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/182,175A
/ FILING DATE:
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/743,006
/ FILING DATE: 9 August 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Linda Axamethy Floyd
/ REGISTRATION NUMBER: 33,692
/ REFERENCE/DOCKET NUMBER: BB-1031
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (302) 992-4929
/ TELEFAX: (302) 892-7949
/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 80:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ FILING DATE:
```

```
; MOLECULE TYPE: protein
US-08-182-175A-80

Query Match          60.0%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4.
   |||
Db 3 EEM 5

RESULT 39
US-08-486-721A-7
; Sequence 7, Application US/08486721A
; Patent No. 5739025
; GENERAL INFORMATION:
; APPLICANT: Fukazawa, Chikafusa
; TITLE OF INVENTION: Method of Producing
; TITLE OF INVENTION: Asparaginyl Endoprotease
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frishauf, Holtz, Goodman, Langer & Chick
; STREET: 767 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017-2023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3+ inch, 1.4 mb
; OPERATING SYSTEM: MS DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,721A
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/091,991
; FILING DATE: 12-JULY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Barth, Richard S.
; REGISTRATION NUMBER: 28,180
; REFERENCE/DOCKET NUMBER: 930587/HG
; TELEPHONE: (212) 319-4900
; TELEFAX: (212) 319-5101
; TELEX: 236268
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:

; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; US-08-486-721A-7

Query Match          60.0%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3
   |||
Db 4 SEE 6

RESULT 40
US-09-024-020B-25
; Sequence 25, Application US/09024020B
; Patent No. 6030810
; GENERAL INFORMATION:
; APPLICANT: DELGADO, STEPHEN G.
; APPLICANT: DIETRICH, PAUL S.
; APPLICANT: FISH, LINDA M.
; APPLICANT: HERMAN, RONALD C.
; APPLICANT: SANGAMESWARAN, LAKSHMI
; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JANET PAULINE CLARK
; STREET: 3401 HILLVIEW AVENUE, MS A2-250
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94304-1397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,020B
; FILING DATE: 16-FEB-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,447
; FILING DATE: 26-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: R0020B-REG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-3097
; TELEFAX: (650) 855-5322
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-024-020B-25

Query Match          60.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 SEE 3  
|||  
Db 4 SEE 6

## RESULT 41

US-08-931-858E-91  
; Sequence 91, Application US/08931858E  
; Patent No. 6222022  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; APPLICANT: KLEIN, ROBERT  
; APPLICANT: DESAUVAGE, FRED  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
; NUMBER OF SEQUENCES: 239  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/931,858E  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 971486  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: linear  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-931-858E-91

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

## RESULT 42

US-08-981-739-91  
; Sequence 91, Application US/08981739  
; Patent No. 6232449  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.

; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,739  
; FILING DATE: 31-Aug-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/03461  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 976163  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 91:  
US-08-981-739-91

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

## RESULT 43

US-09-425-043-25  
; Sequence 25, Application US/09425043  
; Patent No. 6335172  
; GENERAL INFORMATION:  
; APPLICANT: DELGADO, STEPHEN G.  
; APPLICANT: DIETRICH, PAUL S.  
; APPLICANT: FISH, LINDA M.  
; APPLICANT: HERMAN, RONALD C.  
; APPLICANT: SANGAMESWARAN, LAKSHMI  
; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE  
; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: JANET PAULINE CLARK  
; STREET: 3401 HILLVIEW AVENUE, MS A2-250  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 94304-1397  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/425,043  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/024,020  
FILING DATE: 16-FEB-1998  
APPLICATION NUMBER: US 60/039,447  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, JANET P.  
REGISTRATION NUMBER: 34,799  
REFERENCE/DOCKET NUMBER: R0020B-REG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-25

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 4 SEE 6

## RESULT 44

US-09-187-789-32  
Sequence 32, Application US/09187789  
Patent No. 6340740  
GENERAL INFORMATION:  
APPLICANT: Alnemzi, Emad S.  
APPLICANT: Fernandez-Alnemzi, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
TITLE OF INVENTION: AND METHODS OF USE  
FILE REFERENCE: 480140.434C1  
CURRENT APPLICATION NUMBER: US/09/187,789  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-187-789-32

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
Db 3 EEM 5

## RESULT 45

US-08-979-608A-41  
Sequence 41, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Ariona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-08-979-608A-41

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 4 SEE 6

## RESULT 46

US-09-187-859-1245  
Sequence 1245, Application US/09187859A  
Patent No. 6358920  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
FILE REFERENCE: 100086.407C1  
CURRENT APPLICATION NUMBER: US/09/187,859A  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 4052  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1245  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Representative cyclic modulating agent based on  
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-09-187-859-1245

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 5 SEE 7



RESULT 47  
US-09-128-026-91  
; Sequence 91, Application US/09128026  
; Patent No. 6403335  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/128,026  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 976163  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-128-026-91

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 2 SEE 4

RESULT 48  
US-09-139-600-27  
; Sequence 27, Application US/09139600  
; Patent No. 6432628  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandez-Alnemri, Teresa  
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
; FILE REFERENCE: 480140.434  
; CURRENT APPLICATION NUMBER: US/09/139,600  
; CURRENT FILING DATE: 1998-08-25  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-139-600-27

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEE 4  
|||  
Db 3 SEE 5

RESULT 49  
US-09-206-576-5  
; Sequence 5, Application US/09206576  
; Patent No. 6551990  
; GENERAL INFORMATION:  
; APPLICANT: Giachelli, Cecilia M.  
; APPLICANT: Steitz, Susie  
; TITLE OF INVENTION: Methods of Inhibiting Ectopic Calcification  
; FILE REFERENCE: P-UW 3244  
; CURRENT APPLICATION NUMBER: US/09/206,576  
; CURRENT FILING DATE: 1998-12-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-206-576-5

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 4 SEE 6

RESULT 50  
US-09-839-542B-1245  
; Sequence 1245, Application US/09839542B  
; Patent No. 6569996  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; FILE REFERENCE: 100086.407D1  
; CURRENT APPLICATION NUMBER: US/09/839,542B  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1245  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-09-839-542B-1245

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
|||  
Db 5 SEE 7

RESULT 51  
PCT-US92-06412-71

; Sequence 71, Application PC/TUS9206412

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/06412

; FILING DATE: 19920807

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/743,006

; FILING DATE: 9 August 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Linda Axamethy Floyd

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: BB-1031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 992-4929

; TELEFAX: (302) 892-7949

; TELEX: 835420

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; PCT-US92-06412-71

Query Match 60.0%; Score 3; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4

Db 3 EEM 5

RESULT 52

PCT-US92-06412-74

; Sequence 74, Application PC/TUS9206412

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/06412

; FILING DATE: 19920807

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/743,006

; FILING DATE: 9 August 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Linda Axamethy Floyd

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: BB-1031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 992-4929

; TELEFAX: (302) 892-7949

; TELEX: 835420

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; PCT-US92-06412-74

Query Match 60.0%; Score 3; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4

Db 3 EEM 5

RESULT 53

PCT-US92-06412-77

; Sequence 77, Application PC/TUS9206412

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/06412

; FILING DATE: 19920807

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/743,006

; FILING DATE: 9 August 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Linda Axamethy Floyd

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: BB-1031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 992-4929

; TELEFAX: (302) 892-7949

; TELEX: 835420

; INFORMATION FOR SEQ ID NO: 77:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: AMINO ACID

STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
PCT-US92-06412-77

Query Match 60.0%; Score 3; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
Db 3 EEM 5

## RESULT 54

PCT-US92-06412-79  
Sequence 79, Application PC/TUS9206412  
GENERAL INFORMATION:

APPLICANT: Saverio Carl Falco  
APPLICANT: Sharon J. Keeler  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E.I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06412  
FILING DATE: 19920807  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/743,006  
FILING DATE: 9 August 1991

ATTORNEY/AGENT INFORMATION:  
NAME: Linda Axamethy Floyd  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-4929  
TELEFAX: (302) 892-7949  
TELEX: 835420

INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
PCT-US92-06412-79

Query Match 60.0%; Score 3; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
Db 3 EEM 5

## RESULT 55

PCT-US92-06412-80  
Sequence 80, Application PC/TUS9206412  
GENERAL INFORMATION:

APPLICANT: Saverio Carl Falco

APPLICANT: Sharon J. Keeler  
APPLICANT: Janet A. Rice  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:

ADDRESSEE: E.I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06412  
FILING DATE: 19920807  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/743,006  
FILING DATE: 9 August 1991

ATTORNEY/AGENT INFORMATION:  
NAME: Linda Axamethy Floyd  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-4929  
TELEFAX: (302) 892-7949  
TELEX: 835420

INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
PCT-US92-06412-80

Query Match 60.0%; Score 3; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
Db 3 EEM 5

## RESULT 56

5472855-31  
Patent No. 5472855  
APPLICANT: CARTER, PAUL J.; WELLS, JAMES A.  
TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS  
NUMBER OF SEQUENCES: 31  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/287,964  
FILING DATE: 22-SEP-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 90,902  
FILING DATE: 12-JUL-1993  
APPLICATION NUMBER: 823,039  
FILING DATE: 14-JAN-1992  
APPLICATION NUMBER: 35,652  
FILING DATE: 06-APR-1987  
APPLICATION NUMBER: 334,081  
FILING DATE: 04-APR-1989  
APPLICATION NUMBER: 127,134  
FILING DATE: 01-DEC-1987  
APPLICATION NUMBER: 846,627  
FILING DATE: 01-APR-1986  
APPLICATION NUMBER: 858,594  
FILING DATE: 30-APR-1986

APPLICATION NUMBER: 614,612  
FILING DATE: 29-MAY-1984  
APPLICATION NUMBER: 614,615  
FILING DATE: 29-MAY-1984  
APPLICATION NUMBER: 614,617  
FILING DATE: 29-MAY-1984  
APPLICATION NUMBER: 614,491  
FILING DATE: 29-MAY-1984  
SEQ ID NO:31:  
LENGTH: 7  
5472855-31

Query Match 60.0%; Score 3; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5  
|||  
Db 5 EMP 7

RESULT 57  
US-07-872-644-4  
Sequence 4, Application US/07872644  
Patent No. 5389527  
GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/872,644  
FILING DATE: 19920420  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5389527and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-07-872-644-4  
Query Match 60.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 4 EEM 6

RESULT 58  
US-08-045-264A-24  
Sequence 24, Application US/08045264A  
Patent No. 5436131  
GENERAL INFORMATION:

APPLICANT: CONDR, JON H.  
APPLICANT: GRAHAM, DONALD J.  
APPLICANT: GOTLIB, LEAH  
TITLE OF INVENTION: COLOR SCREENING ASSAY FOR IDENTIFYING  
TITLE OF INVENTION: DRUG-RESISTANT HIV PROTEASE MUTANTS AND INHIBITORS  
TITLE OF INVENTION: THEREOF.  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: PO Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh Iicx  
OPERATING SYSTEM: System 7  
SOFTWARE: Microsoft Word 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,264A  
FILING DATE: 02-APR-1993  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: MEREDITH, ROY, D.  
REGISTRATION NUMBER: 30,777  
REFERENCE/DOCKET NUMBER: 18936  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-4678  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: peptide  
DESCRIPTION: NO  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal fragment

US-08-045-264A-24

Query Match 60.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
|||  
Db 5 EEM 7

RESULT 59  
US-08-014-426-56  
Sequence 56, Application US/08014426  
Patent No. 5512435  
GENERAL INFORMATION:

APPLICANT: Renschler, Markus F.  
APPLICANT: Levy, Ronald  
APPLICANT: Bhatt, Ramesh  
APPLICANT: Dower, William  
TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE  
TITLE OF INVENTION: PEPTIDES

```
/
/ NUMBER OF SEQUENCES: 65
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Khourie and Crew
/ STREET: 379 Lytton Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: US
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/014,426
/ FILING DATE: 05-FEB-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 5490A-204
/ TELEPHONE: (415) 326-2400
/ TELEFAX: (415) 326-2422
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/
/ US-08-014-426-56
/
/ Query Match 60.0%; Score 3; DB 1; Length 8;
/ Best Local Similarity 100.0%; Pred. No. 2.5e+05;
/ Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 3 EMP 5
/ |||
/ Db 2 EMP 4
/
/ RESULT 60
/ US-08-297-494-4
/ Sequence 4, Application US/08297494
/ Patent No. 5580771
/ GENERAL INFORMATION:
/ APPLICANT: Beavo, Joseph A.
/ APPLICANT: Bentley, Kelley
/ APPLICANT: Charbonneau, Harry
/ APPLICANT: Sonnenburg, William K.
/ TITLE OF INVENTION: DNA Encoding Mammalian
/ CURRENT APPLICATION DATA:
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ ADDRESSEE: Bicknell
/ STREET: Two First National Plaza, 20 South Clark
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/297,494
/ FILING DATE:
/ CLASSIFICATION: 435
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/688,356
/ FILING DATE: 04-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5602019and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 27866/30822
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 346-5750
/ TELEFAX: (312) 984-9740
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ CLASSIFICATION: 435
```

```
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/688,356
/ FILING DATE: 04-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5580771and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 27866/30822
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 346-5750
/ TELEFAX: (312) 984-9740
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
/ US-08-297-494-4
/
/ Query Match 60.0%; Score 3; DB 1; Length 8;
/ Best Local Similarity 100.0%; Pred. No. 2.5e+05;
/ Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 2 EMP 4
/ |||
/ Db 4 EMP 6
/
/ RESULT 61
/ US-08-297-510-4
/ Sequence 4, Application US/08297510
/ Patent No. 5602019
/ GENERAL INFORMATION:
/ APPLICANT: Beavo, Joseph A.
/ APPLICANT: Bentley, Kelley
/ APPLICANT: Charbonneau, Harry
/ APPLICANT: Sonnenburg, William K.
/ TITLE OF INVENTION: DNA Encoding Mammalian
/ CURRENT APPLICATION DATA:
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ ADDRESSEE: Bicknell
/ STREET: Two First National Plaza, 20 South Clark
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/297,510
/ FILING DATE:
/ CLASSIFICATION: 435
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/688,356
/ FILING DATE: 04-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5602019and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 27866/30822
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 346-5750
/ TELEFAX: (312) 984-9740
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-297-510-4

Query Match      60.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EEM 4
        |||
Db      4 EEM 6

RESULT 62
US-08-066-325-154
; Sequence 154, Application US/08066325
; Patent No. 5667967
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Oksenberg, Jorge
; APPLICANT: Bernard, Claude
; TITLE OF INVENTION: T-CELL RECEPTOR VARIABLE TRANSCRIPTS AS DISEASE RELATED MARKER
; NUMBER OF SEQUENCES: 157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/066,325
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5667967tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 690068.408C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-066-325-155

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/066,325
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5667967tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 690068.408C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-066-325-154

Query Match      60.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEE 3
        |||
Db      6 SEE 8

RESULT 63
US-08-066-325-155
; Sequence 155, Application US/08066325
; Patent No. 5667967
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Oksenberg, Jorge
; APPLICANT: Bernard, Claude
; TITLE OF INVENTION: T-CELL RECEPTOR VARIABLE TRANSCRIPTS AS DISEASE RELATED MARKER
```

```
;
; NUMBER OF SEQUENCES: 157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/066,325
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5667967tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 690068.408C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-066-325-155

Query Match      60.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEE 3
        |||
Db      6 SEE 8

RESULT 64
US-08-467-264-15
; Sequence 15, Application US/08467264
; Patent No. 5705156
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Fitzgerald, David
; APPLICANT: Chaudhary, Vijay K.
; TITLE OF INVENTION: Pseudomonas Exotoxins of Low Animal
; TITLE OF INVENTION: Cytotoxicity and High Cytocidal Activity
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market plaza, Steuatt Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,264
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/522,182
; FILING DATE: 11-MAY-1990
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/130,322  
FILING DATE: 01-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 15280-125-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-264-15

Query Match 60.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
DB 3 SEE 5

RESULT 65  
US-08-479-532-4  
Sequence 4, Application US/08479532  
Patent No. 5776752  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,532  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
FILING DATE: 04-APR-1991  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5776752 and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-264-15

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-479-532-4

Query Match 60.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
DB 4 EEM 6

RESULT 66  
US-08-455-526-4  
Sequence 4, Application US/08455526  
Patent No. 5789553  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,526  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/297,494  
FILING DATE: 29-AUG-1994  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5789553 and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-455-526-4

Query Match 60.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EEM 4  
DB 4 EEM 6

RESULT 67  
US-08-455-525-4  
; Sequence 4, Application US/08455525  
; Patent No. 5800987  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,525  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/297,494  
; FILING DATE:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No 5800987and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-455-525-4  
  
Query Match 60.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 EEM 4  
Db 4 EEM 6  
  
RESULT 68  
US-08-467-603-66  
; Sequence 66, Application US/08467603  
; Patent No. 5843672  
; GENERAL INFORMATION:  
; APPLICANT: Morgenstern, Jay P.  
; APPLICANT: Kanieczny, Andrzej  
; APPLICANT: Bizindaukas, Christine B.  
; APPLICANT: Brauer, Andrew W.  
; TITLE OF INVENTION: Allergenic Proteins and  
; TITLE OF INVENTION: Peptides from Dog  
; TITLE OF INVENTION: Dander and Uses Therefor

NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,603  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/156,549  
FILING DATE:  
APPLICATION NUMBER: 07/999,712  
FILING DATE: 31-Dec-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-467-603-66  
  
Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 SEE 3  
Db 5 SEE 7  
  
RESULT 69  
US-08-705-660-39  
; Sequence 39, Application US/08705660  
; Patent No. 585683  
; GENERAL INFORMATION:  
; APPLICANT: KESSEE, SUSAN  
; APPLICANT: OBAR, ROBERT  
; APPLICANT: WU, YING-JYE  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
; TITLE OF INVENTION: DETECTION OF CERVICAL CANCER  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Testa, Hurwitz & Thibault  
; STREET: 125 High St.  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/705,660  
; FILING DATE:



CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: GREENHALGH, DUNCAN A  
REGISTRATION NUMBER: 38,678  
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-705-660-39

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 4 SEE 6

RESULT 70  
US-08-466-793-66  
Sequence 66, Application US/084666793  
Patent No. 5891716  
GENERAL INFORMATION:  
APPLICANT: Morgenstern, Jay P.  
APPLICANT: Kanieczny, Andrzej  
APPLICANT: Bizindaukas, Christine B.  
APPLICANT: Brauer, Andrew W.  
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
TITLE OF INVENTION: Peptides from Dog  
TITLE OF INVENTION: Dander and Uses Therefor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,793  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/156,549  
FILING DATE: 22-NOV-1993  
APPLICATION NUMBER: 07/999,712  
FILING DATE: 31-Dec-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

FRAGMENT TYPE: internal  
US-08-466-793-66

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 5 SEE 7

RESULT 71  
US-08-491-861A-66  
Sequence 66, Application US/08491861A  
Patent No. 5939283  
GENERAL INFORMATION:  
APPLICANT: Morgenstern, Jay P.  
APPLICANT: Kanieczny, Andrzej  
APPLICANT: Bizindaukas, Christine B.  
APPLICANT: Brauer, Andrew W.  
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
TITLE OF INVENTION: Dander and Uses Therefor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/491,861A  
FILING DATE: 27-OCT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/999,712  
FILING DATE: 31-Dec-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-491-861A-66

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEE 3  
Db 5 SEE 7

RESULT 72  
US-09-139-491-4  
Sequence 4, Application US/09139491  
Patent No. 6015677  
GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/139,491  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,525  
FILING DATE: 31-MAY-1995  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6015677and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-139-491-4  
Query Match 60.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 EEM 4  
Db 4 EEM 6  
RESULT 73  
US-08-989-045-39  
Sequence 39, Application US/08989045  
Patent No. 6027905  
GENERAL INFORMATION:  
APPLICANT: KEESEE, SUSAN  
APPLICANT: OBAR, ROBERT  
APPLICANT: WU, YING-JYE  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
TITLE OF INVENTION: DETECTION OF CERVICAL CANCER  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA

COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/989,045  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: GREENHALGH, DUNCAN A  
REGISTRATION NUMBER: 38,678  
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-989-045-39  
Query Match 60.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SEE 3  
Db 4 SEE 6  
RESULT 74  
US-09-258-754-233  
Sequence 233, Application US/09258754  
Patent No. 6174687  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
APPLICANT: Pasqualini, Renata  
APPLICANT: Rajotte, Daniel  
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
TITLE OF INVENTION: Membrane Dipeptidase  
FILE REFERENCE: P-LJ 3443  
CURRENT APPLICATION NUMBER: US/09/258,754  
CURRENT FILING DATE: 1999-02-26  
EARLIER APPLICATION NUMBER: 09/042,107  
EARLIER FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 452  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 233  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-258-754-233  
Query Match 60.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 EMP 5  
Db 5 EMP 7  
RESULT 75  
US-09-042-107-233  
Sequence 233, Application US/09042107

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; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 233
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-233

Query Match      60.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 EMP 5
      |||
Db      5 EMP 7

Search completed: November 25, 2003, 20:16:11
Job time : 6.45213 secs
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 6.44149 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-16

Perfect score: 7  
Sequence: 1 KYKLOPE 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	42.9	6	2	S11556 hydrogensulfite re
2	3	42.9	8	2	S16324 hypothetical prote
3	3	42.9	9	2	S77984 cytochrome-c oxida
4	3	42.9	10	1	RHAQ1 gonadolibirin I -
5	3	42.9	10	2	B61218 alpha-gliadin 6Ha
6	3	42.9	11	2	A38590 transforming prote
7	3	42.9	12	2	A35585 cytochrome-c oxida
8	3	42.9	13	2	S57567 T cell receptor V-
9	3	42.9	14	2	PS0371 hypothetical prote
10	3	42.9	14	2	B39111 Ig heavy chain V r
11	3	42.9	15	2	I52734 gene c-Ki-ras prot
12	3	42.9	15	2	PH1762 T cell receptor al
13	3	42.9	15	2	I65478 c-Ki-ras - hamster
14	3	42.9	15	4	I38032 hypothetical WNI/T
15	3	42.9	16	2	PH1778 T cell receptor al
16	3	42.9	17	2	PN0587 tyrosine 3-monooxy
17	3	42.9	17	2	PN0587 ribosomal protein
18	3	42.9	17	2	S20490 photosystem II chl
19	3	42.9	17	2	S50901 chlorophyll a/b-bi
20	3	42.9	17	2	PD0005 very-high-density
21	3	42.9	18	2	PN0149 beta-Gliadin l3 -
22	3	42.9	18	2	S39009 oviductin - golden
23	3	42.9	19	2	C21182 4K prothoracicotro
24	3	42.9	19	2	B39845 pyrB leader peptid
25	3	42.9	19	2	JP0054 ribosomal protein
26	3	42.9	19	2	JP0057 ribosomal protein
27	3	42.9	19	2	S19532 globin - polychaet
28	3	42.9	19	2	I39327 pre-T/NK cell-asso
29	3	42.9	20	2	JP0053 ribosomal protein

apolipoprotein E -  
gamma subunit of p  
hypothetical prote  
schwannomin - mous  
copper resistance  
photosystem I 10.4  
T-cell receptor be  
transferrin - bovi  
alpha-tubulin - Ch  
Ig mu chain D regi  
cytotoxic T-lympho  
hypothalamic hepta  
peptidyl-dipeptida  
glucose isomerase  
ICL2 protein - Par  
large granule L3 c  
hucolin, 75K chain  
Ig heavy chain CRD  
glycoprotein compo  
DNA topoisomerase  
glucuronosyltransf  
neural cell adhesi  
serine/threonine-s  
T-cell receptor be  
major fat-globule  
carnocin U149 - Ca  
Na+-transporting A  
neuropeptide B - b  
tumor-associated a  
hypothetical prote  
dissimilatory sulf  
nitrate reductase  
protein OA300039 -  
inulinase (EC 3.2.  
aspartate transami  
neural cell adhesi  
tocopherol-binding  
gene Tnfrsfow prote  
probable Na+-trans  
Ca2+-transporting  
sperm-activating p  
hutu protein - Kle  
ATPase R1 subunit  
glycine cleavage s  
phosphoenolpyruvat  
331K exoantigen -  
locustamyotropon I  
gene NF2 protein -  
cytokeatin 4 - bo  
spectrin alpha cha  
bone gla protein -  
seminal vesicle pr  
beta-neoendorphin  
ranatachikin B -  
neurokinin A-relat  
pneumadin - human  
pneumadin - rat  
hypothetical 1.3K  
urease (EC 3.5.1.5  
ribosomal protein  
glutathione transf  
hementin (EC 3.4.-  
cytochrome-c oxida  
Ig heavy chain CRD  
T-cell receptor ga  
acetylcholinestera  
collagen alpha 1(V  
enamelin, 22K - bo  
T-cell receptor al  
cytochrome-c oxida  
lysosome-associate

## ALIGNMENTS

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 1

S11556  
hydrogenulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment)  
N:Alternate names: bisulfite reductase; desulfofuscin  
C:Species: Desulfovibrio thermophilus  
C:Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
C:Accession: S11556  
R:Faugue, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; I Blochim. Biophys. Acta 1040, 112-118, 1990  
A:Title: Purification and characterization of bisulfite reductase (desulfofuscin) from  
A:Reference number: S11024; MUID:90335276; PMID:2165817  
C:Accession: S11556  
A:Molecule type: protein  
A:Residues: 1-6 <FAU>  
C:Keywords: oxidoreductase

Query Match 42.9%; Score 3; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3

DB 4 KYK 6

## RESULT 2

S16324  
hypothetical protein 2 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000  
C:Accession: S16324  
R:Ruberti, I.; Sesca, G.; Lucchetti, S.; Morelli, G.  
EMBO J. 10, 1787-1791, 1991  
A:Title: A novel class of plant proteins containing a homeodomain with a closely linked  
A:Reference number: S16323; MUID:91266907; PMID:1675603  
C:Accession: S16324  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-8 <RUB>  
A:Cross-references: EMBL:X58821; NID:G16327; PIDN:CAA41624.1; PID:G579259

Query Match 42.9%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKL 4

DB 3 YKL 5

## RESULT 3

S77984  
cytochrome-c oxidase (EC 1.9.3.1) chain VIa - bigeye tuna (fragment)  
C:Species: Thunnus obesus (bigeye tuna)  
C:Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 30-Jan-1998  
C:Accession: S77984  
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.  
submitted to the Protein Sequence Database, June 1997  
A:Reference number: S77980  
C:Accession: S77984  
A:Molecule type: protein  
A:Residues: 1-9 <ARN>  
A:Experimental source: heart  
C:Genetics:  
A:Genome: nuclear  
C:Function:  
A:Pathway: oxidative phosphorylation; respiratory chain  
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 42.9%; Score 3; DB 2; Length 9;

## RESULT 4

RHAQ1  
gonadoliberin I - American alligator  
N:Alternate names: gonadotropin-releasing hormone I  
C:Species: Alligator mississippiensis (American alligator)  
C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
C:Accession: A60066  
R:Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson Regul. Pept. 33, 105-116, 1991  
A:Title: Primary structure of two forms of gonadotropin-releasing hormone from brains o  
A:Reference number: A60066; MUID:91352338; PMID:1882082  
C:Accession: A60066  
A:Molecule type: protein  
A:Residues: 1-10 <LOV>  
C:Superfamily: gonadoliberin  
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 42.9%; Score 3; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6

DB 7 LQP 9

## RESULT 5

B61218  
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)  
C:Species: Haynaldia villosa, Dasyphyrum villosum  
C:Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Mar-1999  
C:Accession: B61218  
R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafiandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynal  
A:Reference number: A61218; MUID:91315394; PMID:1859356  
C:Accession: B61218  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <SHE>  
C:Keywords: seed; storage protein

Query Match 42.9%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6

DB 8 LQP 10

## RESULT 6

A38590  
transforming protein (Ddras) - slime mold (Dictyostelium discoideum) (fragment)  
C:Species: Dictyostelium discoideum  
C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 30-Sep-1993  
C:Accession: A38590  
R:Esch, R.K.; Firtel, R.A.  
Genes Dev. 5, 9-21, 1991  
A:Title: cAMP and cell sorting control the spatial expression of a developmentally esse  
A:Reference number: A38590; MUID:91115102; PMID:1703508  
C:Accession: A38590  
A>Status: preliminary

A:Molecule type: DNA  
A:Accession: PS0371  
A:Residues: 1-11 <ESC>  
A:Cross-references: GB:Z11804; GB:K02114; GB:X58190

Query Match 42.9%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKL 4  
|||  
Db 4 YKL 6

## RESULT 7

A35585  
Cytokinin-binding factor 1 - durum wheat  
C:Species: Triticum durum (durum wheat)  
C>Date: 21-Sep-1990 #sequence\_revision 21-Sep-1990 #text\_change 30-Sep-1993  
C:Accession: A35585  
R:Brinegar, A.C.; Cooper, G.; Stevens, A.; Hauer, C.R.; Shabanowitz, J.; Hunt, D.F.; Fox  
Proc. Natl. Acad. Sci. U.S.A. 85, 5927-5931, 1988  
A:Title: Characterization of a benzyladenine binding-site peptide isolated from a wheat  
by mass spectrometry.

A:Reference number: A35585; MUID:88320357; PMID:3413067

A:Accession: A35585  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <BRI>

Query Match 42.9%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
|||  
Db 3 LQP 5

## RESULT 8

S57567  
T cell receptor V-J junctional alpha chain region - human (fragment)

C:Species: Homo sapiens (man)  
C>Date: 19-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S57567  
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argast, V.P.  
submitted to the EMBL Data Library, June 1995  
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b

A:Reference number: S57494

A:Accession: S57567  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <BUR>

A:Cross-references: EMBL:Z49949; NID:9887470; PIDN:CAA90220.1; PID:9887471  
C:Keywords: T-cell receptor

Query Match 42.9%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQ 5  
|||  
Db 9 KLQ 11

## RESULT 9

PS0371  
hypothetical protein (psac region) - Synecococcus sp. (fragment)

C:Species: Synecococcus sp.  
C>Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 08-Oct-1999  
C:Accession: PS0371  
R:Rhier, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.  
Gene 112, 123-128, 1992

A:Title: The psac genes of Synecococcus sp. PCC7002 and Cyanophora paradoxa: cloning an

A:Reference number: JS0694; MUID:92201692; PMID:1551590

A:Accession: PS0371

A:Molecule type: DNA

A:Residues: 1-14 <RHI>

A:Cross-references: GB:M86238; NID:9154574; PIDN:AAA27351.1; PID:9552030

Query Match 42.9%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
|||  
Db 12 LQP 14

## RESULT 10

B39111  
Ig heavy chain V region - Pacific hagfish (fragment)

C:Species: Eptatretus stoutii (Pacific hagfish)

C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 16-Aug-1996

C:Accession: B39111

R:Varner, J.; Neame, P.; Litman, G.W.

Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991

A:Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simi

A:Reference number: A39111; MUID:91156684; PMID:2000382

A:Accession: B39111

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <VAR>

C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPE 7  
|||  
Db 11 QPE 13

## RESULT 11

IS2734

gene c-Ki-ras protein - hamster (fragment)

C:Species: Cricetinae gen. sp. (hamster)

C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 28-May-1999

C:Accession: IS2734

R:Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian,

Carcinogenesis 16, 931-939, 1995

A:Title: Differences in molecular biological, biological and growth characteristics bet

A:Reference number: IS2734; MUID:95246257; PMID:7728976

A:Accession: IS2734

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-15 <RES>

C:Genetics:

A:Gene: c-Ki-ras

C:Superfamily: ras transforming protein; translation elongation factor Tu homology

C:Keywords: GTP binding

Query Match 42.9%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKL 4  
|||  
Db 4 YKL 6

## RESULT 12

PH1762.

T cell receptor alpha chain V region (clone 1V alpha 23-1) - human (fragment)

C:Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C;Accession: PH1762  
R;Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A;Reference number: PH1754; MUID:93301585; PMID:8391057  
A;Accession: PH1762  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-15 <POR>

Query Match 42.9%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKL 4  
|||  
Db 10 YKL 12

RESULT 13  
I65478  
c-Ki-ras - hamster (fragment)  
C;Species: Cricetinae gen. sp. (hamster)  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 28-Feb-1997  
C;Accession: I65478  
R;Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian, C.  
Carcinogenesis 16, 931-939, 1995  
A;Title: Differences in molecular biological, biological and growth characteristics between  
A;Reference number: I52734; MUID:95246257; PMID:7728976  
A;Accession: I65478  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-15 <RES>  
A;Cross-references: GB:S77069; NID:g914177  
C;Genetics:  
A;Gene: c-Ki-ras

Query Match 42.9%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKL 4  
|||  
Db 4 YKL 6

RESULT 14  
I38032  
hypoetical MNI/TEL mutant fusion protein type I - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Apr-2000  
C;Accession: I38032  
R;Buils, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.  
Oncogene 10, 1511-1519, 1995  
A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion  
A;Reference number: I38031; MUID:95249265; PMID:7731705  
A;Accession: I38032  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-15 <BU>  
A;Cross-references: EMBL:X5035; NID:g971467; PIDN:CAA59398.1; PID:g971468  
C;Comment: This sequence is the chimeric product of a translocation mutation.  
C;Genetics:  
A;Gene: MNI/ETV6; MNI/TEL  
A;Map position: 22q11/12p13  
C;Keywords: fusion protein

Query Match 42.9%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
|||  
Db 9 LQP 11

RESULT 15  
PH1778  
T cell receptor alpha chain V region (clone IPBL V alpha 24-5) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C;Accession: PH1778  
R;Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A;Reference number: PH1754; MUID:93301585; PMID:8391057  
A;Accession: PH1778  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-16 <POR>

Query Match 42.9%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKL 4  
|||  
Db 12 YKL 14

RESULT 16  
PN0587  
tyrosine 3-monooxygenase (EC 1.14.16.2) type 3 and 4 - Japanese macaque (fragment)  
N;Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase  
C;Species: Macaca fuscata (Japanese macaque)  
C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000  
C;Accession: PN0587  
R;Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.  
Biochem. Biophys. Res. Commun. 195, 158-165, 1993  
A;Title: Increased heterogeneity of tyrosine hydroxylase in humans.  
A;Reference number: PN0575; MUID:93371398; PMID:7689834  
A;Accession: PN0587  
A;Molecule type: genomic RNA  
A;Residues: 1-17 <ICH>  
A;Cross-references: GB:L14801  
A;Experimental source: kidney  
C;Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis.  
C;Superfamily: phenylalanine 4-monooxygenase  
C;Keywords: bipterin; monooxygenase; oxidoreductase

Query Match 42.9%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
|||  
Db 15 LQP 17

RESULT 17  
JP0046  
ribosomal protein L30 - Staphylococcus epidermidis (fragment)  
C;Species: Staphylococcus epidermidis  
C;Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 31-Oct-1997  
C;Accession: JP0046  
R;Ochi, K.  
submitted to JIPID, February 1994  
A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal p  
A;Reference number: JP0042  
A;Accession: JP0046  
A;Molecule type: protein  
A;Residues: 1-17 <OCH>  
C;Superfamily: Escherichia coli ribosomal protein L30



C;Keywords: protein biosynthesis; ribosome

Query Match 42.9%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KIQ 5  
|||  
DB 2 KIQ 4

# RESULT 18

S20490 photosystem II chlorophyll a-binding protein psbB - Chlamydomonas reinhardtii chloroplast

C;Species: chloroplast Chlamydomonas reinhardtii  
C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jul-2000

C;Accession: S20490  
R;Monod, C.; Goldschmidt-Clermont, M.; Rochaix, J.D.  
Mol. Gen. Genet. 231, 449-459, 1992

A;Title: Accumulation of chloroplast psbB RNA requires a nuclear factor in Chlamydomonas

A;Reference number: S20490; MUID:92167965; PMID:1371579  
A;Accession: S20490

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-17 <MON>

A;Cross-references: GB:X64066; GB:S84927; NID:g18199; PID:CAA45421.1; PID:g18200

C;Genetics:

A;Gene: psbB

A;Genome: chloroplast

A;Superfamily: photosystem II chlorophyll a-binding protein psbB

C;Keywords: chloroplast

Query Match 42.9%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3  
|||  
DB 3 KYK 5

# RESULT 19

S50901

chlorophyll a/b-binding protein lhcb4 - spinach (fragment)

N;Alternate names: light-harvesting complex LHClIa protein

C;Species: Spinacia oleracea (spinach)

C;Date: 19-Mar-1997 #sequence\_revision 23-Apr-1999 #text\_change 23-Apr-1999

C;Accession: S50901

R;Walters, R.G.; Ruban, A.V.; Horton, P.

Eur. J. Biochem. 226, 1063-1069, 1994

A;Title: Higher plant light-harvesting complexes LHClIa and LHClIc are bound by dicyclo-

A;Reference number: S50900; MUID:95112835; PMID:7813461

A;Accession: S50901

A;Molecule type: protein

A;Residues: 1-17 <WAL>

C;Superfamily: chlorophyll a/b-binding protein

C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosyn-

Query Match 42.9%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
|||  
DB 4 LQP 6

# RESULT 20

PD0005

very-high-density lipoprotein - sand crayfish (fragment)

N;Alternate names: VHDL

C;Species: Ibacus ciliatus (sand crayfish)

C;Date: 13-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 07-May-1999

C;Accession: PD0005

R;Komatsu, M.; Ando, S.

Biosci. Biotechnol. Biochem. 62, 459-463, 1998

A;Title: A very-high-density lipoprotein with clotting ability from hemolymph of sand c-

A;Reference number: PD0005; MUID:98233268; PMID:9571775

A;Accession: PD0005

A;Molecule type: protein

A;Residues: 1-17 <KOM>

C;Comment: This protein plays an important role in the defense process of crustacea, it

Query Match 42.9%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
|||  
DB 1 LQP 3

# RESULT 21

PN0149

beta-Gliadine 13 - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PN0149

R;Odintsova, T.I.; Egorov, T.A.

Biokhimiia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of

A;Reference number: PN0146; MUID:90283493; PMID:2354218

A;Accession: PN0149

A;Molecule type: protein

A;Residues: 1-18 <ODI>

A;Experimental source: strain K-202

C;Superfamily: gliadin

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
|||  
DB 8 LQP 10

# RESULT 22

S39009

oviductin - golden hamster (fragment)

C;Species: Mesocricetus auratus (golden hamster)

C;Date: 19-Mar-1997 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999

C;Accession: S39009

R;Malette, B.; Bleau, G.

Biochem. J. 295, 437-445, 1993

A;Title: Biochemical characterization of hamster oviductin as a sulphated zona pelluci-

A;Reference number: S39009; MUID:94059981; PMID:8240241

A;Accession: S39009

A;Molecule type: protein

A;Residues: 1-18 <WAL>

C;Keywords: glycoprotein

Query Match

Best Local Similarity 42.9%; Score 3; DB 2; Length 18;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKL 4  
|||  
DB 1 YKL 3

# RESULT 23

C21182

4K prothoracicotropic hormone III - silkworm (fragment)

C;Species: Bombyx mori (silkworm)

C;Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 12-Apr-1995

C:Accession: C21182  
R:Nagasawa, H.; Kataoka, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishizaki, H.; Mizoguchi, S.  
Science 226, 1344-1345, 1984  
A:Title: Amino-terminal amino acid sequence of the silkworm prothoracicotropic hormone:  
A:Reference number: A21182  
A:Accession: C21182  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-19 <NAG>  
C:Superfamily: insulin

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 6  
|||  
DB 8 LQ 10

## RESULT 24

B39845  
pyrB leader peptide - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 12-Dec-1997  
C:Accession: B39845  
R:Quinn, C.L.; Stephenson, B.T.; Switzer, R.L.  
J. Biol. Chem. 266, 9113-9127, 1991  
A:Title: Functional organization and nucleotide sequence of the Bacillus subtilis pyrimidinase gene:  
A:Reference number: A39845; MUID:91225016; PMID:1709162  
A:Accession: B39845  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-19 <QUI>  
A:Cross-references: GB:M59757  
C:Superfamily: unassigned leader peptides

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQ 5  
|||  
DB 5 KLQ 7

## RESULT 25

JP0054  
ribosomal protein L30 - Bacillus alvei (fragment)  
C:Species: Bacillus alvei  
C:Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 28-Oct-1994  
C:Accession: JP0054  
R:Ochi, K.  
submitted to JIPID, February 1994  
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal protein L30:  
A:Reference number: JP0042  
A:Accession: JP0054  
A:Molecule type: protein  
A:Residues: 1-19 <OCH>  
C:Keywords: protein biosynthesis; ribosome

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQ 5  
|||  
DB 2 KLQ 4

## RESULT 26

JP0057  
ribosomal protein L30 - Bacillus brevis (fragment)

C:Species: Bacillus brevis  
C:Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 28-Oct-1994  
C:Accession: JP0057  
R:Ochi, K.  
submitted to JIPID, February 1994  
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal protein L30:  
A:Reference number: JP0042  
A:Accession: JP0057  
A:Molecule type: protein  
A:Residues: 1-19 <OCH>  
C:Keywords: protein biosynthesis; ribosome

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQ 5  
|||  
DB 2 KLQ 4

## RESULT 27

S19532  
Globin - polychaete (Eudistylia vancouveri) (fragment)  
N:Alternate names: chlorocruorin  
C:Species: Eudistylia vancouveri  
C:Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 05-Dec-1998  
C:Accession: S19532  
R:Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O.; J. Mol. Biol. 222, 1109-1129, 1991  
A:Title: Hierarchy of globin complexes. The quaternary structure of the extracellular component:  
A:Reference number: S19532; MUID:92106333; PMID:1762147  
A:Accession: S19532  
A:Molecule type: protein  
A:Residues: 1-19 <QAB>  
A:Experimental source: plume  
C:Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dodecamer; heme; homotetramer; oxygen carrier  
C:Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQ 5  
|||  
DB 11 KLQ 13

## RESULT 28

I39327  
pre-T/NK cell-associated protein 1D12A2 - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I39327  
R:Rames-Goldberg, M.G.; Hori, T.; Mohan-Peterson, S.; Spits, H.; J. Immunol. 151, 5810-5821, 1993  
A:Title: Identification of human pre-T/NK cell-associated genes.  
A:Reference number: I39327; MUID:94044805; PMID:8228263  
A:Accession: I39327  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-19 <RES>  
A:Cross-references: GB:L17325; NID:G306322; PIDN:AAAL6780.1; PID:G306323  
C:Genetics:  
A:Gene: GDB:PTNKAP1  
A:Cross-references: GDB:5507882  
A:Map position: 8p21-8p11.2

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQ 5

Db 13 KLQ 15  
|||

## RESULT 29

JP0053

ribosomal protein L30 - Bacillus macerans (fragment)

C:Species: Bacillus macerans

C&gt;Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 02-Sep-2000

C:Accession: JP0053

R:Ochi, K.

submitted to JIPID, February 1994

A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal p

A:Reference number: JP0042

A:Accession: JP0053

A:Molecule type: protein

A:Residues: 1-20 &lt;OCH&gt;

C:Superfamily: Escherichia coli ribosomal protein L30

C:Keywords: protein biosynthesis; ribosome

Query Match 42.9%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQ 5

|||

Db 2 KLQ 4

## RESULT 30

A05310

apolipoprotein E - dog (fragment)

N:Alternate names: apo-E

C:Species: Canis lupus familiaris (dog)

C&gt;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2003

C:Accession: A05310

R:Weigraeber, K.H.; Troxler, R.F.; Rall, S.C.; Mahley, R.W.

Biochem. Biophys. Res. Commun. 95, 374-380, 1980

A:Reference number: A90221; MUID:81021043; PMID:7417263

A:Accession: A05310

A:Molecule type: protein

A:Residues: 1-20 &lt;WRI&gt;

C:Keywords: chylomicron; HDL; lipid binding; lipid transport; lipoprotein; plasma; VLDL

Query Match 42.9%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPE 7

|||

Db 3 QPE 5

## RESULT 31

A48360

gamma subunit of Protein A - Methylosinus trichosporium (fragment)

C:Species: Methylosinus trichosporium

C&gt;Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999

C:Accession: A48360

R:Cardy, D.L.; Laidler, V.; Salmond, G.P.; Murrell, J.C.

Arch. Microbiol. 156, 477-483, 1991

A:Title: The methane monooxygenase gene cluster of Methylosinus trichosporium: cloning a

A:Reference number: A48360; MUID:92153031; PMID:1785954

A:Contents: OB3b

A:Accession: A48360

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-4 &lt;CAR&gt;

A:Cross-references: GB:S81887; NID:G245213; PIDN:AAB21391.1; PID:G245214

A&gt;Note: sequence extracted from NCBI backbone (NCBIN:81887, NCBI:P:81912)

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 5

|||

Db 2 LQ 3

## RESULT 32

T46627

hypothetical protein c4 - loblolly pine

C:Species: Pinus taeda (loblolly pine)

C&gt;Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000

C:Accession: T46627

R;Chang, S.; Purves, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.

submitted to the EMBL Data Library, July 1995

A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is d

A:Reference number: Z23105

A:Accession: T46627

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-4 &lt;CHA&gt;

A:Cross-references: EMBL:U31309; NID:G974285; PID:G974292

A:Experimental source: strain s6P72xs6PT3; 8 month seedlings

Query Match 28.6%; Score 2; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4

|||

Db 2 KL 3

## RESULT 33

I54357

schwannomin - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999

C:Accession: I54357

R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.

Hum. Mol. Genet. 3, 1075-1079, 1994

A:Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are c

A:Reference number: I54357; MUID:95072570; PMID:7981675

A:Accession: I54357

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-4 &lt;RES&gt;

A:Cross-references: GB:L28838; NID:9454836; PIDN:AAA57150.1; PID:G601923

C:Genetics:

A:Gene: NF2

Query Match 28.6%; Score 2; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7

|||

Db 2 PE 3

## RESULT 34

C41225

copper resistance protein - Pseudomonas syringae pv. tomato (fragment)

C:Species: Pseudomonas syringae pv. tomato

C&gt;Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993

C:Accession: C41225

R;Cha, J.S.; Cooksey, D.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991

A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer me

A:Reference number: A41225; MUID:92020961; PMID:1924351

A:Accession: C41225

A:Status: preliminary

A:Molecule type: protein

A;Residues: 1-5 <CHA>

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4  
||  
Db 3 KL 4

#### RESULT 35

P00689  
Photosystem I 10.4K H1 chain - common tobacco (fragment)  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C;Accession: P00689  
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.  
Plant Physiol. 102, 1259-1267, 1993  
A;Title: Molecular heterogeneity of photosystem I. psad, psae, psaf, psah and psal are  
A;Reference number: P00667; MUID:94105345; PMID:8278548  
A;Accession: P00689  
A;Molecule type: protein  
A;Residues: 1-5 <OBO>  
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KY 2  
||  
Db 1 KY 2

#### RESULT 36

PT0625  
T-cell receptor beta chain V-D-J region (120-28) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0625  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0625  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <PEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 5  
||  
Db 4 LQ 5

#### RESULT 37

A19780  
transferrin - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 18-Jun-1993  
C;Accession: A19780  
R;Brock, J.H.; Esparza, I.; Oliver, R.A.; Spooner, R.L.  
Biochem. Genet. 18, 851-860, 1980  
A;Title: Electrophoretic mobility of N- and C-terminal monoferric fragments of bovine th  
A;Reference number: A19780; MUID:91183891; PMID:7225082  
A;Accession: A19780  
A;Molecule type: protein

A;Residues: 1-6 <BRO>

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7  
||  
Db 2 PE 3

#### RESULT 38

I48126  
alpha-tubulin - Chinese hamster (fragment)  
C;Species: Cricetus griseus (Chinese hamster)  
C;Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 05-Nov-1999  
C;Accession: I48126  
R;Elliot, E.M.; Sarangi, F.; Henderson, G.; Ling, V.  
Can. J. Biochem. Cell Biol. 63, 511-518, 1985  
A;Title: Cloning of 11 alpha-tubulin gene sequences from the genome of Chinese hamster  
A;Reference number: I48126; MUID:86001952; PMID:2931165  
A;Accession: I48126  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-6 <RES>  
A;Cross-references: GB:M25895; NID:9341417; PIDN:AAA74493.1; PID:9516601  
C;Genetics:  
A;Introns: 3/3

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4  
||  
Db 2 KL 3

#### RESULT 39

B33932  
Ig mu chain D region (D23) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 16-Aug-1996  
C;Accession: B33932  
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989  
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-  
A;Reference number: A33932; MUID:89282823; PMID:2499887  
A;Accession: B33932  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-6 <BAC>  
A;Cross-references: GB:M27107  
C;Keywords: immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4  
||  
Db 2 KL 3

#### RESULT 40

I49424  
cytotoxic T-lymphocyte proteinase 3 (EC 3.4.21.-) - western wild mouse (fragment)  
C;Species: Mus spretus (western wild mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C;Accession: I49424  
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.  
Mamm. Genome 5, 349-355, 1994  
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: I48934; MUID:94119082; PMID:8043949  
 A:Accession: I49424  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-6 <RES>  
 A:Cross-references: EMBL:U05745; NID:9497084; PIDN:AAB60481.1; PID:9642831  
 C:Keywords: hydrolase; serine proteinase

Query Match 28.6%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4  
 ||  
 Db 4 KL 5

## RESULT 41

NYPG7  
 hypothalamic heptapeptide - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 23-Aug-1996  
 C:Accession: A01417  
 R:Chang, R.C.-C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, Horm. Metab. Res. 13, 228-232, 1981  
 A:Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-release  
 A:Reference number: A01417; MUID:81213980; PMID:6263778  
 A:Accession: A01417  
 A:Molecule type: protein  
 A:Residues: 1-7 <CHA>  
 C:Superfamily: hypothalamic heptapeptide  
 C:Keywords: hypothalamus

Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YK 3  
 ||  
 Db . 6 YK 7

## RESULT 42

JN0859  
 peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito  
 C:Species: Sarda orientalis (striped bonito)  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C:Accession: JN0859  
 R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T. Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
 A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide  
 A:Reference number: JN0859; MUID:94080036; PMID:7764272  
 A:Accession: JN0859  
 A:Molecule type: protein  
 A:Residues: 1-7 <MAT>  
 A:Experimental source: intestine  
 C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin  
 C:Superfamily: bradykinin-potentiating peptide  
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4  
 ||  
 Db 4 KL 5

## RESULT 43

SI7976  
 glucose isomerase - Thermoanaerobacterium saccharolyticum (fragment)  
 C:Species: Thermoanaerobacterium saccharolyticum

C:Date: 12-Feb-1998 #sequence\_revision 12-Feb-1998 #text\_change 17-Apr-1998  
 C:Accession: SI7976  
 R:Lee, C.; Zeikus, J.G. Biochem. J. 273, 565-571, 1991  
 A:Title: Purification and characterization of thermostable glucose isomerase from Clostr.  
 A:Reference number: SI5119; MUID:91144536; PMID:1996956  
 A:Accession: SI7976  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <LSE>  
 A:Note: the sequence from page 568 is inconsistent with that from page 565 in having 6-  
 A:Note: the source is designated as Thermoanaerobacter strain B6A

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KY 2  
 ||  
 Db 3 KY 4

## RESULT 44

SI1299  
 IL2 protein - Paramesium tetraurelia (fragment)  
 C:Species: Paramesium tetraurelia  
 C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999  
 C:Accession: SI1299  
 R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J. Eur. J. Biochem. 238, 121-128, 1996  
 A:Title: Characterization of centrin genes in Paramesium.  
 A:Reference number: SI1299; MUID:96248429; PMID:8665928  
 A:Accession: SI1299  
 A:Molecule type: protein  
 A:Residues: 1-7 <MAD>  
 A:Experimental source: strain d4-2  
 C:Genetics:  
 A:Genetic code: SGC5

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 Db 2 QP 3

## RESULT 45

PC1316  
 large granule L3 chain - horseshoe crab (Tachypleus tridentatus) (fragment)  
 C:Species: Tachypleus tridentatus  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C:Accession: PC1316  
 R:Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iw J. Biochem. 114, 307-316, 1993  
 A:Title: Separation of large and small granules from horseshoe crab (Tachypleus trident.  
 A:Reference number: PC1309; MUID:94110249; PMID:8282718  
 A:Accession: PC1316  
 A:Molecule type: protein  
 A:Residues: 1-7 <SHI>  
 C:Comment: This protein participates in immobilization of invading microbes.

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 Db 3 QP 4

## RESULT 46

S68004  
hucolin, 75K chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C:Accession: S68004  
R:Edgar, P.F.  
FEBS Lett. 375, 159-161, 1995  
A:Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural  
A:Reference number: S68004; MUID:96087107; PMID:7498469  
A:Accession: S68004  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <EDG>  
  
Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 LQ 5  
||  
6 LQ 7  
  
Db  
  
RESULT 47  
PT0283  
Ig heavy chain CDR3 region (clone 4-94B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0283  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0283  
A:Molecule type: DNA  
A:Residues: 1-7 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotrimer; immunoglobulin  
  
Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 QP 6  
||  
5 QP 6  
  
Db  
  
RESULT 48  
E48394  
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C:Accession: E48394  
R:Mather, I.H.; Banghart, L.R.; Lane, W.S.  
Biochem. Mol. Biol. Int. 29, 545-554, 1993  
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
II-like sequences.  
A:Reference number: A48394; MUID:93250576; PMID:8485470  
A:Accession: E48394  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <MAT>  
A:Experimental source: milk  
A:Note: sequence extracted from NCBI backbone (NCBIP:131450)  
C:Keywords: glycoprotein  
  
Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 PE 7  
||  
||

Db 3 PE 4  
  
RESULT 49  
I48086  
DNA topoisomerase II alpha - Chinese hamster (fragment)  
C:Species: Cricetulus griseus (Chinese hamster)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I48086  
R:Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.  
J. Biol. Chem. 270, 25850-25858, 1995  
A:Title: Molecular cloning and characterization of the promoter for the Chinese hamster  
A:Reference number: I48086; MUID:96029684; PMID:7592770  
A:Accession: I48086  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-7 <RES>  
A:Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232  
  
Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 LQ 5  
||  
6 LQ 7  
  
Db  
  
RESULT 50  
PX0008  
glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)  
N:Alternate names: UDP-glucuronyltransferase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 07-Feb-1997  
C:Accession: PX0008  
R:Yokota, H.; Yuasa, A.; Sato, R.  
J. Biochem. 104, 531-536, 1988  
A:Title: Purification and properties of a form of UDP-glucuronyltransferase from liver  
A:Reference number: PX0008; MUID:89197852; PMID:3149280  
A:Accession: PX0008  
A:Molecule type: protein  
A:Residues: 1-7 <YOK>  
C:Keywords: glucosyltransferase; hexosyltransferase; liver  
  
Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 KL 4  
||  
2 KL 3  
  
Db  
  
RESULT 51  
A39690  
neural cell adhesion molecule, cardiac splice form -, -, - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
C:Accession: A39690  
R:Reyes, A.A.; Small, S.J.; Akeson, R.  
Mol. Cell. Biol. 11, 1654-1661, 1991  
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule m  
A:Reference number: A39690; MUID:91141516; PMID:1996115  
A:Accession: A39690  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr  
A:Molecule type: mRNA  
A:Residues: 1-7 <REY>  
A:Cross-references: GB:M63970  
C:Keywords: cardiac muscle; cell adhesion; heart  
  
Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
||

Db 1 QP 2

# RESULT 52

S58797

C:Species: Rattus norvegicus (Norway rat)

C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 23-Feb-1997

C:Accession: S58797

R:Nagao, Y.

Biochim. Biophys. Acta 1245, 130-143, 1995

A:Title: Expression of c-mos protein in cultured rat spermatogenic cells and evidence th

A:Reference number: S58797; PMID:95383384; PMID:7654761

A:Accession: S58797

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <NAG>

C:Genetics:

A:Gene: c-mos

C:Keywords: phosphotransferase; protein kinase

Query Match 28.6%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 5  
||

Db 6 LQ 7

# RESULT 53

PH0932

T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C:Accession: PH0932

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi

A:Reference number: PH0891; PMID:92078857; PMID:1836012

A:Accession: PH0932

A:Molecule type: mRNA

A:Residues: 1-7 <GO>

A:Experimental source: complete Freund's adjuvant-immunized lymph node

C:Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7  
||

Db 4 PE 5

# RESULT 54

B48394

major fat-globule membrane protein GP 55 - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995

C:Accession: B48394

R:Wather, I.H.; Banghart, L.R.; Lane, W.S.

Biochem. Mol. Biol. Int. 29, 545-554, 1993

A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig

II-like sequences.

A:Reference number: A48394; PMID:93250576; PMID:8485470

A:Accession: B48394

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MAT>

A:Experimental source: milk

A:Note: sequence extracted from NCBI backbone (NCBIP:131444)

Query Match 28.6%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7  
||

Db 3 PE 4

# RESULT 55

A58718

carnocin U149 - Carnobacterium sp. (fragment)

C:Species: Carnobacterium sp.

C:Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998

C:Accession: A58718

R:Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.

Appl. Environ. Microbiol. 58, 1417-1422, 1992

A:Title: Purification and characterization of a new bacteriocin isolated from a Carnoba

A:Reference number: A58718; PMID:92321768; PMID:1622206

A:Accession: A58718

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <STO>

C:Keywords: antibiotic; lanthionine

Query Match 28.6%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
||

Db 5 QP 6

# RESULT 56

S45648

Na+-transporting ATP synthase (EC 3.6.1.-) alpha chain - Acetobacterium woodii (fragment)

N:Alternate names: ATPase alpha chain

C:Species: Acetobacterium woodii

C:Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07-May-1999

C:Accession: S45648

R:Reidlinger, J.; Mueller, V.

Eur. J. Biochem. 223, 275-283, 1994

A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as

A:Reference number: S45648; PMID:94307271; PMID:8033902

A:Accession: S45648

A:Molecule type: protein

A:Residues: 1-3; 4-7 <REI>

A:Experimental source: DSM 1030

C:Keywords: hydrolase

Query Match 28.6%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7  
||

Db 4 PE 5

# RESULT 57

B24749

neuropeptide B - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Aug-2000

C:Accession: B24749

R:Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.

Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985

A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two

A:Reference number: A94074; PMID:86067985; PMID:3865193

A:Accession: B24749  
A:Molecule type: protein  
A:Residues: 1-8 <YAN>  
C:Superfamily: unassigned animal peptides  
C:Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
||  
Db 4 QP 5

## RESULT 58

S43971  
tumor-associated antigen MUT1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000  
C:Accession: S43971  
R:Wandelboim, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.  
Nature 369, 67-71, 1994  
A:Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine  
A:Reference number: S43971; MUID:94217811; PMID:8164742  
A:Accession: S43971  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <MAN>  
C:Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
||  
Db 7 QP 8

## RESULT 59

T10077  
hypothetical protein N - Methylophilus methylotrophus (fragment)  
C:Species: Methylophilus methylotrophus  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C:Accession: T10077  
R:Chistoserdov, A.Y.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.  
J. Bacteriol. 176, 4073-4080, 1994  
A:Title: Organization of the methylamine utilization (mau) genes in Methylophilus methylotrophus  
A:Reference number: Z16936; MUID:94292427; PMID:8021188  
A:Accession: T10077  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-8 <CHA>  
A:Cross-references: EMBL:L26407; NID:g561931; PIDN:AA646955.1; PID:g561933  
A:Experimental source: strain W3A1  
C:Genetics:  
A:Gene: mauN

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 5  
||  
Db 4 LQ 5

## RESULT 60

S63493  
dissimilatory sulfite reductase gamma chain, membrane-bound and soluble - Desulfovibrio  
C:Species: Desulfovibrio desulfuricans  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C:Accession: S63493; S63494  
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.  
Eur. J. Biochem. 233, 873-879, 1995  
A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio  
A:Reference number: S63489; MUID:96085152; PMID:8521853  
A:Accession: S63493  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <STE>  
A:Accession: S63494  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <ST2>

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YK 3  
||  
Db 5 YK 6

## RESULT 61

S68802  
nitrate reductase (NADH) inhibitor - spinach (fragment)  
C:Species: Spinacia oleracea (spinach)  
C:Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
C:Accession: S68802  
R:Bachmann, M.; Huber, J.L.; Liao, P.C.; Gage, D.A.; Huber, S.C.  
FEBS Lett. 387, 127-131, 1996

A:Title: The inhibitor protein of phosphorylated nitrate reductase from spinach (Spinach)  
A:Reference number: S68802; MUID:96244508; PMID:86745533  
A:Accession: S68802  
A:Molecule type: protein  
A:Residues: 1-8 <BAC>  
A:Experimental source: leaves; strain cv. Bloomsdale

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YK 3  
||  
Db 7 YK 8

## RESULT 62

PA0035  
protein QA300039 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C:Accession: PA0035  
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional  
A:Reference number: PA0001  
A:Accession: PA0035  
A:Molecule type: protein  
A:Residues: 1-8 <KAM>  
A:Experimental source: stem

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 5  
||  
Db 1 LQ 2

## RESULT 63

PT0030



inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)  
 N:Alternate names: inulase  
 C:Species: Aspergillus ficuum  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 07-May-1999  
 C:Accession: PT0030  
 R:Etalibi, M.; Baratti, J.C. 1990  
 Agric. Biol. Chem. 54, 61-68, 1990  
 A:Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.  
 A:Reference number: PT0030; MUID:90344234; PMID:1368526  
 A:Accession: PT0030  
 A:Molecule type: protein  
 A:Residues: 1-8 <ETI>  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 Db 5 QP 6

RESULT 64  
 A14683  
 aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragment)  
 N:Alternate names: aspartate aminotransferase, mitochondrial  
 C:Species: Gallus gallus (chicken)  
 C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000  
 C:Accession: A14683  
 R:Wilson, K.J.; Hunziker, P.; Hughes, G.J. 1979  
 FEBS Lett. 108, 98-102, 1979  
 A:Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.  
 A:Reference number: A14683; MUID:80092116; PMID:520566  
 A:Accession: A14683  
 A:Molecule type: protein  
 A:Residues: 1-8 <WIL>  
 C:Keywords: aminotransferase; mitochondrion

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 Db 6 QP 7

RESULT 65  
 C39690  
 neural cell adhesion molecule, cardiac splice form -, -, + - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
 C:Accession: C39690  
 R:Reyes, A.A.; Small, S.J.; Akerson, R. 1991  
 Mol. Cell. Biol. 11, 1654-1661, 1991  
 A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA.  
 A:Reference number: A39690; MUID:91141516; PMID:1996115  
 A:Accession: C39690  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <REV>  
 A:CROSS-references: GB:M63970  
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 Db 1 QP 2

RESULT 66  
 S29272  
 tocopherol-binding protein, 81K - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996  
 C:Accession: S29272  
 R:Nalecz, K.A.; Nalecz, M.J.; Azzi, A. 1992  
 Eur. J. Biochem. 209, 37-42, 1992  
 A:Title: Isolation of tocopherol-binding proteins from the cytosol of smooth muscle A7r5 cells  
 A:Reference number: S29272; MUID:93011150; PMID:1396710  
 A:Accession: S29272  
 A:Molecule type: protein  
 A:Residues: 1-8 <NAL>  
 A:Experimental source: smooth muscle A7r5 cells

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7  
 ||  
 Db 1 PE 2

RESULT 67  
 I57532  
 gene Tnslow protein - rat (fragment)  
 C:Species: Rattus sp. (rat)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: I57532  
 R:Banerjee-Basu, S.; Buonanno, A. 1993  
 Mol. Cell. Biol. 13, 7019-7028, 1993  
 A:Title: cis-acting sequences of the rat troponin I slow gene confer tissue- and developmental regulation  
 A:Reference number: I57532; MUID:94019373; PMID:8413291  
 A:Accession: I57532  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <RES>  
 A:CROSS-references: GB:S66172; MUID:9432603  
 C:Genetics:  
 A:Gene: Tnslow

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7  
 ||  
 Db 2 PE 3

RESULT 68  
 S45651  
 probable Na+-transporting ATP synthase (EC 3.6.1.-) - Acetobacterium woodii (fragment)  
 C:Species: Acetobacterium woodii  
 C:Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07-May-1999  
 C:Accession: S45651  
 R:Reidlinger, J.; Mueller, V. 1994  
 Eur. J. Biochem. 223, 275-283, 1994  
 A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as a  
 A:Reference number: S45648; MUID:94307271; PMID:8033902  
 A:Accession: S45651  
 A:Molecule type: protein  
 A:Residues: 1-8 <REI>  
 A:Experimental source: DSM 1030  
 C:Keywords: hydrolase

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KY 2

```

Db          ||
           6 KY 7

Query Match      28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 69
I64832
Ca2+-transporting ATPase (EC 3.6.3.8) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-Apr-2002
C:Accession: I64832
R;Wu, K.
Am. J. Physiol. 264, 333-341, 1993
A:Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase
A:Reference number: I51892
A:Accession: I64832
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-8 <RES>
A:Cross-references: GB:M99223; NID:G203644; PIDN:AAA40992.1; PID:G203646
C:Genetics:
C:Gene: SERCALB
C:Keywords: hydrolase

Query Match      28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 PE 7
           ||
           2 PE 3

Db

RESULT 70
S19329
sperm-activating peptide SAP - sea urchin (Stomopneustes variolus)
C:Species: Stomopneustes variolus
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Aug-2000
C:Accession: S19329
R;Toshino, K.; Takao, T.; Shimonishi, Y.; Suzuki, N.
FEBS Lett. 294, 179-182, 1991
A:Title: Determination of the amino acid sequence of an intramolecular disulfide linkage
A:Reference number: S19329; MUID:92097763; PMID:1756858
A:Accession: S19329
A:Molecule type: protein
A:Residues: 1-9 <FOS>
A:Superfamily: unassigned animal peptides
F;3-8/Disulfide bonds: #status predicted

Query Match      28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 PE 7
           ||
           4 PE 5

Db

RESULT 71
C36730
hutu protein - Klebsiella pneumoniae (fragment)
C:Species: Klebsiella pneumoniae
C>Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 08-Oct-1999
C:Accession: C36730
R;Schwacha, A.; Bender, R.A.
J. Bacteriol. 172, 5477-5481, 1990
A:Title: Nucleotide sequence of the gene encoding the repressor for the histidine utilization
A:Reference number: A36730; MUID:90368611; PMID:2203754
A:Accession: C36730
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-9 <SCH>
A:Cross-references: GB:M34604; NID:G149203; PIDN:AAA25076.1; PID:G149206

Query Match      28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 KY 2
           ||
           8 KY 9

Db

RESULT 72
D48186
ATPase R1 subunit - wood tobacco (fragment)
C:Species: Nicotiana sylvestris (wood tobacco)
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
C:Accession: D48186
R;De Paeppe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
A:Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase
A:Reference number: A48186; MUID:93317598; PMID:8327463
A:Accession: D48186
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DEI>
A:Experimental source: pollen
A>Note: sequence extracted from NCBI backbone (NCBIP:134871)

Query Match      28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 YK 3
           ||
           8 YK 9

Db

RESULT 73
PS0253
glycine cleavage system protein H - rice (strain Nihonbare) (fragment)
N:Alternate names: glycine decarboxylase complex H protein
C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Feb-1994
C:Accession: PS0253
R;Tsugita, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0253
A:Molecule type: protein
A:Residues: 1-9 <TSU>

Query Match      28.6%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 KY 2
           ||
           8 KY 9

Db

RESULT 74
S55696
phosphoenolpyruvate carboxykinase - Trypanosoma brucei
C:Species: Trypanosoma brucei
C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S55696
R;Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A:Title: Purification and characterization of phosphoenolpyruvate carboxykinase from T.
A:Reference number: S55696; MUID:95284106; PMID:7766679
A:Accession: S55696
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <HUN>
```

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OP 6  
||  
Db 1 QP 2

## RESULT 75

B33098  
231K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum  
C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C:Accession: B33098  
R:Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A:Reference number: A33098  
A:Accession: B33098  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <NIC>

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 5  
||  
Db 2 LQ 3

Search completed: November 25, 2003, 18:28:24  
Job time : 7.44149 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 3.3883 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-16

Perfect score: 7  
Sequence: 1 KYKLOPE 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	42.9	9	1 BUK_CLOPA	P81337 clostridium
2	3	42.9	9	1 COXE_THUOB	P80975 thunnus obe
3	3	42.9	10	1 GONI_ALLMI	P37041 alligator m
4	3	42.9	11	1 CXLI_CONMR	P58807 conus marmo
5	3	42.9	13	1 XCL4_CONMR	P58810 conus marmo
6	3	42.9	15	1 GTS_ASADI	P83246 asaphis dic
7	2	28.6	6	1 OVM_LEPDE	P42985 leptonotars
8	2	28.6	7	1 EIO5_LITRU	P82101 litoria rub
9	2	28.6	7	1 FAR5_HIRME	P42564 hirudo medi
10	2	28.6	7	1 HY7_PIG	P01153 sus scrofa
11	2	28.6	7	1 LANC_CARUI	P36960 carnobacter
12	2	28.6	8	1 NPB_BOVIN	P15507 bos taurus
13	2	28.6	8	1 UHO3_RAT	P56575 rattus norv
14	2	28.6	9	1 ALIO_CARMA	P81813 carcinus ma
15	2	28.6	9	1 FAR3_PENMO	P83318 penaeus mon
16	2	28.6	9	1 FAR4_PENMO	P83319 penaeus mon
17	2	28.6	9	1 FRF1_SARBU	P83350 sarcophaga
18	2	28.6	9	1 HUTU_KLEAE	P12381 klebsiella
19	2	28.6	9	1 LMT3_LOCMI	P41489 locusta mig
20	2	28.6	9	1 RT33_BOVIN	P82926 bos taurus
21	2	28.6	9	1 SAP_STOVA	P24047 stomopneute
22	2	28.6	9	1 UPA7_HUMAN	P30093 homo sapien
23	2	28.6	10	1 COXK_ONCMY	P80332 oncorhynch
24	2	28.6	10	1 FAR5_PANRE	P82660 panagrellus
25	2	28.6	10	1 PNEU_HUMAN	P22103 homo sapien
26	2	28.6	10	1 PNEU_RAT	P21996 rattus norv
27	2	28.6	10	1 PORE_METTM	P80901 methanobact
28	2	28.6	10	1 RL16_ACHLA	P29221 acholeplasm
29	2	28.6	10	1 TKNE_RANCA	P22689 rana cateeb
30	2	28.6	10	1 TKNE_RANRI	P29135 rana ridibu
31	2	28.6	10	1 UPAS_HUMAN	P30091 homo sapien
32	2	28.6	10	1 URE3_MORMO	P17339 morganella
33	2	28.6	10	1 UXA6_CHLTR	P38007 chlamydia t

## ALIGNMENTS

RESULT 1

11	1	EFG_CLOPA	P81350 clostridium
11	1	MHB1_KLEPN	P80580 klebsiella
11	1	MORN_HUMAN	P01163 homo sapien
11	1	TKSN_PSETE	P59072 pseudonaja
11	1	TKN1_PSEGU	P42986 pseudophryn
11	1	TKN1_PPERU	P08612 uperoleia f
11	1	TKN2_PSEGU	P42987 pseudophryn
11	1	TKN3_PSEGU	P42988 pseudophryn
11	1	TKN4_PSEGU	P42989 pseudophryn
11	1	TKN5_PSEGU	P42990 pseudophryn
11	1	TKNA_RANRI	P29207 rana ridibu
11	1	TKND_RANCA	P22591 rana cateeb
11	1	TKN_ELEMO	P01293 eledeone mos
11	1	UF05_MOUSE	P38643 mus musculu
12	1	FAR1_CALVO	P41869 calliphora
12	1	FIF1_SARBU	P83149 sarcophaga
12	1	HEP1_BACSE	P83054 bacteroides
12	1	HS9A_RAT	P82995 rattus norv
12	1	NUD0_SESRO	O24369 sesbania ro
12	1	NUDM_CANFA	P54713 canis famil
12	1	RR16_GINBI	P36207 ginkgo bilo
12	1	TM2A_METMA	P80652 methanosarc
12	1	UR2A_CATCO	P04558 catostomus
12	1	UR2B_CATCO	P04559 catostomus
12	1	UR2B_CYPCA	P04561 cyprinus ca
12	1	UR2_GILMI	P01147 gilllichthys
12	1	UR2_POLSP	P81022 polycodon ep
12	1	UR2_SCYCA	P35490 scyliorhinu
12	1	ACT7_SOYBN	P15987 glycine max
13	1	ADFB_TENMO	P83109 tenebrio mo
13	1	BPPI_BOTJA	P01020 bothrops ja
13	1	CRBL_VESAN	P17233 vespa anali
13	1	CRBL_VESLE	P17235 vespa lew
13	1	CRBL_VESMA	P17232 vespa manda
13	1	CRBL_VESXA	P17234 vespa xanth
13	1	EI22_LITRU	P82098 litoria rub
13	1	EP65_HUMAN	P54963 homo sapien
13	1	GER1_HORVU	P28526 hordeum vul
13	1	GER2_HORVU	P28526 hordeum vul
13	1	HPB9_RANES	P32416 rana escul
13	1	NO40_VICSA	P55961 vicia sativ
13	1	PEDI_HYDAT	P80578 hydra atten
13	1	RPOC_MYCGA	P47716 mycoplasma
13	1	UN12_CLOPA	P81353 clostridium
14	1	CAL1_CALGI	P20728 calotropis
14	1	CRBL_VESOR	P17236 vespa orien
14	1	CXAI_CONCN	P56373 conus conso
14	1	GLGS_SPIOL	P55235 spinacia ol
14	1	KARA_BROPL	P22442 bromelia pl
14	1	MARI_ALTSP	P29399 alteromonas
14	1	MAST_VESBA	P21654 vespa baal
14	1	MAST_VESMA	P04205 vespa manda
14	1	MAST_VESXA	P01515 vespa xanth
14	1	MCRX_METTM	P58815 methanobact
14	1	MCRZ_METTM	P58816 methanobact
14	1	TAT_HVIW2	P12509 human immun
14	1	TAT_HVI28	P12511 human immun
15	1	AFP3_MALPA	P83137 malva parvi
15	1	ARCA_STRPS	P58827 streptococc
15	1	ATP2_PINPS	P81663 pinus pinas
15	1	COXJ_THUOB	P80979 thunnus obe
15	1	FGF1_CANFA	P18651 canis famil
15	1	FKB7_PINPS	P81104 pinus pinas
15	1	IRBP_CRISP	P12665 cricetidae
15	1	LEC1_PSOSC	P22582 psophocarpu
15	1	LEC3_PSOSC	P22583 psophocarpu
15	1	METK_MAIZE	P80616 zea mays (m

BUK\_CLOPA  
ID BUK\_CLOPA STANDARD; PRT; 9 AA.  
AC F81337;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).  
GN BUK.  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl  
phosphate to butyrate (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.  
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Belongs to the acetokinase family.  
DR HAMAP; MF\_00542; -, 1.  
DR InterPro; IPR000890; Acetate kin.  
DR PROSITE; PS01075; ACETATE KINASE 1; PARTIAL.  
DR PROSITE; PS01076; ACETATE\_KINASE\_2; PARTIAL.  
KW Transferase; Kinase.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1104 MW; 05504050572732B CRC64;  
  
Query Match 42.9%; Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 YKL 4  
DB 2 YKL 4  
  
RESULT 2  
COXE\_THUOB STANDARD; PRT; 9 AA.  
AC P80975;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).  
OS Thynnus obesus (Bigeye tuna).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
OC Scombridae; Thunnus.  
OX NCBI\_TaxID=8241;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart;  
RX MEDLINE=97454291; PubMed=9310366;  
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,  
RT "The subunit structure of cytochrome-c oxidase from tuna heart and  
liver.";  
RL Eur. J. Biochem. 248:99-103(1997).  
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
MITOCHONDRIAL ELECTRON TRANSPORT.  
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
c + 2 H(2)O.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.

DR PIR; S77984; S77984.  
DR InterPro; IPR001349; COX6A.  
DR PROSITE; PS01329; COX6A; PARTIAL.  
KW Oxidoreductase; inner membrane; Mitochondrion.  
FT NON\_TER 1  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;  
  
Query Match 42.9%; Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 QPE 7  
DB 3 QPE 5  
  
RESULT 3  
GONL\_ALLMI STANDARD; PRT; 10 AA.  
AC P37041; P20407; (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)  
(Luliberin I).  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
OX NCBI\_TaxID=8496;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=91352338; PubMed=1882082;  
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,  
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;  
RT "Primary structure of two forms of gonadotropin-releasing hormone  
from brains of the American alligator (Alligator mississippiensis).";  
RL Regul. Pept. 33:105-116(1991).  
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the GNRH family.  
DR PIR; A60066; RHAQ1.  
DR InterPro; IPR002012; GNRH.  
DR Pfam; PF00446; GNRH; 1.  
DR PROSITE; PS00473; GNRH; 1.  
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;  
  
Query Match 42.9%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 LOP 6  
DB 7 LOP 9  
  
RESULT 4  
CXLL\_CONMR STANDARD; PRT; 11 AA.  
AC P58807;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lambda-conotoxin CMrVIA.  
OS Conus marmoreus (Marble cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=42752;

```

RN  [1]
RP  SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RX  TISSUE=Venom;
RA  MEDLINE=20564325; PubMed=10988292;
RA  Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA  Seow K.T., Bay B.-H.;
RT  "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT  pattern and protein folding. Isolation and characterization from the
RT  venom of Conus marmoreus.";
RL  J. Biol. Chem. 275:39516-39522(2000).
CC  -1- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -1- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
CC  -1- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
KW  Neurotoxin; Toxin; Hydroxylation.
FT  DISULFID 2 11
FT  DISULFID 3 8
FT  MOD_RES 10 10 HYDROXYLATION.
SQ  SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 2 YKL 4
DB 5 YKL 7

RESULT 5
CXLL4_CONMR
ID CXLL4_CONMR STANDARD; PRT; 13 AA.
AC P5810;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda/chi-conotoxin MrIB (Chi-MrIB).
OS Conus marmoreus (Marble Cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP TISSUE=Venom;
RX MEDLINE=21419681; PubMed=11528421;
RA Sharpe I.A., Gehrman J., Loughnan M.L., Thomas L., Adams D.A.,
RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
RA Lewis R.J.;
RT "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
RT noradrenaline transporter.";
RL Nat. Neurosci. 4:902-907(2001).
CC -1- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- PTM: Exists in two forms, due to cis-trans isomerization at His-
CC 11-Hyp-12.
CC -1- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
DR PDB; 1IEO; 03-APR-02.
DR KW Neurotoxin; Toxin; Hydroxylation; 3D-structure.
FT DISULFID 4 13
FT DISULFID 5 10 HYDROXYLATION.
FT MOD_RES 12 12
SQ SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 2 YKL 4
DB 5 YKL 7

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Db 7 YKL 9

RESULT 6
GTS_ASADI STANDARD; PRT; 15 AA.
ID P83246;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutathione S-transferase (EC 2.5.1.18) (GST class-sigma) (adGST)
DE (Fragment).
OS Asaphis dichotoma.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Tellinoidea; Peamobiidae; Asaphis.
OX NCBI_TaxID=184428;
RN [1]
RP SEQUENCE, FUNCTION, SUBUNIT, MASS SPECTROMETRY, AND CIRCULAR DICHROISM
RP ANALYSIS.
RC TISSUE=Intestine, and Liver;
RX MEDLINE=2213252; PubMed=12139969;
RA Yang H.-L., Nie L.-J., Zhu S.-G., Zhou X.-W.;
RT "Purification and characterization of a novel glutathione S-
RT transferase from Asaphis dichotoma.";
RL Arch. Biochem. Biophys. 403:202-208(2002).
CC -1- FUNCTION: Has a strong specific activity toward 1-chloro-2,4-
CC dinitrobenzene and etharynic acid.
CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -1- SUBUNIT: Homodimer.
CC -1- MASS SPECTROMETRY: MW=23138; METHOD=MALDI.
CC -1- MISCELLANEOUS: In A.dichotoma there are at least two isozymes of
CC glutathione S-transferase.
CC -1- MISCELLANEOUS: Optimal pH is 8.5 with 1-chloro-2,4-dinitrobenzene
CC as the substrate.
CC -1- MISCELLANEOUS: The Km for 1-chloro-2,4-dinitrobenzene and
CC glutathione are 0.68 +/-0.05 and 0.106 +/-0.005 mM, and the Vmax
CC is 0.1446 +/-0.0072 and 0.033 +/-0.002 mmol/min x mg enzyme,
CC respectively.
CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. SIGMA FAMILY.
DR GO; GO:0004364; F:glutathione transferase activity; NAS.
DR GO; GO:0008603; P:glutathione conjugation reaction; NAS.
KW Transferase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1767 MW; CB3E4BF92D3CB0B9 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.5e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 2 YKL 4
DB 3 YKL 5

RESULT 7
OVM_LEPDE STANDARD; PRT; 6 AA.
ID P42385;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Oviductal motility stimulating peptide (LeD-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phyllophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=91271080; PubMed=2052497;
RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,

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RA Proost P., Torrekens S., de Loof A.;  
RT "Isolation, identification and synthesis of novel oviductal motility  
stimulating head peptide in the Colorado potato beetle, Leptinotarsa  
decehlineata.";  
RL Peptides 12:31-36(1991).  
CC -|- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE  
OVIDUCT.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 6 6 AMIDATION.  
SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YK 3  
DB 3 YK 4

RESULT 8  
EI05\_LITRU STANDARD; PRT; 7 AA.  
AC P82101;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 5.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]

RP TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litoria electrica. Comparison with the skin peptides from Litoria  
rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PE 7  
DB 4 PE 5

RESULT 9  
FAR5\_HIRME STANDARD; PRT; 7 AA.  
AC P42564;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRamide-like neuropeptide GGYMRP-amide.  
OS Hirudo medicinalis (Medicinal leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Arthropoda; Hirudini; Hirudiniformes; Hirudinidae; Hirudo.  
OX NCBI\_TaxID=6421;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=92195954; PubMed=1686933;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of RFamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).  
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 858 MW; 69D406B853387810 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KY 2  
DB 3 KY 4

RESULT 10  
HV7\_PIG STANDARD; PRT; 7 AA.  
AC P01153;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last annotation update)  
DE Hypothalamic heptapeptide.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]

RP SEQUENCE, AND SYNTHESIS.  
RX MEDLINE=81213980; PubMed=6263778;  
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,  
RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;  
RT "Isolation, structure and synthesis of a heptapeptide with in vitro  
ACTH-releasing activity from porcine hypothalamus.";  
RL Horm. Metab. Res. 13:228-232(1981).  
DR PIR; A01417; NYPG7.  
SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YK 3  
DB 6 YK 7

RESULT 11  
LANC\_CARUI STANDARD; PRT; 7 AA.  
AC F36960;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lantibiotic carnocin UI49 (Fragment).  
OS Carnobacterium sp. (strain UI49).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium.  
OX NCBI\_TaxID=35782;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=92321768; PubMed=1622206;  
RA Stoffels G., Missen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
RA Nes I.F.;  
RT "Purification and characterization of a new bacteriocin isolated from  
a Carnobacterium sp.";  
RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
CC -|- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).  
KW Antibiotic; Bacteriocin; Lantibiotic.  
FT NON\_TER 7 7  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;



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Query Match      28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 5 QP 6

RESULT 12
NPB_BOVIN
ID NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
characterization of two brain neuropeptides that modulate the action
of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR: B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 4 QP 5

RESULT 13
UH09_RAT
ID UH09_RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleisner K.-P., Scheller C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 4 QP 5

RESULT 14
AL10_CARMA
ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 963 MW; 372D79CDB4776C7 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 3 QP 4

RESULT 15
FAR3_PENMO
ID FAR3_PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP3 (AQPSMRLRF-amide).
OS Penaeus monodon (Pencoid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivuthangkur P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

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Query Match 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 DB 2 QP 3

RESULT 16  
 FAR4 PENMO  
 ID FAR4 PENMO STANDARD; PRT; 9 AA.  
 AC P8319;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRamide-like neuropeptide FLP4 (SQPSMRLRF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,  
 RA Chaiwisutangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk  
 of the giant tiger prawn Penaeus monodon.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MASS SPECTROMETRY: MW=1119.8; METHOD=WALDI.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 SQ SEQUENCE -9 AA; 1121 MW; DA0807340685A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 DB 2 QP 3

RESULT 17  
 FRFL\_SARBU  
 ID FRFL\_SARBU STANDARD; PRT; 9 AA.  
 AC P8350;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neb-FMRamide 1.  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE, AMIDATION, AND FUNCTION.  
 RC TISSUE=CNS;  
 RX MEDLINE=22342733; PubMed=12438685;  
 RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;  
 RT "Identification in *Drosophila melanogaster* of the invertebrate G  
 protein-coupled FMRamide receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
 CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular  
 junctions.  
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 FAMILY.  
 CC Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 KW MOD RES 1 1  
 FT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 DB 1 QP 2

RESULT 18  
 HUTU KLEAE  
 ID HUTU KLEAE STANDARD; PRT; 9 AA.  
 AC P12381;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate  
 dehydratase) (Fragment).  
 GN HUTU  
 OS Klebsiella aerogenes.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=28451;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88198018; PubMed=2834335;  
 RA Newkooop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;  
 RT "Bidirectional promoter in the hut(P) region of the histidine  
 utilization (hut) operons from *Klebsiella aerogenes*.";  
 RL J. Bacteriol. 170:2240-2246(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90368611; PubMed=2203754;  
 RA Schwacha A., Bender R.A.;  
 RT "Nucleotide sequence of the gene encoding the repressor for the  
 histidine utilization genes of *Klebsiella aerogenes*.";  
 RL J. Bacteriol. 172:5477-5481(1990).  
 CC -1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-  
 yl)propanoate = urocanate + H(2)O.  
 CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).  
 CC -1- PATHWAY: Histidine degradation; second step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.

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CC EMBL; M19665; AAA25078.1; -  
 CC EMBL; M34604; AAA25076.1; -  
 DR HAMAP; MF 00577; -; 1.  
 DR InterPro; IPR000193; Urocanase.  
 DR PROSITE; PS01233; UROCANASE; PARTIAL.  
 KW Histidine metabolism; Lyase; NAD.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1140 MW; 970FC41B5325A6C5 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KY 2

```
DB 5 KY 6
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 5 QP 6

RESULT 21
SAP_STOVA
ID_ SAP_STOVA STANDARD; PRT; 9 AA.
AC P24047;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Sperm-activating peptide (SAP).
OS Stomopneustes variolaris (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomeschinidae;
OC Stomopneustes
OC NCBI_TaxID=7663;
RN [1]
RP SEQUENCE, AND DISULFIDE BOND.
RC TISSUE=Egg jelly;
RX MEDLINE=92097763; PubMed=1756858;
RA Yoshino K.-I., Takao T., Shimonishi Y., Suzuki N.;
RT "determination of the amino acid sequence of an intramolecular
RT disulfide linkage-containing sperm-activating peptide by tandem mass
RT spectrometry.";
RL FEBS Lett. 294:179-182(1991).
CC -!- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY
CC THROUGH INTRACELLULAR ALKALINIZATION. TRANSIENT ELEVATIONS OF
CC CAMP, CGMP AND CLACIUM LEVELS IN SPERM CELLS, AND TRANSIENT
CC ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF
CC GUANYLATE CYCLASE.
CC DISULFID 3
FT DISULFID 8
SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;
Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7
DB 4 PE 5

RESULT 22
UPA7_HUMAN
ID_ UPA7_HUMAN STANDARD; PRT; 9 AA.
AC P30093;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.
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DR SWISS-2DPAGE; P30093; HUMAN.
FT NON_TER 1 1
FT UNSURE 5 5
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7
DB 4 PE 5

RESULT 23
COXK_ONCMY STANDARD; PRT; 10 AA.
AC P80332;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE Cytochrome c oxidase polypeptide Viia-heart (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=942717150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR PIR; S43631; S43631.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1174 MW; 4C8D81CAFAF772C3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 9 KL 10

RESULT 24
FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82650;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
Maule A.G.;

RT "Isolation, characterization and pharmacology of RMRFamide-related
peptides (FarPe) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1132 MW; CB13B4C9D776C76D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 5 QP 6

RESULT 25
PNEU_HUMAN STANDARD; PRT; 10 AA.
AC P22103;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: ANTI-DIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
DR PIR; B33143; B33143.
DR GO; GO:0030103; P:vasopressin secretion; NAS.
KW Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 5 KL 6

RESULT 26
PNEU_RAT STANDARD; PRT; 10 AA.
AC P21996;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNM).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
```

CC -!- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.  
DR PIR; A33143; A33143.  
KW Amidation.  
FT MOD\_RES 10 10 AMIDATION  
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KL 4  
DB 5 KL 6  
RESULT 27  
PORB\_METTM STANDARD; PRT; 10 AA.  
AC P80901;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase  
beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)  
DE (Fragment).  
GN PORB.  
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=79929;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=97261844; PubMed=9108259;  
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;  
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases  
in Methanobacterium thermoautotrophicum.";  
RL Eur. J. Biochem. 244:862-868(1997).  
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-  
CoA + CO(2) + reduced ferredoxin.  
CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE  
GAMMA CHAIN.  
CC -!- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature  
of 80 degrees Celsius.  
KW Oxidoreductase.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1232 MW; 167011DAP6DB0760 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 PE 7  
DB 4 PE 5  
RESULT 28  
RL16\_ACHLA STANDARD; PRT; 10 AA.  
AC P29221;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE 50S ribosomal protein L16 (Fragment).  
GN rPLP.  
OS Achleplasma laidlawii.  
OC Bacteria; Firmicutes; Mollicutes; Achleplasmatales;  
OC Achleplasmataceae; Achleplasma.  
OX NCBI\_TaxID=2148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92210505; PubMed=1556079;  
RA Lim P.O., Sears B.B.;

RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like  
organism and Achleplasma laidlawii deduced from two ribosomal protein  
gene sequences.";  
RL J. Bacteriol. 174:2606-2611(1992).  
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS  
LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER  
(BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M74771; AAA21914.1; -.  
DR PIR; F41839; F41839.  
DR InterPro; IPR000114; Ribosomal L16.  
DR PROSITE; PS00586; RIBOSOMAL\_L16\_1; PARTIAL.  
DR PROSITE; PS00701; RIBOSOMAL\_L16\_2; PARTIAL.  
KW Ribosomal protein; rRNA-binding.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KY 2  
DB 8 KY 9  
RESULT 29  
TKNB\_RANCA STANDARD; PRT; 10 AA.  
AC P22689;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ranatachikin B (RTK B).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RX MEDLINE=91254337; PubMed=2043143;  
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
brain and intestine.";  
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=94023216; PubMed=8210506;  
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and  
intestine.";  
RL Regul. Pept. 46:81-88(1993).  
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
MUSCLES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
CC PIR; B61033; B61033.  
DR InterPro; IPR002040; Tachykinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation.

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FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1210 MW; 917E556B59D5B5B5 CRC64;

Query Match
Best Local Similarity 28.6%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YK 3
   ||
Db 1 YK 2

RESULT 30
TKNB_RANRI
ID TKNB_RANRI STANDARD; PRT; 10 AA.
AC F29135;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurokinin A.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine; PubMed=1332683;
RX MEDLINE=93075037;
RA Wang Y., Badgery-Parker T., Lovas S., Chartrel N., Vaudry H.,
RA Burcher E., Conlon J.M.;
RT "Primary structure and receptor-binding properties of a neurokinin A-
RT related peptide from frog gut.";
RL Biochem. J. 287:827-832(1992).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S27178; S27178.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION
SQ SEQUENCE 10 AA; 1160 MW; 526B407059D5B5AA7 CRC64;

Query Match
Best Local Similarity 28.6%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
   ||
Db 2 KL 3

RESULT 31
UPA5_HUMAN
ID UPA5_HUMAN STANDARD; PRT; 10 AA.
AC P30091;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
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RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON_TER 1 1
FT VARIANT 9 9 G -> Y.
FT /FTIG=VAR_000002.
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match
Best Local Similarity 28.6%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
   ||
Db 3 QP 4

RESULT 32
URE3_MORMO
ID URE3_MORMO STANDARD; PRT; 10 AA.
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
DE amidohydrolase) (Fragment).
GN UREA.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
DR PIR; C35389; C35389.
KW Hydrolase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match
Best Local Similarity 28.6%; Score 2; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7
   ||
Db 6 PE 7

RESULT 33
UXA6_CHLTR
ID UXA6_CHLTR STANDARD; PRT; 10 AA.
AC P38007;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
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OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
DR Siena-2DPAGE; P38007; -
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1243 MW; DAD39A3330485339 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KY 2
DB 4 KY 5

RESULT 34
EFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Fleggsrud R., Skjoldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71FD9C33B17 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KY 2
DB 1 KY 2

RESULT 35
MHBI_KLEPN STANDARD; PRT; 11 AA.
AC P80580;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).

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GN MHBI.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE.
RX MEDLINE=96349117; PubMed=8760924;
RA Robson N.D., Parrott S., Cooper R.A.;
RT "In vitro formation of a catabolic plasmid carrying Klebsiella
RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-
RT hydroxybenzoate.";
RL Microbiology 142:2115-2120(1996).
CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
KW Isomerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 2 KL 3

RESULT 36
MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuroepitope (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuroepitope, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuroepitope, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
CC IN THE G2/MITOSIS TRANSITION.

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CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA  
 CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED  
 CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS  
 CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.

DR PIR; A01427; YHRT.  
 DR PIR; A93900; YHXA.  
 DR PIR; B01427; YHUU.  
 DR PIR; B93900; YHJPHY.  
 DR PIR; C01427; YHBO.

DR GK; P01163; -.  
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1  
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 DB 1 QP 2

RESULT 37  
 NXSN PSETE STANDARD; PRT; 11 AA.  
 AC P59072;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).  
 OS Pseudonaja textilis (Eastern brown snake).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Elapidae; Acanthophiinae; Pseudonaja.  
 OX NCBI\_TaxID=8673;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99449602; PubMed=10518793;  
 RA Gong N.L., Armugam A., Jayaseelan K.;  
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA  
 RT cloning, expression and protein characterization.";  
 RL Eur. J. Biochem. 265:982-989(1999).  
 CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic  
 CC acetylcholine receptors (nAChR).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.  
 CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.  
 CC -!- SIMILARITY: Belongs to the snake toxin family.  
 DR InterPro; IPR003571; Snake toxin.  
 DR PROSITE; PS00272; SNAKE\_TOXIN; PARTIAL.  
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;  
 FT UNSURE 3 3  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1319 MW; 0D1EFC081B58732B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YK 3  
 DB 4 YK 5

RESULT 38  
 TKNI\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42986;  
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-1 (PG-KI).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guntheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; B60409; B60409.  
 DR InterPro; IPR003580; Protachykinin.  
 DR InterPro; IPR002040; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 11 11  
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9C81AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 DB 1 QP 2

RESULT 39  
 TKNI\_UPERU STANDARD; PRT; 11 AA.  
 AC P08612;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Uperolein.  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=75131227; PubMed=1120493;  
 RA Anastasi A., Erspamer V., Endean R.;  
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring  
 RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";  
 RL Experientia 31:394-395(1975).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.



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DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 1 QP 2

RESULT 40
TKN2_PSEGU
ID TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP TISSUE=Skin secretion;
RC MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri."
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: D60409; C60409.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CBIAB7 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 1 QP 2

RESULT 41
TKN3_PSEGU
ID TKN3_PSEGU STANDARD; PRT; 11 AA.

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AC P42988;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-III (PG-KIII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP TISSUE=Skin secretion;
RC MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri."
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: D60409; D60409.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 1 QP 2

RESULT 42
TKN4_PSEGU
ID TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP TISSUE=Skin secretion;
RC MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri."
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; E60409; E60409.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 1 QP 2

RESULT 43
TKN5_PSEGU
ID TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).
OS Pseudophryne guentheri (Guenther's coadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304 (1990).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7
DB 4 PE 5

RESULT 45
TKND_RANCA
ID TKND_RANCA STANDARD; PRT; 11 AA.
AC P22691;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin D (RTK D).
OS Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595 (1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";
RL Regul. Pept. 46:81-88 (1993).

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RESULT 44
TKNA_RANRI
ID TKNA_RANRI STANDARD; PRT; 11 AA.
AC P29207;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ranakinin (Substance-P-related peptide).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091 (1991).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro; IPR003580; Protachykinin.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7
DB 4 PE 5

RESULT 45
TKND_RANCA
ID TKND_RANCA STANDARD; PRT; 11 AA.
AC P22691;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin D (RTK D).
OS Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595 (1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";
RL Regul. Pept. 46:81-88 (1993).

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CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
CC MUSCLES.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR; D61033; D61033.  
DR InterPro; IPR002040; Tachykinin.  
DR PROSITE; PS00267; TACHYKININ; FALSE NEG.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION  
SQ SEQUENCE 11 AA; 1350 MW; 3A34256C9D40B07 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 PE 7  
DB 4 PE 5  
  
RESULT 46  
TKN\_ELEMO STANDARD; PRT; 11 AA.  
ID TKN\_ELEMO  
AC P01293;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Eledoisin.  
OS Eledone moschata (Musky octopus) (Ozaena moschata), and  
OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.  
OX NCBI\_TaxID=6641, 102876;  
RN [1]  
RP SEQUENCE.  
RA Anastasi A., Erespamer V.;  
RT "The isolation and amino acid sequence of eledoisin, the active  
RT endecapeptide of the posterior salivary glands of Eledone.";  
RL Arch. Biochem. Biophys. 101:56-65(1963).  
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
CC MUSCLES.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR; A01561; EOCC.  
DR PIR; B01561; EOCC.  
DR PDB; 1MXQ; 18-FEB-03.  
DR InterPro; IPR002040; Tachykinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;  
KW 3D-structure.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION  
SQ SEQUENCE 11 AA; 1206 MW; 570D7C2595CDDAA3 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 QP 6  
DB 1 QP 2  
  
RESULT 47  
UF05\_MOUSE STANDARD; PRT; 11 AA.  
ID UF05\_MOUSE  
AC F38643;  
DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
RT using preparative two-dimensional gel electrophoresis";  
RL Electrophoresis 15:735-745(1994).  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.5, ITS MW IS: 48 kDa.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAF6 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KY 2  
DB 1 KY 2  
  
RESULT 48  
FARI\_CALVO STANDARD; PRT; 12 AA.  
ID FARI\_CALVO  
AC P41869;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Callimyramide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated callimyramides) from the blowfly  
RT Calliphora vomitoria";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; E44787; E44787.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 12 12 AMIDATION  
SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 QP 6  
DB 4 QP 5  
  
RESULT 49  
FIFI\_SARBU STANDARD; PRT; 12 AA.  
ID FIFI\_SARBU  
AC P83349;  
DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE, AMIDATION, AND FUNCTION.  
RC TISSUE=CNS;  
RA MEDLINE=22342733; PubMed=12438685;  
RX Meeusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;  
RT "Identification in Drosophila melanogaster of the invertebrate G  
protein-coupled FMR1-like receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular  
CC junctions.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE FMRP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 12 12  
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 5 QP 6  
DB 4 QP 5  
  
RESULT 50  
HEP1\_BACSE STANDARD; PRT; 12 AA.  
AC P83054;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Heparin lyase (EC 4.2.2.7) (Heparin eliminase) (Heparinase)  
(Fragment).  
OS Bacteroides stercoris.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=46506;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=HJ-15;  
RX MEDLINE=20381043; PubMed=10920269;  
RA Kim B.-T., Kim W.-S., Kim Y.-S., Linhardt R.J., Kim D.-H.;  
RT "Purification and characterization of a novel heparinase from  
Bacteroides stercoris HJ-15.";  
RL J. Biochem. 128:323-328(2000).  
CC -!- FUNCTION: Degrades heparin and heparan sulfate.  
CC CATALYTIC ACTIVITY: Eliminative cleavage of polysaccharides  
containing 1,4-linked glucuronate or iduronate residues and 1,4-  
alpha-linked 2-sulfoamino-2-deoxy-6-sulfo-D-glucose residues to  
give oligosaccharides with terminal 4-deoxy-alpha-D-gluc-4-  
enuronoyl groups at their non-reducing ends.  
CC -!- ENZYME REGULATION: Inhibited by cupric ion, lead and some agents  
that modify histidine and cysteine residues. Activated by KCL and  
by reducing agents, such as dithiothreitol and 2-  
mercaptoethanol.  
CC -!- PTM: The N-terminus is blocked.  
CC -!- MISCELLANEOUS: The enzyme has an isoelectric point of 8.7. Its  
optimum pH is 7.2 and the optimum temperature is 45 degrees  
Celsius.  
KW Lyase; Heparin-binding.  
FT NON\_TER 1 1  
FT NON\_TER 12 12

SQ SEQUENCE 12 AA; 1381 MW; CD9CCD8B98F6D72D CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 4 LQ 5  
DB 6 LQ 7  
  
RESULT 51  
HS9A\_RAT STANDARD; PRT; 12 AA.  
ID HS9A\_RAT  
AC P8295;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Heat shock protein HSP 90-alpha (Fragment).  
GN HSPCA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=21589773; PubMed=11732320;  
RA Langer T., Fasold H.;  
RT "Isolation and quantification of the heat shock protein 90 alpha and  
beta isoforms from rat liver.";  
RL Protoplasma 218:54-56(2001).  
CC -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY  
(BY SIMILARITY).  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.  
DR InterPro; IPR001404; Hsp90.  
KW PROSITE; PS00298; HSP90; PARTIAL.  
FT MOD\_RES 4 4  
FT MOD\_RES 6 6  
FT MOD\_RES 12 12  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B5 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 6 PE 7  
DB 1 PE 2  
  
RESULT 52  
N040\_SESRO STANDARD; PRT; 12 AA.  
ID N040\_SESRO  
AC O24369;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Early nodulin 40.  
GN ENOD40.  
OS Sesbania rostrata.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.  
OX NCBI\_TaxID=3895;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Stem nodules;

RX MEDLINE=98281575; PubMed=9620265;  
 RA Corich V., Goormachtig S., Lievens S., van Montagu M., Holsters M.;  
 RT "Patterns of ENOD40 gene expression in stem-borne nodules of Sesbania  
 RL rostrata.";  
 CC Plant Mol. Biol. 37:67-76(1998).  
 CC -!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT  
 CC GROWTH REGULATOR THAT ALTERS PHYTHORMONE RESPONSES (BY  
 CC SIMILARITY).  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE  
 CC DEVELOPMENT.  
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 CC -----  
 CC EMBL; Y12714; CAA73252.1; -.  
 KW Nodulation.  
 SQ SEQUENCE 12 AA; 1418 MW; 3C6955187CB326C3 CRC64;  
  
 Query Match 28.6%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 3 KL 4  
 DB 2 KL 3  
  
 RESULT 53  
 NUDM\_CANFA STANDARD; PRT; 12 AA.  
 ID NUDM\_CANFA  
 AC P54713;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 42 kDa subunit (EC 1.6.5.3)  
 DE (EC 1.6.9.3) (Complex 1-42KD) (CI-42KD) (Fragment).  
 GN NDUFA10.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
 CC TO BE UBIQUINONE.  
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
 CC -!- COFACTOR: Binds 1 FAD per subunit.  
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.  
 CC THIS A COMPONENT OF THE HYDROPHOBIC PROTEIN FRACTION.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 DR HSC-2DPAGE; P54713; DOG.  
 KW Oxidoreductase; NAD; Ubiquinone; Flavoprotein; FAD; Mitochondrion.  
 FT NON TER 12  
 FT NON TER 12  
 SQ SEQUENCE 12 AA; 1284 MW; 3CCD4E2B36EDD737 CRC64;  
  
 Query Match 28.6%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 LQ 5

Db 1 LQ 2  
 RESULT 54  
 RRI6\_GINBI STANDARD; PRT; 12 AA.  
 ID RRI6\_GINBI  
 AC P36207;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Chloroplast 30S ribosomal protein S16 (Fragment).  
 GN RPS16.  
 OS Ginkgo biloba (Ginkgo).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.  
 OX NCBI\_TaxID=3311;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95094313; PubMed=8001171;  
 RA Richard M., Tremblay C., Bellemare G.;  
 RT "Chloroplastic genomes of Ginkgo biloba and Chlamydomonas moewusii  
 RT contain a chlB gene encoding one subunit of a light-independent  
 RT protochlorophyllide reductase.";  
 RL Curr. Genet. 26:159-165(1994).  
 CC -!- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC -----  
 CC EMBL; U01531; AAA66977.1; -.  
 DR HAMAP; MF 00385; -; 1.  
 DR InterPro: IPR000307; Ribosomal\_S16.  
 DR PROSITE; P500732; RIBOSOMAL\_S16; 1.  
 KW Ribosomal protein; Chloroplast.  
 FT NON TER 12  
 FT NON TER 12  
 SQ SEQUENCE 12 AA; 1488 MW; 6700EDAF9D033734 CRC64;  
  
 Query Match 28.6%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 3 KL 4  
 DB 3 KL 4  
  
 RESULT 55  
 TM2A\_METMA STANDARD; PRT; 12 AA.  
 ID TM2A\_METMA  
 AC P8052;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit  
 DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M  
 DE methyltransferase 28 kDa subunit) (Fragment).  
 DE Methanosarcina mazei (Methanosarcina frisia).  
 OS Methanosarcina mazei (Methanosarcina frisia).  
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;  
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2209;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;  
 RX MEDLINE=96370840; PubMed=8774736;  
 RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;  
 RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:



RESULT 59  
UR2\_GILMI  
ID UR2\_GILMI STANDARD; PRT; 12 AA.  
AC P01147;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Urotensin II (U-II) (UII).  
OS Gillichthys mirabilis (Long-jawed mudsucker).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidae;  
OC Gobiidae; Gillichthys.  
OX NCBI\_TaxID=8222;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81054904; PubMed=6107911;  
RA Pearson D., Shively J.E., Clark B.R., Geschwind I.I., Barkley M.,  
RA Nishioka R., Bern H.A.;  
RT "Urotensin II: a somatostatin-like peptide in the caudal  
RT neurosecretory system of fishes."  
RL Proc. Natl. Acad. Sci. U.S.A. 77:5021-5024(1980).  
CC -!- FUNCTION: UROSENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY  
CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A  
CC CORTICOTROPIN-RELEASING FACTOR.  
CC -!- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.  
DR PIR; A01409; UOGM2.  
DR PIR; S42765; S42765.  
DR InterPro; IPR001483; Urotensin\_II.  
DR Pfam; PF02083; Urotensin\_II; 1.  
DR PROSITE; PS00984; UROSENSIN\_II; 1.  
KW Hormone.  
FT DISULFID 6 11  
SQ SEQUENCE 12 AA; 1364 MW; 969BF9892679CEBA CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KY 2  
DB |||  
9 KY 10

RESULT 60  
UR2\_POLSP  
ID UR2\_POLSP STANDARD; PRT; 12 AA.  
AC P81022;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Urotensin II (U-II) (UII).  
OS Polyodon spathula (North American paddlefish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;  
OC Polyodon.  
OX NCBI\_TaxID=7913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spinal cord;  
RX MEDLINE=96051494; PubMed=8536944;  
RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;  
RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea  
RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon  
RT spathula)."  
RL Gen. Comp. Endocrinol. 99:323-332(1995).  
CC -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A  
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH  
CC MUSCLE STIMULATION.  
CC -!- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.  
DR InterPro; IPR001483; Urotensin\_II.  
DR Pfam; PF02083; Urotensin\_II; 1.

RESULT 61  
UR2\_SCVCA  
ID UR2\_SCVCA STANDARD; PRT; 12 AA.  
AC P35490;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Urotensin II (U-II) (UII).  
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
OC Scyliorhinidae; Scyliorhinus.  
OX NCBI\_TaxID=7830;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Spinal cord;  
RX MEDLINE=92319231; PubMed=1620290;  
RA Conlon J.M., O'Harte F., Smith D.D., Balmert R.J., Hazen N.;  
RT "Purification and characterization of urotensin II and parvalbumin  
RT from an elasmobranch fish, Scyliorhinus canicula (common dogfish)."  
RL Neuroendocrinology 55:230-235(1992).  
CC -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A  
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH  
CC MUSCLE STIMULATION.  
CC -!- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.  
DR InterPro; IPR001483; Urotensin\_II.  
DR Pfam; PF02083; Urotensin\_II; 1.  
DR PROSITE; PS00984; UROSENSIN\_II; 1.  
KW Hormone.  
FT DISULFID 6 11  
SQ SEQUENCE 12 AA; 1526 MW; 804729FD579CEBA CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KY 2  
DB |||  
9 KY 10

RESULT 62  
ACT7\_SOYBN  
ID ACT7\_SOYBN STANDARD; PRT; 13 AA.  
AC P15987;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Actin 7 (Fragment).  
GN SACT7.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Wayne;  
RX MEDLINE=91346640; PubMed=2102831;

Pearson L., Meagher R.B.;  
RT "Diverse soybean actin transcripts contain a large intron in the 5'  
RT untranslated leader: structural similarity to vertebrate muscle actin  
genes.";  
RL Plant Mol. Biol. 14:513-526(1990).  
CC -|- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED  
CC IN ALL EUKARYOTIC CELLS.  
CC -|- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN  
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,  
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.  
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -|- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.  
CC -|- SIMILARITY: Belongs to the actin family.  
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DR EMBL; X17120; CAA34980.1; -.  
DR PIR; S15755; S15755.  
DR InterPro; IPR004001; Actin.  
DR InterPro; IPR004000; Actin-like.  
DR PROSITE; PS00406; ACTINS\_1; PARTIAL.  
DR PROSITE; PS00432; ACTINS\_2; PARTIAL.  
DR PROSITE; PS01132; ACTINS\_ACT LIKE; PARTIAL.  
KW Structural protein; Multigene family.  
FT NON TER 13  
FT SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 QP 6  
DB 8 QP 9  
  
RESULT 63  
ADFB\_TENNO STANDARD; PRT; 13 AA.  
ID ADFB\_TENNO  
AC P83109;  
DT 15-SEP-2003 (Rel. 42, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Antidiuretic factor B (ADFB).  
OS Tenebrio molitor (Yellow mealworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Tenebrionidae; Tenebrio.  
OX NCBI\_TaxID=7067;  
RN [1]  
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND  
RP SYNTHESIS.  
RC TISSUE=Head;  
RX MEDLINE=22465067; PubMed=12576082;  
RA Eigenheer R.A., Wihart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,  
RA Hull J.J., Schooley D.A.;  
RT "Isolation, identification and localization of a second beetle  
RT antidiuretic peptide.";  
RL Peptides 24:27-34(2003).  
CC -|- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses  
CC CGMP as second messenger. May function as an antidiuretic  
CC hormone.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two  
CC pairs of bilaterally symmetrical cells in the protocerebrum.  
CC -|- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI.

KW Neuropeptide; Hormone.  
SQ SEQUENCE 13 AA; 1562 MW; 0240A4504B8A632B CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 YK 3  
DB 6 YK 7  
  
RESULT 64  
BP1\_BOTJA STANDARD; PRT; 13 AA.  
ID BP1\_BOTJA  
AC P01020; P30421;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S3.1 (13A). (Angiotensin-converting  
DE enzyme inhibitor V-9).  
OS Bothrops jararaca (Jararaca), and  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724, 8723;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=B.jararaca; TISSUE=Venom;  
RX MEDLINE=72118526; PubMed=4334402;  
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,  
RA Kocy O.;  
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops  
RT jararaca. Isolation, elucidation of structure, and synthesis.";  
RL Biochemistry 10:4033-4039(1971).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=B.insularis; TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -|- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; A01253; XAVI9B.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1  
FT SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;  
SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;  
  
Query Match 28.6%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 PE 7  
DB 9 PE 10  
  
RESULT 65  
CRBL\_VESAN STANDARD; PRT; 13 AA.  
ID CRBL\_VESAN  
AC P17233;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vespid chemotactic peptide A (VESCP-A).  
OS Vespa analis (Hornet).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;



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OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7449;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA Fujino M.;
RL (In) Munekata E. (eds.);
RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
RL Osaka (1984).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1386 MW; C85554365DF9233D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 7 KL 8

RESULT 66
CRBL_VESLE
ID CRBL_VESLE STANDARD; PRT; 13 AA.
AC P17235;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespil chemotactic peptide L (VESCP-L).
OS Vespa lewisii (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7452;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (In) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1384 MW; C850402B8819233D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 7 KL 8

RESULT 67
CRBL_VESMA
ID CRBL_VESMA STANDARD; PRT; 13 AA.
AC P17232;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespil chemotactic peptide M (VESCP-M).
OS Vespa mandarinia (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7446;

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RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA Fujino M.;
RL (In) Munekata E. (eds.);
RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
RL Osaka (1984).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1384 MW; 2650402B9DF92338 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 7 KL 8

RESULT 68
CRBL_VESXA
ID CRBL_VESXA STANDARD; PRT; 13 AA.
AC P17234;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespil chemotactic peptide X (VESCP-X).
OS Vespa xanthoptera (Japanese hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7448;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (In) Izumiya N. (eds.);
RL Peptide chemistry 1994, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 7 KL 8

RESULT 69
E122_LITRU
ID E122_LITRU STANDARD; PRT; 13 AA.
AC P82058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.

```

RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645 (1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1598 MW; C1808EF3B357322 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 Db 9 QP 10

RESULT 70  
 EP65\_HUMAN STANDARD; PRT; 13 AA.  
 ID EP65\_HUMAN  
 AC P54963;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Erythrocyte 65 kDa protein (P65) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.  
 RX MEDLINE=90004678; PubMed=2507249;  
 RA Hart G.W., Haltiwanger R.S., Holt G.D., Kelly W.G.;  
 RT "Nucleoplasmic and cytoplasmic glycoproteins.";  
 RL Ciba Found. Symp. 145:102-118 (1989).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 DR GO: GO:0005737; Cytoplasm; NAS.  
 KW Glycoprotein.  
 FT NON\_TER 1 1  
 FT CARBOHYD 2 2 O-LINKED (GLCNAC).  
 FT NON\_TER 13 13  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1300 MW; D08873344C61A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 Db 6 QP 7

RESULT 71  
 GER1\_HORVU STANDARD; PRT; 13 AA.  
 ID GER1\_HORVU  
 AC P28525;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Germin GSI (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Harkman W.J., Tao H.P., Tanaka C.K.;

RT "Germin-like polypeptides increase in barley roots during salt  
 stress.";  
 RL Plant Physiol. 97:366-374 (1991).  
 CC -1- FUNCTION: MAY PLAY A ROLE IN ALTERING THE PROPERTIES OF CELL  
 CC WALLS DURING GERMINATIVE GROWTH.  
 CC -1- SUBUNIT: OLIGOMER (BELIEVED TO BE A PENTAMER BUT PROBABLY  
 CC HEXAMER) (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: SOLUBLE, MICROSMAL AND CELL WALL FRACTIONS.  
 CC -1- TISSUE SPECIFICITY: ROOTS AND COLEOPTILE. IN ROOTS, PRESENT IN  
 CC THE MATURE REGION, BUT NOT IN THE TIP. NOT DETECTED IN LEAVES.  
 CC -1- INDUCTION: INCREASED BY SALT STRESS IN ROOTS AND DECREASED BY SALT  
 CC STRESS IN COLEOPTILE.  
 CC -1- PTM: GLYCOSYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE GERMIN FAMILY.  
 DR InterPro: IPR001929; Germin.  
 DR PROSITE: PS00725; GERMIN; PARTIAL.  
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
 FT UNSURE 10 10  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1470 MW; 43FB588AA3B7B6D7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 5  
 ||  
 Db 6 LQ 7

RESULT 72  
 GER2\_HORVU STANDARD; PRT; 13 AA.  
 ID GER2\_HORVU  
 AC F28526;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Germin GS2 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Harkman W.J., Tao H.P., Tanaka C.K.;  
 RT "Germin-like polypeptides increase in barley roots during salt  
 stress.";  
 RL Plant Physiol. 97:366-374 (1991).  
 CC -1- FUNCTION: MAY PLAY A ROLE IN ALTERING THE PROPERTIES OF CELL  
 CC WALLS DURING GERMINATIVE GROWTH.  
 CC -1- SUBUNIT: OLIGOMER (BELIEVED TO BE A PENTAMER BUT PROBABLY  
 CC HEXAMER) (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: SOLUBLE, MICROSMAL AND CELL WALL FRACTIONS.  
 CC -1- TISSUE SPECIFICITY: ROOTS AND COLEOPTILE. IN ROOTS, PRESENT IN  
 CC THE MATURE REGION, BUT NOT IN THE TIP. NOT DETECTED IN LEAVES.  
 CC -1- INDUCTION: INCREASED BY SALT STRESS IN ROOTS AND DECREASED BY SALT  
 CC STRESS IN COLEOPTILE.  
 CC -1- PTM: GLYCOSYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE GERMIN FAMILY.  
 DR InterPro: IPR001929; Germin.  
 DR PROSITE: PS00725; GERMIN; PARTIAL.  
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
 FT UNSURE 10 10  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7B6D7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 5

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Db      6 LQ 7
RESULT 73
HPB9_RANES
ID_HPB9_RANES STANDARD; PRT; 13 AA.
AC P32416;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hemolytic protein B9 (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RN SEQUENCE
RC TISSUE=Skin secretion;
RX MEDLINE=90198965; PubMed=23117508;
RA Simmaco M., de Biase D., Severini C., Alta M., Erspamer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -!- FUNCTION: Shows hemolytic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; S09019; S09019.
KW Amphibian defense peptide; Amidation; Hemolysis.
FT MOD_RES 13 13
FT NON_TER 13 13
FT SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 11 KL 12

RESULT 74
NO40_VICSA STANDARD; PRT; 13 AA.
AC P55961;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Early nodulin 40.
GN ENOD40.
OS Vicia sativa (Spring vetch) (Tare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.
OX NCBI_TaxID=3908;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Nigra; TISSUE=Root nodules;
RX MEDLINE=96011756; PubMed=7548828;
RA Vijn I., Yang W.-C., Pallisgaard N., Oestergaard Jensen E.,
RA van Kammen A., Bissegling T.;
RT "VseNOD5, VseNOD12 and VseNOD40 expression during Rhizobium-induced
RT nodule formation on Vicia sativa roots.";
RL Plant Mol. Biol. 28:1111-1119(1995).
CC -!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
CC GROWTH REGULATOR THAT ALTERS PHYTHORMONE RESPONSES (BY
CC SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING RHIZOBIUM-INDUCED NODULE
CC FORMATION. IN 4-DAY OLD NODULES IT IS FOUND IN ALL THE CELLS OF
CC THE CENTRE OF THE NODULE PRIMORDIUM AND ALSO OCCURS IN THE REGION
CC OF THE ROOT PERICYCLE FACING THE NODULE PRIMORDIUM. AT DAY 5,

EXPRESSON IS SEEN IN THE COMPLETE CENTRAL TISSUE. AT DAY 20
EXPRESSED IN THE COMPLETE PREFIXATION ZONE II, AND IN THE PROXIMAL
PART OF THIS ZONE IT IS FOUND ONLY IN THE INFECTED CELLS BUT NOT
IN THE UNINFECTED CELLS. AT THE TRANSITION OF PREFIXATION ZONE II
INTO INTERZONE II-III EXPRESSION DECREASES IN THE INFECTED CELLS.
IN THE FIXATION ZONE III, EXPRESSION IS INDUCED IN THE UNINFECTED
CELLS AND IN THE PROXIMAL PART OF THIS ZONE IT IS UNDETECTABLE.
PRESENT AT HIGH LEVELS IN THE PERICYCLE OF THE NODULE VASCULAR
BUNDLE.

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CC -----
DR EMBL; X83683; CAB37926.1; -.
DR PIR; S60046; S60046.
KW Nodulation.
SQ SEQUENCE 13 AA; 1531 MW; 3C6953C4BD8A26C3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 2 KL 3

RESULT 75
PEDI_HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RN SEQUENCE.
RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RT peptides from Hydra vulgaris.";
RL Development 122:1941-1948(1996).
CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
CC DEVELOPMENT.
CC Morphogen.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PE 7
DB 5 PE 6

Search completed: November 25, 2003, 18:17:34
Job time : 3.3883 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 16.867 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-16

Perfect score: 7

Sequence: 1 KYKLQPE 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	57.1	16	2 Q9F9S4	Q9F9S4 helicobacte
2	4	57.1	17	2 Q9E1L3	Q9E1L3 helicobacte
3	4	57.1	18	12 Q919D5	Q919D5 human papil
4	4	57.1	18	12 Q919B3	Q919B3 human papil
5	4	57.1	18	12 Q919B5	Q919B5 human papil
6	4	57.1	18	12 Q919B7	Q919B7 human papil
7	4	57.1	18	12 Q919C5	Q919C5 human papil
8	4	57.1	18	12 Q919D1	Q919D1 human papil
9	4	57.1	18	12 Q919D3	Q919D3 human papil
10	4	57.1	18	12 Q919B9	Q919B9 human papil
11	4	57.1	18	12 Q919A8	Q919A8 human papil
12	4	57.1	18	12 Q919C7	Q919C7 human papil
13	4	57.1	18	12 Q919C9	Q919C9 human papil
14	3	42.9	9	2 Q47556	Q47556 escherichia
15	3	42.9	9	10 P82440	P82440 nicotiana t
16	3	42.9	9	13 Q8AYL5	Q8AYL5 carassius a

Q8AUM7 carassius a  
Q9UMK9 homo sapien  
P83091 spinacia ol  
Q86324 rous sarcom  
Q86325 rous sarcom  
Q86326 rous sarcom  
Q9Y392 homo sapien  
Q19718 homo sapien  
Q8UUP1 xenopus lae  
Q88176 mus musculu  
Q55326 synechococ  
Q9P2A2 homo sapien  
Q16045 homo sapien  
Q852V1 zea mays m  
Q9UR63 emericeila  
Q9UCY1 homo sapien  
Q9T264 oryctolagus  
Q988N8 hordeum vul  
Q852V2 zea mays m  
Q8VME2 pseudomonas  
Q14001 homo sapien  
Q9T2S2 solanum tub  
Q9T2H4 spinacia ol  
Q9JK08 mus musculu  
Q919B0 human papil  
Q81nn9 oryza sativ  
Q9S888 narcissus p  
Q9JIE9 mus musculu  
Q57600 gallus gall  
Q07603 homo sapien  
Q9UC80 homo sapien  
Q9UJ18 homo sapien  
Q9TVC3 sus scrofa  
Q9TR12 ovis aries  
Q8SPM3 bos taurus  
Q8W128 scaevola pr  
Q9J1A2 rattus norv  
Q9R4H7 micrococcc  
Q9R4H6 bacillus su  
Q9R4H8 arthrobacte  
Q96KZ0 homo sapien  
Q9TGW3 lucilia cup  
Q9TWF1 drosophila  
Q90X92 gallus gall  
Q90X91 gallus gall  
Q8G100 borrelia bu  
Q9S345 saccharomyc  
Q66205 transmissib  
Q66113 cherry leaf  
Q9VQ10 transmissib  
Q9RQ49 buchnera ap  
P72279 rhodococcus  
Q87471 haemophilus  
Q51594 escherichia  
Q15889 homo sapien  
Q15901 homo sapien  
Q15888 homo sapien  
Q15893 homo sapien  
Q94Vf6 varanus job  
Q34909 locusta mig  
Q9GV15 rattus sp.  
Q9ET21 mus musculu  
Q8R4D8 mus musculu  
Q64971 alfalfa mos  
P87488 oncorhynch  
Q53914 streptomyc  
Q46179 clostridium  
Q9R735 streptomyc  
P72149 pseudomonas  
P83222 streptomyc  
Q8G131 borrelia bu  
Q8G126 borrelia bu  
Q16276 homo sapien

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90      2 28.6      9 4 Q16605 homo sapien
91      2 28.6      9 4 P78484 homo sapien
92      2 28.6      9 4 Q9UK44 homo sapien
93      2 28.6      9 5 Q8WT19 drosophila
94      2 28.6      9 6 Q28093 bos taurus
95      2 28.6      9 8 Q8WFT4 diadema ant
96      2 28.6      9 8 Q94VG2 varanus ind
97      2 28.6      9 10 P82429 nicotiana t
98      2 28.6      9 10 Q9FEC0 hordeum vul
99      2 28.6      9 11 Q9QZA7 mus musculus
100     2 28.6      9 11 Q62530 mus spretus

```

## ALIGNMENTS

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RESULT 1
Q9F9S4 PRELIMINARY; PRT; 16 AA.
AC Q9F9S4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Methylase HpyI (Fragment).
GN M.HPYI.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Finland 9496;
RA Yan Y., Karhukorpi J., Lahti M., Sirvio A., Riipinen K., Kolho K.-L.,
RA Lindahl H., Verkasalo M., Fagerholm R., Rautelin H., Karttunen R.;
RT "Subtypes of the H. pylori iceA gene in Finnish pediatric patients.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF176822; AAG13123.1; -.
DR InterPro; IPR002294; D12N6.mtfrase.
DR Pfam; PF02086; MethyltransfD12; 1.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1944 MW; 7306D1D11603768A CRC64;

Query Match 57.1%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4
DB 7 KYKL 10

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RESULT 2
Q9ETL3 PRELIMINARY; PRT; 17 AA.
AC Q9ETL3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Methylase HpyI (Fragment).
GN M.HPYI OR HPYI.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Finland 18696;
RA Yan Y., Karhukorpi J., Lahti M., Sirvio A., Riipinen K., Kolho K.-L.,
RA Lindahl H., Verkasalo M., Fagerholm R., Rautelin H., Karttunen R.;
RT "Subtypes of the H. pylori iceA gene in Finnish pediatric patients.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

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```

RC STRAIN=7796;
RA Yan Y., Karhukorpi J., Lahti M., Sirvio A., Riipinen K., Kolho K.-L.,
RA Lindahl H., Verkasalo M., Fagerholm R., Rautelin H., Karttunen R.;
RT "The subtype of Helicobacter pylori iceA gene in the Finnish pediatric
patients.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF176823; AAG13125.1; -.
DR EMBL; AF176090; AAG09227.1; -.
DR InterPro; IPR002294; D12N6.mtfrase.
DR Pfam; PF02086; MethyltransfD12; 1.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2058 MW; B2B306D1D1160376 CRC64;

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Query Match 57.1%; Score 4; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KYKL 4
DB 7 KYKL 10

```

```

RESULT 3
Q919D5 PRELIMINARY; PRT; 18 AA.
AC Q919D5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC1;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404692; AAL01341.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB68F77688 CRC64;

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Query Match 57.1%; Score 4; DB 12; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 4 LOPE 7
DB 15 LOPE 18

```

```

RESULT 4
Q919B3 PRELIMINARY; PRT; 18 AA.
AC Q919B3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC12;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16

```

RT cervical cancer isolates from Australia and New Caledonia."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF404703; AAL01364.1; -  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 15 LOPE 18

## RESULT 5

Q919B5 ID Q919B5 PRELIMINARY; PRT; 18 AA.

AC Q919B5; DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.

OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.

OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=HPV16E6C11;

RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF404702; AAL01362.1; -  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 15 LOPE 18

## RESULT 6

Q919B7 ID Q919B7 PRELIMINARY; PRT; 18 AA.

AC Q919B7; DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.

OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.

OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=HPV16E6C10;

RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF404701; AAL01360.1; -  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 15 LOPE 18

## RESULT 7

Q919C5 ID Q919C5 PRELIMINARY; PRT; 18 AA.

AC Q919C5; DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.

OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.

OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=HPV16E6CC6;

RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF404697; AAL01352.1; -  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 15 LOPE 18

## RESULT 8

Q919D1 ID Q919D1 PRELIMINARY; PRT; 18 AA.

AC Q919D1; DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE E7 protein (Fragment).  
GN E7.

OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.

OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=HPV16E6CC3;

RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF404694; AAL01346.1; -  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 15 LOPE 18

```
RESULT 9
Q919D3 ID Q919D3 PRELIMINARY; PRT; 18 AA.
AC Q919D3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_TaxID=10581;
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC2;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404693; AAL01344.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
Db 15 LOPE 18

RESULT 10
Q919B9 ID Q919B9 PRELIMINARY; PRT; 18 AA.
AC Q919B9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_TaxID=10581;
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC9;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404700; AAL01358.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
Db 15 LOPE 18

RESULT 11
Q919A8 ID Q919A8 PRELIMINARY; PRT; 18 AA.
AC Q919A8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
```

```
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_TaxID=10581;
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC15;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404706; AAL01369.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
Db 15 LOPE 18

RESULT 12
Q919C7 ID Q919C7 PRELIMINARY; PRT; 18 AA.
AC Q919C7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_TaxID=10581;
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC5;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404696; AAL01350.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 57.1%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
Db 15 LOPE 18

RESULT 13
Q919C9 ID Q919C9 PRELIMINARY; PRT; 18 AA.
AC Q919C9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
```



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RN  SEQUENCE FROM N.A.
RP  STRAIN=HPV16E6C4;
RA  Wattle K.J., Thompson C.H., Coseart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human papillomavirus type 16
RL  cervical cancer isolates from Australia and New Caledonia.";
RR  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF404695; AAL01348.1; -.
FT  NON_TER 18
SQ  SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match      57.1%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 LOPE 7
DB  15 LOPE 18

RESULT 14
Q47556
ID  Q47556 PRELIMINARY; PRT; 9 AA.
AC  Q47556;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE  Aspartate transcarbamoylase regulatory chain (Fragment).
GN  PYR1.
OS  Escherichia coli.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Escherichia.
OX  NCBI_TaxID=562;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=82275057; PubMed=7051000;
RA  Pauza C.D., Karels M.J., Navre M., Schachman H.K.;
RT  "Genes encoding Escherichia coli aspartate transcarbamoylase: The
RT  pyrB-pyri operon.";
RL  Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
RN  [2]
RP  SEQUENCE OF 1-5 FROM N.A.
RX  MEDLINE=83195078; PubMed=6302686;
RA  Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
RA  Wild J.R.;
RT  "Nucleotide sequence of the structural gene (pyrB) that encodes the
RT  catalytic polypeptide of aspartate transcarbamoylase of Escherichia
RT  coli.";
RL  Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
DR  EMBL; J01670; AAA24475.1; -.
FT  NON_TER 9
SQ  SEQUENCE 9 AA; 1085 MW; 99BFD72334AA1F1 CRC64;

Query Match      42.9%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 KLO 5
DB  6 KLO 8

RESULT 15
P82440
ID  P82440 PRELIMINARY; PRT; 9 AA.
AC  P82440;
DT  01-JUN-2000 (TrEMBLrel. 14, Created)
DT  01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT  01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE  42 kDa cell wall protein (Fragment).
OS  Nicotiana tabacum (Common tobacco).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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OC  Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX  NCBI_TaxID=4097;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=CV. PETIT HAVANA;
RA  Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA  Wojtaszek P., Bolwell G.P.;
RT  "Proteomic study of secondary cell wall proteins from transformed
RT  tobacco culture.";
RL  Planta 0:0-0(2000).
CC  -!- SUBCELLULAR LOCATION: CELL WALL.
CC  -!- TISSUE SPECIFICITY: XYLEM.
KW  Cell wall.
FT  NON_TER 9
SQ  SEQUENCE 9 AA; 1053 MW; 298CC9D2D5BB1B07 CRC64;

Query Match      42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 QPE 7
DB  1 QPE 3

RESULT 16
Q8AYL5
ID  Q8AYL5 PRELIMINARY; PRT; 9 AA.
AC  Q8AYL5;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Cytochrome P450 aromatase (Fragment).
GN  CYP19A.
OS  Carassius auratus (Goldfish).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Carassius.
OX  NCBI_TaxID=7957;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
RT  "Promoter characteristics of two Cyp19 genes differentially expressed
RT  in the brain and ovary of teleost fish.";
RL  J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
DR  EMBL; AF324897; AAN32618.1; -.
FT  NON_TER 9
SQ  SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;

Query Match      42.9%; Score 3; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 LQP 6
DB  6 LQP 8

RESULT 17
Q8AUM7
ID  Q8AUM7 PRELIMINARY; PRT; 9 AA.
AC  Q8AUM7;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Cytochrome P450 aromatase (Fragment).
GN  CYP19A.
OS  Carassius auratus (Goldfish).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Carassius.
OX  NCBI_TaxID=7957;
RN  [1]

```

RP SEQUENCE FROM N.A.  
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;  
 RT "promoter characteristics of two CYP19 genes differentially expressed  
 in the brain and ovary of teleost fish.";  
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).  
 DR EMBL; AF324895; AAN32616.1; -.  
 DR EMBL; AF324896; AAN32617.1; -.  
 FT 'NON\_TER' 9 9  
 SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;

Query Match 42.9%; Score 3; DB 13; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LQP 6  
 |||  
 Db 6 LQP 8

RESULT 18  
 Q9UMK9 PRELIMINARY; PRT; 10 AA.  
 ID Q9UMK9  
 AC Q9UMK9  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Dystrophin (Fragment).  
 GN DAG1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Saad F.A., Moatacciuolo M.L., Merlini L., Trevisan C., Tomelleri G.,  
 RA Angelini C., Danieli G.A.;  
 RT "Novel point mutations in the human dystrophin gene detected by double  
 strand conformation analysis";  
 RT Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; L41643; AAB59464.1; -.  
 FT 'NON\_TER' 1 1  
 SQ SEQUENCE 10 AA; 1223 MW; 5D3C9185A2ACAB6D7 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KLQ 5  
 |||  
 Db 2 KLQ 4

RESULT 19  
 P83091 PRELIMINARY; PRT; 10 AA.  
 ID P83091  
 AC P83091  
 DT 01-OCT-2001 (TREMBLrel. 18, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Protease Do-like (EC 3.4.21.-) (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE, AND SUBCELLULAR LOCATION.  
 RA Schubert M., Petersen U., Funk C., Schroeder W.P., Kieselbach T.;  
 RL Submitted (AUG-2001) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: SERINE PROTEASE THAT IS REQUIRED AT HIGH TEMPERATURE.  
 CC MAY BE INVOLVED IN THE DEGRADATION OF DAMAGED PROTEINS (BY  
 SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C; ALSO KNOWN AS THE  
 CC DEGP/DEGO/DEGS FAMILY.  
 DR InterPro; IPR001478; PDZ.  
 KW Hydrolyase; Serine protease; Chloroplast; Thylakoid.  
 FT 'NON\_TER' 10 10  
 SQ SEQUENCE 10 AA; 1128 MW; DA0FED2AF771B5A2 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KLQ 5  
 |||  
 Db 8 KLQ 10

RESULT 20  
 Q86324 PRELIMINARY; PRT; 10 AA.  
 ID Q86324  
 AC Q86324  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Gp37 (Fragment).  
 GN ENV.  
 OS Rous sarcoma virus.  
 OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.  
 OX NCBI\_TaxID=11886;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Schmidt-Ruppin subgroup A;  
 RX MEDLINE=98083689; PubMed=9421881;  
 RA Hara H., Kaji A.;  
 RT "The U3 region of the long terminal repeat of a subgroup A  
 RT transformation-defective rous sarcoma virus (tdPH2010) converts a  
 RL noncytopathic virus to a cytopathic virus.";  
 RL Virus Genes 15:171-180(1997).  
 DR EMBL; U41726; AAB60580.1; -.  
 FT 'NON\_TER' 1 1  
 SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPE 7  
 |||  
 Db 4 QPE 6

RESULT 21  
 Q86325 PRELIMINARY; PRT; 10 AA.  
 ID Q86325  
 AC Q86325  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Gp37 (Fragment).  
 GN ENV.  
 OS Rous sarcoma virus.  
 OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.  
 OX NCBI\_TaxID=11886;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Schmidt-Ruppin subgroup A;  
 RX MEDLINE=98083689; PubMed=9421881;  
 RA Hara H., Kaji A.;  
 RT "The U3 region of the long terminal repeat of a subgroup A  
 RT transformation-defective rous sarcoma virus (tdPH2010) converts a  
 RL noncytopathic virus to a cytopathic virus.";  
 RL Virus Genes 15:171-180(1997).  
 DR EMBL; U41727; AAB60581.1; -.  
 FT 'NON\_TER' 1 1

SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;  
 Query Match 42.9%; Score 3; DB 15; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPE 7  
 Db 4 QPE 6

## RESULT 22

Q86326 PRELIMINARY; PRT; 10 AA.  
 AC Q86326;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Gp37 (Fragment).  
 GN ENV.  
 OS Rous sarcoma virus.  
 OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.  
 OX NCBI\_TaxID=11886;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Schmidt-Ruppin subgroup A;  
 RX MEDLINE=98083689; PubMed=9421881;  
 RA Hara H., Kaji A.;  
 RT "The U3' region of the long terminal repeat of a subgroup A  
 RT transformation-defective rous sarcoma virus (tdPH2010) converts a  
 RT noncytopathic virus to a cytopathic virus.";  
 RL Virus Genes 15:171-180(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Schmidt-Ruppin subgroup A;  
 RX MEDLINE=82271824; PubMed=6287213;  
 RA Takeya T., Hanafusa H., Jungmans R.P., Ju G., Skalka A.M.;  
 RT "Comparison between the viral transforming gene (src) of recovered  
 RT avian sarcoma virus and its cellular homolog.";  
 RL Mol. Cell. Biol. 1:1024-1037(1981).  
 DR EMBL; U41729; AAA84421.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPE 7  
 Db 4 QPE 6

## RESULT 23

Q9Y3G2 PRELIMINARY; PRT; 11 AA.  
 AC Q9Y3G2;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE LSF2 protein (Fragment).  
 GN LSF2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9929247; PubMed=10369878;  
 RA Gilley J., Fried M.;  
 RT "Extensive gene order differences within regions of conserved synteny  
 RT between the Fugu and human genomes: implications for chromosomal  
 RT evolution and the cloning of disease genes.";

RL Hum. Mol. Genet. 8:1313-1320(1999).  
 DR EMBL; Y17456; CAB44349.1; -;  
 FT NON\_TER 1  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1342 MW; 68C5B5D7A8772324 CRC64;  
 Query Match 42.9%; Score 3; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KIQ 5  
 Db 9 KIQ 11

## RESULT 24

O19718 PRELIMINARY; PRT; 11 AA.  
 AC O19718;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II antigen (Fragment).  
 GN HLA-DRB1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86206008; PubMed=3458223;  
 RA Gregersen P.K., Shen M., Song Q.-L., Merryman P., Degar S., Seki T.,  
 RA Maccari J., Goldberg D., Murphy H., Schwenzer J., Wang C.Y.,  
 RA Winchester R.J., Nepom G.T., Silver J.;  
 RT "Molecular diversity of HLA-DR4 haplotypes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2642-2646(1986).  
 DR EMBL; M15074; AAA59810.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 11 AA; 1143 MW; 4E6AADA061B776D7 CRC64;

Query Match 42.9%; Score 3; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
 Db 4 LQP 6

## RESULT 25

Q8UUP1 PRELIMINARY; PRT; 11 AA.  
 AC Q8UUP1;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Beta-TrCP protein (Fragment).  
 GN BETA-TRCP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carnevali F.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ballarino M.;  
 RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus  
 RT laevis.";  
 RL Thesis (2001), Department of Genetica e Biologia Molecolare,

RL University of Rome La Sapienza, Rome, Italy.  
DR EMBL; AJ428930; CAD21927.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
DB 8 LQP 10

RESULT 26  
O88176 PRELIMINARY; PRT; 13 AA.  
AC O88176; (Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Neural cell adhesion molecule (fragment).  
GN NCAM1 OR NCAM.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb-C; TISSUE=Liver;  
RX MEDLINE=98250618; PubMed=9582442;  
RA Kawahigashi H., Harada Y., Aeano A., Nakamura M.;  
RT "A cis-acting regulatory element that affects the alternative splicing  
of a muscle-specific exon in the mouse NCAM gene.";  
RL Biochim. Biophys. Acta 1397:305-315(1998).  
DR EMBL; AB001873; BAA31275.1; -.  
DR MGD; MGI:97281; Ncam1.  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
DB 7 LQP 9

RESULT 27  
Q55326 PRELIMINARY; PRT; 14 AA.  
ID Q55326  
AC Q55326; (Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Putative ORF1 (fragment).  
OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
OX NCBI\_TaxID=32049;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PR6;  
RX MEDLINE=92201692; PubMed=1551590;  
RA Rhiel E., Stirewalt V.L., Gasparich G.E., Bryant D.A.;  
RT "The psac genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa:  
cloning and sequence analysis.";  
RT Cloning and sequence analysis."  
RL Gene 112:123-128(1992).  
DR EMBL; M86238; AAA27351.1; -.  
DR NON\_TER 14 14  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1590 MW; 9D5226BDCB998BCA CRC64;

Query Match 42.9%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
DB 12 LQP 14

RESULT 28  
Q9P2A2 PRELIMINARY; PRT; 14 AA.  
ID Q9P2A2  
AC Q9P2A2; (Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Truncated aldo-keto reductase (fragment).  
GN TRUNCATED AKR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20138537; PubMed=10672042;  
RA Nishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,  
RA Watanabe K., Ito S.;  
RT "Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with  
three aldo-keto reductase genes.";  
RL Genes Cells 5:111-125(2000).  
DR EMBL; AB037903; BAA92888.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
DB 7 LQP 9

RESULT 29  
Q16045 PRELIMINARY; PRT; 14 AA.  
ID Q16045  
AC Q16045; (Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE D3 dopamine receptor (fragment).  
GN D3R.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=93326145; PubMed=7916609;  
RA Nagai Y., Ueno S., Saeki Y., Soga F., Yanagihara T.;  
RT "Expression of the D3 dopamine receptor gene and a novel variant  
transcript generated by alternative splicing in human peripheral blood  
lymphocytes.";  
RT Lymphocytes."  
RL Biochem. Biophys. Res. Commun. 194:368-374(1993).  
DR EMBL; S63845; AAB27543.2; -.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1586 MW; EA310BEFE94CF1B1 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
|||  
Db 12 LQP 14

## RESULT 30

Q8S2V1 ID Q8S2V1 PRELIMINARY; PRT; 14 AA.  
AC Q8S2V1; 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hydroxymethyltransferase-like protein (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. CL23;  
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,  
RA Morgante M., Rafalski J.A.;  
RT "SNP frequency, haplotype structure and linkage disequilibrium in  
RT elite maize inbred lines."  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF498513; AAM18693.1; -;  
KW Transferase; Methyltransferase.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1676 MW; 4741A28D79E8EF17 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3  
|||  
Db 11 KYK 13

## RESULT 31

Q9UR63 ID Q9UR63 PRELIMINARY; PRT; 15 AA.  
AC Q9UR63; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight  
DE isoform (EC 3.2.1.26) (Fragment).  
OS Emericella nidulans (Aspergillus nidulans).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; Emericella.  
OX NCBI\_TaxID=162425;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96409246; PubMed=8814228;  
RA Chen J.S., Saxton J., Henning F.W., Peberdy J.F.;  
RT "Purification and partial characterization of the high and low  
RT molecular weight form (S- and F-form) of invertase secreted by  
RT Aspergillus nidulans."  
RL Biochim. Biophys. Acta 1296:207-218(1996).  
SQ SEQUENCE 15 AA; 1568 MW; 2C992B42211366BB CRC64;

Query Match 42.9%; Score 3; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
|||  
Db 1 LQP 3

## RESULT 32

Q9UCY1 ID Q9UCY1 PRELIMINARY; PRT; 15 AA.  
AC Q9UCY1; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Thromboxane A2 receptor isoform alpha (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96193877; PubMed=8613548;  
RA Hirata T., Ushikubi F., Kakizuka A., Okuma M., Narumiya S.;  
RT "Two thromboxane A2 receptor isoforms in human platelets. Opposite  
RT coupling to adenylyl cyclase with different sensitivity to Arg60 to Leu  
RT mutation."  
RL J. Clin. Invest. 97:949-956(1996).  
SQ SEQUENCE 15 AA; 1656 MW; 5EC77C6B9E97FB78 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
|||  
Db 4 LQP 6

## RESULT 33

Q9TR64 ID Q9TR64 PRELIMINARY; PRT; 15 AA.  
AC Q9TR64; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Nucleoside diphosphate kinase, NDK, p19=17.143 kDa A subunit  
DE (Fragment).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95285334; PubMed=7767789;  
RA Weber B., Weber W., Buck F., Hilz H.;  
RT "Isolation of the myc transcription factor nucleoside diphosphate  
RT kinase and the multifunctional enzyme glyceraldehyde-3-phosphate  
RT dehydrogenase by CAMP affinity chromatography."  
RL Int. J. Biochem. Cell Biol. 27:215-224(1995).  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1820 MW; 2728CBD4FDA56316 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPE 7  
|||  
Db 7 QPE 9

## RESULT 34

Q9S8N8 ID Q9S8N8 PRELIMINARY; PRT; 15 AA.  
AC Q9S8N8; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE Protein E-22 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 ON NCBI\_TaxID=4513;  
 RN [1]  
 RN SEQUENCE  
 RP MEDLINE=94170739; PubMed=8125056;  
 RX "Flengsrud R.;  
 RA "Separation of acidic barley endosperm proteins by two-dimensional  
 RT electrophoresis.";  
 RL Electrophoresis 14:1060-1066(1993).  
 SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
 DB 3 LQP 5

RESULT 35  
 ID Q8S2V2 PRELIMINARY; PRT; 15 AA.  
 AC Q8S2V2;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hydroxymethyltransferase-like protein (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 ON NCBI\_TaxID=4577;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=cv. H98;  
 RC Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,  
 RA Morgante M., Rafalski J.A.;  
 RT "SNP frequency, haplotype structure and linkage disequilibrium in  
 RT elite maize inbred lines";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF498512; AAW18692.1;  
 KW Transferase; Methyltransferase.  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1823 MW; 4741A28D79E8B9C9 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3  
 DB 12 KYK 14

RESULT 36  
 ID Q8VME2 PRELIMINARY; PRT; 17 AA.  
 AC Q8VME2;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE ParC protein (Fragment).  
 GN PARC  
 OS Pseudomonas putida.  
 OG Plasmid pWMO.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 ON NCBI\_TaxID=303;

RN [1]  
 RN SEQUENCE FROM N.A.  
 RP Greated A., Lambertson L., Williams P.A., Thomas C.M.;  
 RT "Complete nucleotide sequence of IncP-9 plasmid pWMO.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ344068; CAC86875.1;  
 KW Plasmid.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 1903 MW; A58E0B85C365A999 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
 DB 13 LQP 15

RESULT 37  
 ID Q14001 PRELIMINARY; PRT; 17 AA.  
 AC Q14001;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Cyclic nucleotide phosphodiesterase (Fragment).  
 GN CGIPDE1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=97079687; PubMed=8921398;  
 RX Loebert R.W., Winterpacht A., Seipel B., Zabel B.U.;  
 RT "Molecular cloning and chromosomal assignment of the human homologue  
 RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved  
 RT in fat metabolism located at 11p15.1";  
 RL Genomics 37:211-218(1996).  
 DR EMBL; X95522; CAA64776.1;  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6  
 DB 14 LQP 16

RESULT 38  
 ID Q9T2S2 PRELIMINARY; PRT; 17 AA.  
 AC Q9T2S2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Cytochrome-C reductase 55 kDa subunit (EC 1.10.2.2) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OG Mitochondrion.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.  
 ON NCBI\_TaxID=4113;  
 RN [1]  
 RN SEQUENCE  
 RP MEDLINE=94198758; PubMed=7764624;  
 RX Braun H.P., Kruft V., Schmitz U.K.;  
 RL Planta 193:99-106(1994).  
 SQ SEQUENCE 17 AA; 2031 MW; DDC159AE6AE5B362 CRC64;

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Query Match      42.9%; Score 3; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPE 7
   |||
Db 2 QPE 4

RESULT 39
Q9T2H4          PRELIMINARY; PRT; 17 AA.
AC Q9T2H4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Photosystem II light-harvesting complex 30 kDa component (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=95112835; PubMed=7813461;
RA Walters R.G., Ruban A.V., Horton P.;
RT "Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound
RT by dicyclohexylcarbodiimide during inhibition of energy dissipation.";
RL Eur. J. Biochem. 226:1063-1069(1994).
SQ SEQUENCE 17 AA; 2015 MW; A098D5E8323434D CRC64;

Query Match      42.9%; Score 3; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6
   |||
Db 4 LQP 6

RESULT 40
Q9JK08          PRELIMINARY; PRT; 17 AA.
AC Q9JK08;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 22, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
GN FBP2 OR FBPASE 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=20337676; PubMed=10773464;
RA Tillmann H., Stein S., Liehr T., Eschrich K.;
RT "Structure and chromosomal localization of the human and mouse muscle
RT fructose-1,6-bisphosphatase genes.";
RL Gene 247:241-253(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Stein S.;
RT "Mouse liver fructose-1,6-bisphosphatase: Gene structure,
RT transcriptional start point, chromosomal localization, cDNA cloning,
RT characterization of the recombinant protein, and analysis of tissue-
RT specific expression.";
RL Arch. Biochem. Biophys. 0:0-0(0).
RN [3]
DB EMBL; AJ243021; CAB90668.1; -.

DR MGD; MGI:95491; Fbp2.
KW Hydrolase.
FT NON_TER 1 17
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1887 MW; E2609FFD33922C8B CRC64;

Query Match      42.9%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6
   |||
Db 12 LQP 14

RESULT 41
Q919B0          PRELIMINARY; PRT; 17 AA.
ID Q919B0;
AC Q919B0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16B6CC14;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404705; AAL01367.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1998 MW; 4471DB6BF776889B CRC64;

Query Match      42.9%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6
   |||
Db 15 LQP 17

RESULT 42
Q8LNN9          PRELIMINARY; PRT; 18 AA.
ID Q8LNN9;
AC Q8LNN9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0040D23.8.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buehl C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Taitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBA0040D23 genomic sequence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC074196; AAM76354.1; -.

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DR Gramene; Q8LNN9; -  
KW Hypothetical protein.  
SQ SEQUENCE 18 AA; 2005 MW; 23DBF28FF63C1608 CRC64;  
Query Match 42.9%; Score 3; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KLQ 5  
DB 15 KLQ 17  
RESULT 43  
Q9S888 PRELIMINARY; PRT; 18 AA.  
AC Q9S888; DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Chaparonin 60 beta chain (Fragment);  
OS Narcissus pseudonarcissus (Daffodil);  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;  
OC Narcissus;  
OX NCBI\_TaxID=39639;  
RN [1] SEQUENCE  
RP MEDLINE=96291727; PubMed=8754688;  
RA Bonk M., Tadros M., Vandekerckhove J., Al-Babli S., Beyer P.;  
RT "Purification and characterization of chaparonin 60 and heat-shock  
RT protein 70 from chromoplasts of Narcissus pseudonarcissus";  
RL Plant Physiol. 111:931-939(1996).  
SQ SEQUENCE 18 AA; 2108 MW; E324CCA884907EE8 CRC64;  
Query Match 42.9%; Score 3; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KLQ 5  
DB 15 KLQ 17  
RESULT 44  
Q9JIE9 PRELIMINARY; PRT; 18 AA.  
AC Q9JIE9; DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Protein arginine N-methyltransferase 1 (Fragment).  
GN MRMT1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1] SEQUENCE FROM N.A.  
RP MEDLINE=20307889; PubMed=10848611;  
RA Pawlak M.R., Scherer C.A., Chen J., Roehon M.J., Ruley H.E.;  
RT "Arginine N-methyltransferase 1 is required for early postimplantation  
RT mouse development, but cells deficient in the enzyme are viable.";  
RL Mol. Cell. Biol. 20:4859-4869(2000).  
RL EMBL; AF232718; AAF37294.1; -  
KW Methyltransferase; Transferase.  
FT NON\_TER 1 1  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 1931 MW; 392E2C312C4A8372 CRC64;  
Query Match 42.9%; Score 3; DB 11; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOP 6  
DB 12 LOP 14  
RESULT 45  
O57600 PRELIMINARY; PRT; 18 AA.  
ID O57600; DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Thrombomucin (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1] SEQUENCE FROM N.A.  
RP MEDLINE=97444372; PubMed=9298993;  
RX McNaghy K.M., Petterson I., Rossi F., Flamme I., Shevchenko A.,  
RA Mann M., Graf T.;  
RT "Thrombomucin, a novel cell surface protein that defines thrombocytes  
RT and multipotent hematopoietic progenitors";  
RL J. Cell Biol. 138:1395-1407(1997).  
DR EMBL; Y13976; CAA74309.1; -  
FT NON\_TER 1 1  
SQ SEQUENCE 18 AA; 1973 MW; CA71002CD77FE4F9 CRC64;  
Query Match 42.9%; Score 3; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LOP 6  
DB 14 LOP 16  
RESULT 46  
Q07603 PRELIMINARY; PRT; 19 AA.  
ID Q07603; DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 1D12A protein.  
GN 1D12A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1] SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RX MEDLINE=94044805; PubMed=8228263;  
RA Ranes-Goldberg M.G., Hori T., Mohan-Peterson S., Spits H.;  
RT "Identification of human pre-T/NK cell-associated genes";  
RL J. Immunol. 151:5810-5821(1993).  
DR EMBL; L17325; AAA16780.1; -  
SQ SEQUENCE 19 AA; 2259 MW; EDF56A4BFD5BEC78 CRC64;  
Query Match 42.9%; Score 3; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KLQ 5  
DB 13 KLQ 15  
RESULT 47



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Q9UC80
ID Q9UC80 PRELIMINARY; PRT; 19 AA.
AC Q9UC80;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE 21.5 kDa stone matrix protein (EC 1.15.1.1) (Superoxide dismutase
[Mn/Fe]) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95215817; PubMed=7701298;
RA Binette J.P., Binette M.B.;
RT "Sequencing of proteins extracted from stones.";
RL Scanning Microsc. 8:233-239(1994).
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
KW Oxidoreductase.
SQ SEQUENCE 19 AA; 2116 MW; A0D0DAE848E87894 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOP 6
DB 14 LOP 16

RESULT 48
Q9UJ18
ID Q9UJ18 PRELIMINARY; PRT; 19 AA.
AC Q9UJ18;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DJ33A15.2 (Prostaglandin E receptor (EP3e)) (Fragment).
GN PTGER3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Frankland J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031429; CAB52457.1; -.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 19 AA; 2245 MW; 1424503798298FEC CRC64;

Query Match 42.9%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3
DB 13 KYK 15

RESULT 49
Q9TVC3
ID Q9TVC3 PRELIMINARY; PRT; 19 AA.
AC Q9TVC3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Myostatin (Fragment).
GN GDF8; MSTN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20078370; PubMed=10612246;
RA Stratil A., Kopecky M.;
RT "Genomic organization, sequence and polymorphism of the porcine
myostatin (GDF8; MSTN) gene.";
RL Anim. Genet. 30:468-470(1999).
DR EMBL; AJ133580; CAB39561.1; -.
FT NON_TER.
SQ SEQUENCE 19 AA; 2307 MW; 7A1A7F3EA701F0CC CRC64;

Query Match 42.9%; Score 3; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQ 5
DB 3 KLQ 5

RESULT 50
Q9TR12
ID Q9TR12 PRELIMINARY; PRT; 19 AA.
AC Q9TR12;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE 14 kDa anaphylatoxin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=96209140; PubMed=8621983;
RA Johnson R.J., Burchop K.E., Van Epps D.E.;
RT "Infusion of ovine C5a into sheep mimics the inflammatory response of
RT hemodialysis.";
RL J. Lab. Clin. Med. 127:456-469(1996).
SQ SEQUENCE 19 AA; 2301 MW; D47290F525A85EAC CRC64;

Query Match 42.9%; Score 3; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3
DB 12 KYK 14

RESULT 51
Q8SPM3
ID Q8SPM3 PRELIMINARY; PRT; 19 AA.
AC Q8SPM3;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN GDF-8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

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RN  (1)
RP  SEQUENCE FROM N.A.
RA  Cria A., Marchitelli C., Savarese M., Valentini A.;
RT  "Sequence analysis of the myostatin promoter region in cattle.";
RL  Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AJ438578; CAD27441.1; -.
FT  NON_TER 19
SQ  SEQUENCE 19 AA; 231 MW; 7A1A7F3EAF3F0CC CRC64;

Query Match 42.9%; Score 3; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQ 5
DB 3 KLQ 5

RESULT 52
Q8W128 PRELIMINARY; PRT; 19 AA.
ID Q8W128
AC Q8W128;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nitrate reductase (Fragment).
GN NIA.
OS Scaevola procera.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Goodeniaceae; Scaevola.
OC NCBI_TaxID=184417;
OX (1)
RN SEQUENCE FROM N.A.
RA Howarth D.G., Baum D.A.;
RT "Phylogenetic utility of a nuclear intron from nitrate reductase for
RT the study of closely related plant species.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF460205; ALU66737.1; -.
DR InterPro; IPR005066; Mo-co_dimer.
DR Pfam; PF03404; Mo-co_dimer; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2357 MW; 5C0582771535B26A CRC64;

Query Match 42.9%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OPE 7
DB 2 OPE 4

RESULT 53
Q9JIA2 PRELIMINARY; PRT; 19 AA.
ID Q9JIA2
AC Q9JIA2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Norepinephrine transporter (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX (1)
RN SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley;
RX MEDLINE=20525705; PubMed=11072103;
RA Padbury J.F., McGonnigal B., Tseng Y.T., Nguyen T.T., Stabila J.P.;
RT "Cloning and sequence analysis of the rat norepinephrine transporter
RT promoter.";

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RL Brain Res. Mol. Brain Res. 83:128-132 (2000).
DR EMBL; AF246668; AAF78041.1; -.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2082 MW; 4AA83339008F55CD CRC64;

Query Match 42.9%; Score 3; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OPE 7
DB 11 OPE 13

RESULT 54
Q9R4H7 PRELIMINARY; PRT; 20 AA.
ID Q9R4H7
AC Q9R4H7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE L2 like ribosomal protein (Fragment).
OS Micrococcus luteus (Micrococcus lysodeikticus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Micrococcaceae; Micrococcus.
OC NCBI_TaxID=1270;
OX (1)
RN SEQUENCE.
RX MEDLINE=96014410; PubMed=8520111;
RA Ochiai K., Kawamoto I.;
RT "Two-dimensional gel electrophoresis of ribosomal proteins as a novel
RT approach to bacterial taxonomy: application to the genus
RT Arthrobacter.";
RL Biosci. Biotechnol. Biochem. 59:1679-1687 (1995).
SQ SEQUENCE 20 AA; 2164 MW; 5C137D96694F08D CRC64;

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3
DB 4 KYK 6

RESULT 55
Q9R4H6 PRELIMINARY; PRT; 20 AA.
ID Q9R4H6
AC Q9R4H6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE L2 like ribosomal protein (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1423;
OX (1)
RN SEQUENCE.
RX MEDLINE=96014410; PubMed=8520111;
RA Ochiai K., Kawamoto I.;
RT "Two-dimensional gel electrophoresis of ribosomal proteins as a novel
RT approach to bacterial taxonomy: application to the genus
RT Arthrobacter.";
RL Biosci. Biotechnol. Biochem. 59:1679-1687 (1995).
SQ SEQUENCE 20 AA; 2259 MW; 45E771AD997D08D CRC64;

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3
DB 4 KYK 6

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RESULT 56
Q9R4H8
ID Q9R4H8 PRELIMINARY; PRT; 20 AA.
AC Q9R4H8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE L2 like ribosomal protein (Fragment).
OS Arthropoda; Insecta; Hexapoda; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
RN NCBI_TaxID=7375;
RX MEDLINE=96035600; PubMed=7553348;
RA Trowell S.C., Hines E.R., Herlt A.J., Rickards R.W.;
RT "Characterization of a juvenile hormone binding lipophorin from the
RT blowfly Lucilia cuprina.";
RL Comp. Biochem. Physiol. 109B:339-357(1994).
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2188 MW; 11BA745A4B303C7B CRC64;

Query Match 42.9%; Score 3; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3
DB 12 KYK 14

RESULT 57
Q9SKZ0
ID Q9SKZ0 PRELIMINARY; PRT; 20 AA.
AC Q9SKZ0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RX MEDLINE=96087104; PubMed=7498465;
RA Hintermann E., Jeno P., Meyer U.A.;
RT "Isolation and characterization of an arylalkylamine N-
RT acetyltransferase from Drosophila melanogaster.";
RL FEBS Lett. 375:148-150(1995).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2215 MW; 7DF5E20D67C13F34 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPE 7
DB 13 QPE 15

RESULT 60
Q90X92
ID Q90X92 PRELIMINARY; PRT; 20 AA.
AC Q90X92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tyrosinase (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN NCBI_TaxID=9031;
RX MEDLINE=96014410; PubMed=8520111;
RA Ochiai K., Kawamoto I.;
RT "Two-dimensional gel electrophoresis of ribosomal proteins as a novel
RT approach to bacterial taxonomy: application to the genus
RT Arthrobacter.";
RL Biosci. Biotechnol. Biochem. 59:1679-1687(1995).
SQ SEQUENCE 20 AA; 2193 MW; 45F5C7DDBDB4F08D CRC64;

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3
DB 4 KYK 6

RESULT 58
Q9TWG3
ID Q9TWG3 PRELIMINARY; PRT; 20 AA.
AC Q9TWG3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Apolipophorin I (Fragment).
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).

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RA Deng X., Yang Y., Liu W.;
RT "Single nucleotide polymorphism analysis on chicken tyrosinase gene
RT and its associations with melanin traits.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416915; AAL14561.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2300 MW; AD237F25FA1BA696 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6
DB 1 LQP 3

RESULT 61
Q90X91 PRELIMINARY; PRT; 20 AA.
ID Q90X91
AC Q90X91;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Tyrosinase (Fragment).
GN TYR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Deng X., Yang Y., Liu W.;
RT "Single nucleotide polymorphism analysis on chicken tyrosinase gene
RT and its associations with melanin traits.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416916; AAL14562.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2217 MW; BC677F25FA1BA696 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQP 6
DB 1 LQP 3

RESULT 62
Q8GL00 PRELIMINARY; PRT; 7 AA.
ID Q8GL00
AC Q8GL00;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-13.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amid diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AX142106; AAN17857.1; -.
SQ SEQUENCE 7 AA; 869 MW; 72C691E727233B70 CRC64;
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KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 5 KL 6

RESULT 63
Q95945 PRELIMINARY; PRT; 7 AA.
ID Q95945
AC Q95945;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Inside intron 5 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D273-10B;
RX MEDLINE=8106985; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system: Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24066.1; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4
DB 5 KL 6

RESULT 64
Q66205 PRELIMINARY; PRT; 7 AA.
ID Q66205
AC Q66205;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Membrane protein (1 is 3rd base in codon) (Fragment).
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FS772/70;
RX MEDLINE=88216185; PubMed=28355592;
RA Britton P., Carmenes R.S., Page K.W., Garwes D.J., Parra F.;
RT "Sequence of the Nucleoprotein Gene from a Virulent British Field
RT Isolate of Transmissible Gastroenteritis Virus and its Expression in
RT Saccharomyces Cerevisiae.";
RL Mol. Microbiol. 2:89-99(1988).
DR EMBL; Y00542; CAA68606.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 869 MW; 72C691E727233B70 CRC64;
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Query Match      28.6%; Score 2; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KL 4
DB 2 KL 3

RESULT 65
Q6113 ID Q6113 PRELIMINARY; PRT; 7 AA.
AC Q6113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE C-terminus of the viral replicase (fragment).
OS Cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus.
OX NCBI_TaxID=12615;
RN [1]_TaxID=12615;
RP SEQUENCE FROM N.A.
RC STRAIN=Walnut;
RA Borja M.;
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Walnut;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal
RT regions of the genomic RNAs of cherry leafroll virus (walnut
RT strain).";
RL Virus Genes 10:245-252(1995).
DR EMBL; 234265; CAA84019.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match      28.6%; Score 2; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LQ 5
DB 1 LQ 2

RESULT 66
Q9YQ10 ID Q9YQ10 PRELIMINARY; PRT; 7 AA.
AC Q9YQ10;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical fusion protein.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11149;
RN [1]_TaxID=11149;
RP SEQUENCE FROM N.A.
RX MEDLINE=9909045; PubMed=9882359;
RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
RA Enjuanes L.;
RT "Replication and packaging of transmissible gastroenteritis
RT coronavirus-derived synthetic minigenomes.";
RL J. Virol. 73:1535-1545(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95159435; PubMed=7856095;
RA Eleouet J., Rasschaert D., Lambert P., Levy L., Vende P., Laude H.;

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RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1
RT of transmissible gastroenteritis virus.";
RL Virology 206:817-822(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88078100; PubMed=2825819;
RA Rasschaert D., Gelfi J., Laude H.;
RT "Enteric coronavirus TGEV: partial sequence of the genomic RNA its
RT organization and expression.";
RL Biochimie 69:591-600(1987).
DR EMBL; AJ011482; CAA09625.1; -.
SQ SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;

Query Match      28.6%; Score 2; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LQ 5
DB 5 LQ 6

RESULT 67
Q9RQ49 ID Q9RQ49 PRELIMINARY; PRT; 8 AA.
AC Q9RQ49;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Nifs protein homolog (fragment).
GN NIFS.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022990; PubMed=10555290;
RA Clark M.A., Moran N.A., Baumann P.;
RT "Sequence evolution in bacterial endosymbionts having extreme base
RT compositions.";
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR EMBL; AF130814; AAF13805.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 992 MW; F3A73B5047672336 CRC64;

Query Match      28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KL 4
DB 2 KL 3

RESULT 68
P72279 ID P72279 PRELIMINARY; PRT; 8 AA.
AC P72279;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Biphenyl dioxygenase (fragment).
GN BPHB.
OS Rhodococcus globorulus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=33008;
RN [1]_TaxID=33008;
RP SEQUENCE FROM N.A.
RX MEDLINE=95255652; PubMed=7737502;
RA Asturias J.A., Diaz E., Timmis K.N.;
RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-

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RT positive bacterium Rhodococcus globerulus P6 to multicomponent  
 RT dioxygenases of gram-negative bacteria.";  
 RL Gene 156:11-18(1995)  
 DR EMBL; X80041; CAA56350.1; --  
 KW Dioxxygenase.  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 5  
 ||  
 Db 3 LQ 4

## RESULT 69

OB7471 PRELIMINARY; PRT; 8 AA.  
 AC OB7471; 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DE Hifa (Fragment).  
 GN Hifa.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bagan;  
 RX MEDLINE=98389689; PubMed=9721313;  
 RA Mhalanga-Mutagadura T., Morlin G., Smith A.L., Eisenstark A.,  
 RA Golomb M.;  
 RT "Evolution of the major pilus gene cluster of haemophilus  
 RT influenzae";  
 RL J. Bacteriol. 180:4693-4703(1998).  
 DR EMBL; AF071762; AAC35830.1; --  
 FT NON TER 1  
 SQ SEQUENCE 8 AA; 876 MW; DAB44451A7272325 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4  
 ||  
 Db 2 KL 3

## RESULT 70

Q51594 PRELIMINARY; PRT; 8 AA.  
 AC Q51594; 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE CopB protein (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86223772; PubMed=2423502;  
 RA Weber P.C., Palchaudhuri S.;  
 RT "Incompatibility repressor in a repA-like replicon of the IncFI  
 RT plasmid ColV2-K94.";  
 RL J. Bacteriol. 166:1106-1112(1986).  
 DR EMBL; M13472; AAA23194.1; --

KW Plasmid.  
 FT NON TER 1  
 SQ SEQUENCE 8 AA; 998 MW; 0F37205AA73416D7 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQ 5  
 ||  
 Db 1 LQ 2

## RESULT 71

Q15889 PRELIMINARY; PRT; 8 AA.  
 AC Q15889; 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE (Clone XP15H8B) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries.";  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL; L32070; AAA73879.1; --  
 FT NON TER 1  
 SQ SEQUENCE 8 AA; 865 MW; 0474472325A761E7 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KL 4  
 ||  
 Db 5 KL 6

## RESULT 72

Q15901 PRELIMINARY; PRT; 8 AA.  
 AC Q15901; 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE (Clone XP7B11B) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries.";  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL; L32080; AAA73891.1; --  
 FT NON TER 1  
 SQ SEQUENCE 8 AA; 860 MW; 37D2878676729CB CRC64;

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Query Match      28.6%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LQ 5
Db      7 LQ 8

RESULT 73
Q15893      PRELIMINARY;      PRT;      8 AA.
AC Q15893;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE (Clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32073; AAA73883.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match      28.6%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LQ 5
Db      5 LQ 6

RESULT 74
Q15888      PRELIMINARY;      PRT;      8 AA.
AC Q15888;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE (Clone XP15H8A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32069; AAA73878.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match      28.6%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LQ 5
Db      7 LQ 8

RESULT 75
Q94VF6      PRELIMINARY;      PRT;      8 AA.
AC Q94VF6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
OS COI.
GN Varanus jobiensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169843;
RN [1]_TaxID=169843;
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407507; AAL10075.1; -.
KW Mitochondrion.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1144 MW; EFD729DB436411A6 CRC64;

Query Match      28.6%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LQ 5
Db      7 LQ 8

Search completed: November 25, 2003, 18:25:39
Job time : 17.917 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 22.6755 seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-16

Perfect score: 7

Sequence: 1 KYKLOPE 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	22	Colostrinin derive
2	7	100.0	7	22	Colostrinin peptid
3	7	100.0	7	22	Colostrinin peptid
4	7	100.0	7	22	Ewe colostrinin pe
5	7	100.0	7	23	Colostrinin consti
6	7	100.0	7	23	Colostrinin consti
7	7	100.0	7	23	Neural cell regula
8	5	71.4	8	19	Human HDC peptide
9	5	71.4	10	22	Ewe colostrinin pe

10	4	57.1	7	14	AAR33159	HPV E7 protein - R
11	4	57.1	7	22	AAW43817	H11 binding site c
12	4	57.1	7	22	AAW43822	H11 binding site c
13	4	57.1	7	22	AAW43827	H11 binding site c
14	4	57.1	7	22	AAW43832	H11 binding site c
15	4	57.1	7	22	AAW43837	H11 binding site c
16	4	57.1	7	22	AAW43842	H11 binding site c
17	4	57.1	7	22	AAW43966	H11 binding site c
18	4	57.1	7	22	AAW45364	H11 binding site c
19	4	57.1	7	22	AAW45369	H11 binding site c
20	4	57.1	7	22	AAW45450	H11 binding site c
21	4	57.1	7	22	AAW45455	H11 binding site c
22	4	57.1	7	22	AAW45460	H11 binding site c
23	4	57.1	7	22	AAW45465	H11 binding site c
24	4	57.1	7	22	AAW45470	H11 binding site c
25	4	57.1	7	22	AAW45475	H11 binding site c
26	4	57.1	7	22	AAW45480	H11 binding site c
27	4	57.1	7	22	AAW45485	H11 binding site c
28	4	57.1	7	22	AAW45490	H11 binding site c
29	4	57.1	7	22	AAW45495	H11 binding site c
30	4	57.1	7	22	AAW45672	H11 binding site c
31	4	57.1	7	22	AAW45677	H11 binding site c
32	4	57.1	7	22	AAW45961	H11 binding site c
33	4	57.1	7	22	AAW45966	H11 binding site c
34	4	57.1	7	22	AAW45976	H11 binding site c
35	4	57.1	7	22	AAW45998	H11 binding site c
36	4	57.1	7	22	AAW46003	H11 binding site c
37	4	57.1	7	22	AAW46008	H11 binding site c
38	4	57.1	7	22	AAW46038	H11 binding site c
39	4	57.1	7	22	AAW46062	H11 binding site c
40	4	57.1	7	22	AAW46067	H11 binding site c
41	4	57.1	7	22	AAW46235	H11 binding site c
42	4	57.1	7	23	ABG60340	Selective targetin
43	4	57.1	8	12	AAW10631	Human Papilloma Vi
44	4	57.1	8	14	AAW33158	HPV E7 protein - R
45	4	57.1	8	20	AAW10184	T cell epitope/MHC
46	4	57.1	8	21	AAW83922	HIV-1 gag p17 B8-r
47	4	57.1	8	22	AAU12533	Human HIV-1 Th-CTL
48	4	57.1	8	22	AAW62330	Casein-related pep
49	4	57.1	8	23	ABU57482	HIV cytotoxic lymph
50	4	57.1	8	23	ABG79866	MHC class I molecu
51	4	57.1	9	12	AAW10635	Human Papilloma Vi
52	4	57.1	9	13	AAW25420	Non-homologous aut
53	4	57.1	9	14	AAW33157	HPV E7 protein - R
54	4	57.1	9	14	AAW33163	HPV E7 protein - R
55	4	57.1	9	14	AAW33170	HPV E7 protein - R
56	4	57.1	9	14	AAW43741	MHC Class I allele
57	4	57.1	9	14	AAW43742	MHC Class I allele
58	4	57.1	9	15	AAW59257	Peptide fragment (
59	4	57.1	9	15	AAW59246	Peptide fragment (
60	4	57.1	9	15	AAW73799	Antigen fragment 1
61	4	57.1	9	15	AAW73800	Antigen fragment 1
62	4	57.1	9	15	AAW73796	Antigen fragment 1
63	4	57.1	9	16	AAW80939	Peptide for increa
64	4	57.1	9	16	AAW78889	HPV16 E7 11-19 cyt
65	4	57.1	9	16	AAW78894	HPV16 E7 12-20 cyt
66	4	57.1	9	16	AAW78853	HIV gap p17.3 cyto
67	4	57.1	9	18	AAW39661	HPV16/18 E7 peptid
68	4	57.1	9	18	AAW39662	HPV16/18 E7 peptid
69	4	57.1	9	18	AAW36590	Hepatitis B virus
70	4	57.1	9	19	AAW78893	Human papillomavir
71	4	57.1	9	19	AAW54766	Peptide from HPV 1
72	4	57.1	9	19	AAW54767	Peptide from HPV 1
73	4	57.1	9	20	AAW53459	HIV-1 p17 protein
74	4	57.1	9	20	AAW53432	HLA binding plu-1
75	4	57.1	9	20	AAW45656	Immunogenic peptid
76	4	57.1	9	20	AAW40308	Amino acid sequenc
77	4	57.1	9	20	AAW26800	HIV-derived lipope
78	4	57.1	9	20	AAW10346	T cell epitope/MHC
79	4	57.1	9	20	AAW10253	T cell epitope/MHC
80	4	57.1	9	20	AAW10511	HLA Class I motif
81	4	57.1	9	21	AAW33705	MHC Class I associ
82	4	57.1	9	21	AAW66456	HLA-A24-binding H

83 4 57.1 9 21 AAY73309 Plasmodium falcipa  
 84 4 57.1 9 22 ABP17126 HIV B27 super moti  
 85 4 57.1 9 22 ABP20400 HIV A03 motif gag  
 86 4 57.1 9 22 ABP22667 HIV A11 motif gag  
 87 4 57.1 9 22 ABP24122 HIV A24 motif gag  
 88 4 57.1 9 22 AAG93801 Human papilloma vi  
 89 4 57.1 9 22 AAG88611 HER2/NEU DR superm  
 90 4 57.1 9 22 AAG88725 HER2/NEU DR 3a mot  
 91 4 57.1 9 22 AAB95951 MHC class-I associ  
 92 4 57.1 9 22 AAB95999 HPV 16 E7 A2 MHC-b  
 93 4 57.1 9 22 AAB96001 HPV 16 E7 A2 MHC-b  
 94 4 57.1 9 22 AAB96004 HPV 16 E7 A2 MHC-b  
 95 4 57.1 9 22 AAB20215 HPV strain 16 E7 p  
 96 4 57.1 9 22 AAB30975 HPV E7 peptide whi  
 97 4 57.1 9 22 AAB31056 Polyepitopic peptri  
 98 4 57.1 9 22 AAB31145 A polyepitopic pep  
 99 4 57.1 9 23 ABUS7459 HIV cytotoxic lymph  
 100 4 57.1 9 23 ABJ15216 Immunogenic HIV pe

## ALIGNMENTS

RESULT 1  
 AAB72261  
 ID AAB72261 standard; peptide; 7 AA.  
 XX  
 AC AAB72261;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 16.  
 XX  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22818.  
 XX  
 PR 17-AUG-1999; 99US-0149311.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGS-) REGEN THERAPEUTICS PLC.  
 XX  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 XX WPI; 2001-202804/20.  
 DR  
 XX  
 PT Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 7; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KYKLOPE 7  
 Db 1 KYKLOPE 7  
 RESULT 2  
 AAB72514  
 ID AAB72514 standard; Peptide; 7 AA.  
 XX  
 AC AAB72514;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #15.  
 XX  
 KW Dermatological; oxidative stress regulator; colostrinin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22665.  
 XX  
 PR 17-AUG-1999; 99US-0149310.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2001-218342/22.  
 DR  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 7; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KYKLOPE 7  
 Db 1 KYKLOPE 7  
 RESULT 3  
 AAB72546  
 ID AAB72546 standard; Peptide; 7 AA.  
 XX  
 AC AAB72546;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX

DE Colostrinin peptide #15.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 KW Unidentified.  
 OS  
 XX  
 XX WO200112651-A2.  
 PN  
 XX  
 XX 22-FEB-2001.  
 PD  
 XX  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX  
 XX Boldogh I;  
 PI  
 XX  
 XX WPI; 2001-226545/23.  
 DR  
 XX  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 XX  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 100.0%; Score 7; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYKLOPE 7  
 Db 1 KYKLOPE 7

RESULT 5  
 AAE20243  
 ID AAE20243 standard; peptide; 7 AA.  
 XX  
 XX AAE20243;  
 AC  
 XX 18-JUN-2002 (first entry)  
 DT  
 XX  
 XX Colostrinin constituent peptide #15.  
 DE  
 XX  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnary.  
 XX  
 XX Unidentified.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH  
 FT Modified-site 7  
 FT /note= "Optionally C-terminal amide"  
 XX  
 XX WO200213850-A1.  
 PN  
 XX  
 XX 21-FEB-2002.  
 PD  
 XX  
 XX 17-AUG-2000; 2000WO-US22776.  
 PF  
 XX  
 XX 17-AUG-2000; 2000WO-US22776.  
 PR  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 PI  
 XX  
 XX WPI; 2002-269151/31.  
 DR  
 XX  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 XX Claim 6; Page 25; 51pp; English.  
 PS  
 XX  
 XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

DE Colostrinin peptide #15.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 KW Unidentified.  
 OS  
 XX  
 XX WO200112651-A2.  
 PN  
 XX  
 XX 22-FEB-2001.  
 PD  
 XX  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX  
 XX Boldogh I;  
 PI  
 XX  
 XX WPI; 2001-226545/23.  
 DR  
 XX  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 XX  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 100.0%; Score 7; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYKLOPE 7  
 Db 1 KYKLOPE 7

RESULT 4  
 AAB59317  
 ID AAB59317 standard; Peptide; 7 AA.  
 XX  
 XX AAB59317;  
 AC  
 XX 21-MAR-2001 (first entry)  
 DT  
 XX  
 XX Ewe colostrinin peptide fragment B-2.  
 DE  
 XX  
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 KW  
 XX  
 XX Ovis sp.  
 OS  
 XX  
 XX WO200075173-A2.  
 PN  
 XX  
 XX 14-DEC-2000.  
 PD  
 XX  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF  
 XX  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 PA  
 XX  
 XX Georgiades JA;  
 PI  
 XX  
 XX WPI; 2001-071058/08.  
 DR  
 XX  
 XX Peptides having an N-terminal amino acid sequence isolated from

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKLOPE 7  
 |||||  
 Db 1 KYKLOPE 7

#### RESULT 6

AA051050  
 ID AAM51050 standard; Peptide; 7 AA.

XX AC AAM51050;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide.

DE Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; beta-casein; human.  
 KW Homo sapiens.

XX Key Location/Qualifiers  
 FT Modified-site 7 /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. The peptide is  
 CC classified as having a beta-casein homologue precursor. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific, an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKLOPE 7  
 |||||  
 Db 1 KYKLOPE 7

#### RESULT 7

AA014592  
 ID AAO14592 standard; peptide; 7 AA.

XX AC AAO14592;

DT 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 15.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers  
 FT Modified-site 7 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 7; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0; Mismatches 0; Conservative 0;

QY 1 KYKLQPE 7

DB 1 KYKLQPE 7

RESULT 8

AAW63621  
ID AAW63621 standard; peptide; 8 AA.

XX AC AAW63621;

XX DT 16-OCT-1998 (first entry)

XX DE Human HDC peptide fragment (aa 318-325).

XX KW Histidine decarboxylase; HDC; epitope; detection; melanoma; cancer; leukaemia.

XX OS Homo sapiens.

XX PN WQ9830593-A2.

XX PD 16-JUL-1998.

XX PF 06-JAN-1998; 98WO-US06810.

XX PR 06-JAN-1997; 97US-0779814.

XX PA (PROM-) PROMEGA CORP.

XX PI Falus A, Haak-Frendscho M;

XX DR WPI; 1998-399068/34.

XX PT Antibody reactive with human histidine decarboxylase - useful for, e.g. detecting individuals having or being at risk of melanoma and leukaemia

PS Claim 3; Page 26; 36pp; English.

CC AAW63620 and AAW63621 are peptide epitopes from the human histidine decarboxylase (HDC) which are used in a method for detecting a mammal having, or at risk of having, melanoma. The antibodies (Abs) can be used in methods for detecting or determining the amount of histidine decarboxylase in a mammalian physiological sample. The Abs can also be used to detect cancer, especially leukaemia or melanoma, in a mammal at risk or afflicted with cancer. Kits for detecting histidine decarboxylase in cells, and for detecting melanoma are also included.

SQ Sequence 8 AA;

Query Match 71.4%; Score 5; DB 19; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0; Mismatches 0; Conservative 0;

QY 1 KYKLQ 5

DB 4 KYKLQ 8

RESULT 9

AAB59347  
ID AAB59347 standard; Peptide; 10 AA.

XX AC AAB59347;

XX

DT 21-MAR-2001 (first entry)

DE Ewe colostrinin peptide fragment derived sequence #7.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WQ200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques -

PS Claim 8; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques.

SQ Sequence 10 AA;

Query Match 71.4%; Score 5; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 18; Indels 0; Gaps 0; Mismatches 5; Conservative 0; Mismatches 0;

QY 1 KYKLQ 5

DB 5 KYKLQ 9

RESULT 10

AAR33159

ID AAR33159 standard; peptide; 7 AA.

XX AC AAR33159;

XX DT 25-MAR-2003 (updated)

XX DE 25-JUN-1993 (first entry)

XX DE HPV E7 protein - RBG protein binding inhibitor peptide.

XX KW Human papilloma virus; retinoblastoma gene; genital warts; cervical cancer; treatment.

XX OS Synthetic.

XX PN BP531080-A2.

XX PD 10-MAR-1993.

XX PF 01-SEP-1992; 92EP-0307905.

XX

PR 04-SEP-1991; 91US-0754829.  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Oliff AI, Riemen MW;  
 XX  
 DR WPI; 1993-078581/10.  
 XX  
 PT New polypeptide(s) which inhibit human papilloma virus binding to  
 PT RRG protein - useful for treating genital warts and cervical cancer  
 XX  
 PS Claim 7; Page 15; 15pp; English.  
 XX  
 CC The sequence is that of a peptide which inhibits binding of human  
 CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)  
 CC protein. It can be used in the treatment of conditions caused by HPV,  
 CC esp. genital warts and cervical cancer.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 7 AA;  
 Query Match 57.1%; Score 4; DB 14; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 LOPE 7  
 DB 2 LOPE 5  
 RESULT 11  
 AAM43817  
 ID AAM43817 standard; Peptide; 7 AA.  
 XX  
 AC AAM43817;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #88.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 CC Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 XX  
 PS Example 4; Page 101; 154pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell

CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 KLOP 6  
 DB 3 KLOP 6  
 RESULT 12  
 AAM43822  
 ID AAM43822 standard; Peptide; 7 AA.  
 XX  
 AC AAM43822;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #93.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 CC Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 XX  
 PS Example 4; Page 101; 154pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell

CC surface-associated SPPC of TC. (I) has cytostatic activity and can be used in vaccine production and as a tumour-specific immunogenic response inducer. (I) is useful for treating 71 types of cancers or tumours in a subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting or imaging cancer cells, and to monitor the course of amelioration of malignancy in an individual. AAM43707 to AAM47109 represent peptides which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 57.1%; Score 4; DB 22; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6

DB 3 KLOP 6

RESULT 13

AAM43827  
ID AAM43827 standard; Peptide; 7 AA.

XX

AC AAM43827;

XX 25-OCT-2001 (first entry)

XX H11 binding site consensus conforming peptide (CCP) #98.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC; immunogenically cross-reactive; cancer; immunogenic cancer cell; cytostatic; vaccine; tumour-specific immunogenic response inducer; astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma; ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.

OS Synthetic.

XX CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress protein-peptide complexes associated with tumor, and isolated antigen-binding fragments of an antibody that binds specifically to the complex -

PS Example 4; Page 101; 154pp; English.

XX The present invention describes a composition (I) comprising stress protein-peptide complexes (SPPC) associated with tumours that is specifically immunogenically cross-reactive with cell surface-associated SPPCs specific to target cancer (TC). Also described is an isolated antigen-binding fragment of an antibody that binds specifically to SPPCs or a population of different SPPCs consisting of immunogenic cancer cell surface-associated SPPC of TC. (I) has cytostatic activity and can be used in vaccine production and as a tumour-specific immunogenic response inducer. (I) is useful for treating 71 types of cancers or tumours in a subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, CC

CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting or imaging cancer cells, and to monitor the course of amelioration of malignancy in an individual. AAM43707 to AAM47109 represent peptides which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 57.1%; Score 4; DB 22; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6

DB 3 KLOP 6

RESULT 14

AAM43832  
ID AAM43832 standard; Peptide; 7 AA.

XX

AC AAM43832;

XX 25-OCT-2001 (first entry)

XX H11 binding site consensus conforming peptide (CCP) #103.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC; immunogenically cross-reactive; cancer; immunogenic cancer cell; cytostatic; vaccine; tumour-specific immunogenic response inducer; astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma; ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.

OS Synthetic.

XX CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress protein-peptide complexes associated with tumor, and isolated antigen-binding fragments of an antibody that binds specifically to the complex -

PS Example 4; Page 101; 154pp; English.

XX The present invention describes a composition (I) comprising stress protein-peptide complexes (SPPC) associated with tumours that is specifically immunogenically cross-reactive with cell surface-associated SPPCs specific to target cancer (TC). Also described is an isolated antigen-binding fragment of an antibody that binds specifically to SPPCs or a population of different SPPCs consisting of immunogenic cancer cell surface-associated SPPC of TC. (I) has cytostatic activity and can be used in vaccine production and as a tumour-specific immunogenic response inducer. (I) is useful for treating 71 types of cancers or tumours in a subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting or imaging cancer cells, and to monitor the course of amelioration of

CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 57.1%; Score 4; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
|||  
Db 3 KLQP 6

RESULT 15  
AAM43837  
ID AAM43837 standard; Peptide; 7 AA.

XX AAM43837;  
XX 25-OCT-2001 (first entry)  
XX H11 binding site consensus conforming peptide (CCP) #108.  
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;  
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;  
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;  
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.  
OS Synthetic.

XX CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

XX Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
XX protein-peptide complexes associated with tumor, and isolated  
XX antigen-binding fragments of an antibody that binds specifically to the  
XX complex

XX Example 4; Page 101; 154pp; English.

XX The present invention describes a composition (I) comprising stress  
XX protein-peptide complexes (SPCC) associated with tumours that is  
XX specifically immunogenically cross-reactive with cell surface-associated  
XX SPCCs specific to target cancer (TC). Also described is an isolated  
XX antigen-binding fragment of an antibody that binds specifically to SPCCs  
XX or a population of different SPCCs consisting of immunogenic cancer cell  
XX surface-associated SPCC of TC. (I) has cytostatic activity and can be  
XX used in vaccine production and as a tumour-specific immunogenic response  
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a  
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting  
XX or imaging cancer cells, and to monitor the course of amelioration of  
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides  
XX which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 57.1%; Score 4; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
|||  
Db 3 KLQP 6

RESULT 16

AAM43842  
ID AAM43842 standard; Peptide; 7 AA.

XX AAM43842;

XX 25-OCT-2001 (first entry)

XX H11 binding site consensus conforming peptide (CCP) #113.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;  
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;  
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;  
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.

XX Synthetic.

XX CA2290722-A1.

XX 08-JUN-2001.

XX 08-DEC-1999; 99CA-2290722.

XX 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

XX Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
XX protein-peptide complexes associated with tumor, and isolated  
XX antigen-binding fragments of an antibody that binds specifically to the  
XX complex

XX Example 4; Page 101; 154pp; English.

XX The present invention describes a composition (I) comprising stress  
XX protein-peptide complexes (SPCC) associated with tumours that is  
XX specifically immunogenically cross-reactive with cell surface-associated  
XX SPCCs specific to target cancer (TC). Also described is an isolated  
XX antigen-binding fragment of an antibody that binds specifically to SPCCs  
XX or a population of different SPCCs consisting of immunogenic cancer cell  
XX surface-associated SPCC of TC. (I) has cytostatic activity and can be  
XX used in vaccine production and as a tumour-specific immunogenic response  
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a  
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting  
XX or imaging cancer cells, and to monitor the course of amelioration of  
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides  
XX which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 57.1%; Score 4; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 3 KLQP 6  
 DB 3 KLQP 6

## RESULT 17

AAW43966  
 ID AAW43966 standard; Peptide; 7 AA.

AC AAW43966;

DT 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #237.

KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.

OS Synthetic.

PN CA2290722-A1.

PD 08-JUN-2001.

PF 08-DEC-1999; 99CA-2290722.

PR 08-DEC-1999; 99CA-2290722.

PA (NOVO-) NOVOPHARM BIOTECH INC.

PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

DR WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
 protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

PS Example 4; Page 101; 154pp; English.

XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAW43707 to AAW47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
 DB 3 KLQP 6

## RESULT 18

AAW45364

ID AAW45364 standard; Peptide; 7 AA.

XX AAW45364;

DT 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #1635.

KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.

OS Synthetic.

PN CA2290722-A1.

PD 08-JUN-2001.

PF 08-DEC-1999; 99CA-2290722.

PR 08-DEC-1999; 99CA-2290722.

PA (NOVO-) NOVOPHARM BIOTECH INC.

PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

DR WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
 protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

PS Example 4; Page 106; 154pp; English.

XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAW43707 to AAW47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
 DB 3 KLQP 6

## RESULT 19

AAW45369

ID AAM45369 standard; Peptide; 7 AA.  
 XX  
 AC AAM45369;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #1640.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
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 PT Composition useful for treating and diagnosing cancer, comprises stress  
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 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex.  
 XX  
 PS Example 4; Page 106; 154pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising stress  
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 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KLQP 6  
 Db |||||  
 3 KLQP 6  
 RESULT 20  
 AAM45450  
 ID AAM45450 standard; Peptide; 7 AA.  
 XX  
 AC AAM45450;  
 XX

DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #1721.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 PT Composition useful for treating and diagnosing cancer, comprises stress  
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 PS Example 4; Page 107; 154pp; English.  
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 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KLQP 6  
 Db |||||  
 3 KLQP 6  
 RESULT 21  
 AAM45455  
 ID AAM45455 standard; Peptide; 7 AA.  
 XX  
 AC AAM45455;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #1726.  
 XX

KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
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 DR WPI; 2001-425937/46.  
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 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KLOP 6  
 DB 3 KLOP 6  
 RESULT 22  
 AAM45460  
 ID AAM45460 standard; Peptide; 7 AA.  
 XX  
 AC AAM45460;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #1731.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
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 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
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 XX  
 DR WPI; 2001-425937/46.  
 XX  
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 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KLOP 6  
 DB 3 KLOP 6  
 RESULT 23  
 AAM45465  
 ID AAM45465 standard; Peptide; 7 AA.  
 XX  
 AC AAM45465;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #1736.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.



XX PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
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 DR  
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 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
 Db 3 KLQP 6  
 |||||

RESULT 26  
 AAM45480  
 ID AAM45480 standard; Peptide; 7 AA.  
 XX  
 AC AAM45480;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #1751.  
 XX  
 DE  
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
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 PI Entwistle JM, MacDonald GC;  
 XX WPI; 2001-425937/46.  
 DR

PI Entwistle JM, MacDonald GC;  
 XX WPI; 2001-425937/46.  
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 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 XX Sequence 7 AA;  
 SQ

Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
 Db 3 KLQP 6  
 |||||

RESULT 27  
 AAM45485  
 ID AAM45485 standard; Peptide; 7 AA.  
 XX  
 AC AAM45485;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #1756.  
 XX  
 DE  
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PD 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
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 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX WPI; 2001-425937/46.  
 DR

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CC or imaging cancer cells, and to monitor the course of amelioration of  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention.  
XX  
XX Sequence 7 AA;  
SQ  
Query Match 57.1%; Score 4; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KLOP 6  
Db |||||  
3 KLOP 6  
RESULT 28  
AAM45490  
ID AAM45490 standard; Peptide; 7 AA.  
XX  
XX AAM45490;  
XX  
XX 25-OCT-2001 (first entry)  
XX  
XX H11 binding site consensus conforming peptide (CCP) #1761.  
XX  
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;  
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX CA2290722-A1.  
XX  
XX 08-JUN-2001.  
XX  
XX 08-DEC-1999; 99CA-2290722.  
XX  
XX 08-DEC-1999; 99CA-2290722.  
XX  
XX (NOVO-) NOVOPHARM BIOTECH INC.  
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XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
PI Entwistle JM, MacDonald GC;  
XX  
XX WPI; 2001-425937/46.  
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XX  
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CC or imaging cancer cells, and to monitor the course of amelioration of  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention.  
XX  
XX Sequence 7 AA;  
SQ  
Query Match 57.1%; Score 4; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KLOP 6  
Db |||||  
3 KLOP 6  
RESULT 29  
AAM45495  
ID AAM45495 standard; Peptide; 7 AA.  
XX  
XX AAM45495;  
XX  
XX 25-OCT-2001 (first entry)  
XX  
XX H11 binding site consensus conforming peptide (CCP) #1766.  
XX  
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;  
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX CA2290722-A1.  
XX  
XX 08-JUN-2001.  
XX  
XX 08-DEC-1999; 99CA-2290722.  
XX  
XX 08-DEC-1999; 99CA-2290722.  
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XX (NOVO-) NOVOPHARM BIOTECH INC.  
XX  
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PI Entwistle JM, MacDonald GC;  
XX  
XX WPI; 2001-425937/46.  
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 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;  
 SQ Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
 DB 3 KLQP 6

RESULT 30  
 AAM45672  
 ID AAM45672 standard; Peptide; 7 AA.

AC AAM45672;  
 XX 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #1943.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.  
 OS Synthetic.

PN CA2290722-A1.

XX 08-JUN-2001.

PF 08-DEC-1999; 99CA-2290722.

PR 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

PS Example 4; Page 107; 154pp; English.

XX The present invention describes a composition (I) comprising stress

CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs

CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

SQ Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
 DB 3 KLQP 6

RESULT 31  
 AAM45677  
 ID AAM45677 standard; Peptide; 7 AA.

AC AAM45677;

XX 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #1948.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX Homo sapiens.

OS Synthetic.

PN CA2290722-A1.

XX 08-JUN-2001.

PF 08-DEC-1999; 99CA-2290722.

PR 08-DEC-1999; 99CA-2290722.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, MacDonald GC;

XX WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

PS Example 4; Page 107; 154pp; English.

XX The present invention describes a composition (I) comprising stress

CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a

CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6  
 ||||  
 Db 3 KLOP 6

# RESULT 32

AAM45961  
 ID AAM45961 standard; Peptide; 7 AA.

XX AC AAM45961;

XX DT 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #2232.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.  
 OS Synthetic.

XX PN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

XX PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

XX Example 4; Page 109; 154pp; English.

XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPSCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPSCs  
 CC or a population of different SPSCs consisting of immunogenic cancer cell  
 CC surface-associated SPSC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting

CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6  
 ||||  
 Db 3 KLOP 6

# RESULT 33

AAM45966  
 ID AAM45966 standard; Peptide; 7 AA.

XX AC AAM45966;

XX DT 25-OCT-2001 (first entry)

DE H11 binding site consensus conforming peptide (CCP) #2237.

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

OS Homo sapiens.  
 OS Synthetic.

XX PN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

XX PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -

XX Example 4; Page 109; 154pp; English.

XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPSCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPSCs  
 CC or a population of different SPSCs consisting of immunogenic cancer cell  
 CC surface-associated SPSC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.



SQ Sequence 7 AA; Query Match 57.1%; Score 4; DB 22; Length 7; Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
 DB 3 KLQP 6

RESULT 34  
 AAM45976  
 ID AAM45976 standard; Peptide; 7 AA.  
 XX  
 AC AAM45976;  
 XX  
 DT 25-OCT-2001 (first entry)  
 DE H11 binding site consensus conforming peptide (CCP) #2247.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC; immunogenically cross-reactive; cancer; immunogenic cancer cell; cytostatic; vaccine; tumour-specific immunogenic response inducer; astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma; endependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX CA2290722-A1.  
 PN 08-JUN-2001.  
 PD 08-DEC-1999; 99CA-2290722.  
 PF 08-DEC-1999; 99CA-2290722.  
 PR (NOVO-) NOVOPHARM BIOTECH INC.  
 PA Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE; Entwistle JM, MacDonald GC; WPI; 2001-425937/46.  
 PI Composition useful for treating and diagnosing cancer, comprises stress protein-peptide complexes associated with tumor, and isolated antigen-binding fragments of an antibody that binds specifically to the complex -  
 PS Example 4; Page 109; 154pp; English.  
 XX The present invention describes a composition (I) comprising stress protein-peptide complexes (SPPC) associated with tumours that is specifically immunogenically cross-reactive with cell surface-associated SPPCs specific to target cancer (TC). Also described is an isolated antigen-binding fragment of an antibody that binds specifically to SPPCs or a population of different SPPCs consisting of immunogenic cancer cell surface-associated SPPC of TC. (I) has cytostatic activity and can be used in vaccine production and as a tumour-specific immunogenic response inducer. (I) is useful for treating 71 types of cancers or tumours in a subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, endependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting or imaging cancer cells, and to monitor the course of amelioration of malignancy in an individual. AAM43707 to AAM47109 represent peptides which are used in the exemplification of the present invention.

SQ Sequence 7 AA; Query Match 57.1%; Score 4; DB 22; Length 7; Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
 DB 3 KLQP 6

RESULT 35  
 AAM45998  
 ID AAM45998 standard; Peptide; 7 AA.  
 XX  
 AC AAM45998;  
 XX  
 DT 25-OCT-2001 (first entry)  
 DE H11 binding site consensus conforming peptide (CCP) #2269.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC; immunogenically cross-reactive; cancer; immunogenic cancer cell; cytostatic; vaccine; tumour-specific immunogenic response inducer; astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma; endependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX CA2290722-A1.  
 PN 08-JUN-2001.  
 PD 08-DEC-1999; 99CA-2290722.  
 PF 08-DEC-1999; 99CA-2290722.  
 PR (NOVO-) NOVOPHARM BIOTECH INC.  
 PA Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE; Entwistle JM, MacDonald GC; WPI; 2001-425937/46.  
 PI Composition useful for treating and diagnosing cancer, comprises stress protein-peptide complexes associated with tumor, and isolated antigen-binding fragments of an antibody that binds specifically to the complex -  
 PS Example 4; Page 109; 154pp; English.  
 XX The present invention describes a composition (I) comprising stress protein-peptide complexes (SPPC) associated with tumours that is specifically immunogenically cross-reactive with cell surface-associated SPPCs specific to target cancer (TC). Also described is an isolated antigen-binding fragment of an antibody that binds specifically to SPPCs or a population of different SPPCs consisting of immunogenic cancer cell surface-associated SPPC of TC. (I) has cytostatic activity and can be used in vaccine production and as a tumour-specific immunogenic response inducer. (I) is useful for treating 71 types of cancers or tumours in a subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, endependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting or imaging cancer cells, and to monitor the course of amelioration of malignancy in an individual. AAM43707 to AAM47109 represent peptides which are used in the exemplification of the present invention.

SQ Sequence 7 AA; Query Match 57.1%; Score 4; DB 22; Length 7; Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
 DB 3 KLQP 6

```

Db          3 KLOP 6

RESULT 36
AAM46003
ID AAM46003 standard; Peptide; 7 AA.
XX
AC AAM46003;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #2279.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPpC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX Synthetic.
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex.
XX
XX Example 4; Page 109; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPpC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPpCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPpCs
XX or a population of different SPpCs consisting of immunogenic cancer cell
XX surface-associated SPpC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
XX
XX Query Match 57.1%; Score 4; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 KLOP 6
XX ||||
XX Db 3 KLOP 6
XX
XX RESULT 37
AAM46038
ID AAM46038 standard; Peptide; 7 AA.
XX
XX AAM46038;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #2274.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPpC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX Synthetic.
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex.
XX
XX Example 4; Page 109; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPpC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPpCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPpCs
XX or a population of different SPpCs consisting of immunogenic cancer cell
XX surface-associated SPpC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
XX
XX Query Match 57.1%; Score 4; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 KLOP 6
XX ||||
XX Db 3 KLOP 6
XX
XX RESULT 38
AAM46038
ID AAM46038 standard; Peptide; 7 AA.
XX
XX AAM46038;

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```

XX 25-OCT-2001 (first entry)
XX H11 binding site consensus conforming peptide (CCP) #2309.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex.
XX
XX Example 4; Page 109; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
XX
XX Query Match 57.1%; Score 4; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 KLOP 6
XX ||||
XX Db 3 KLOP 6
XX
XX RESULT 39
XX AAM46062
XX ID AAM46062 standard; Peptide; 7 AA.
XX
XX AC AAM46062;
XX
XX DT 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #2333.

```

```

XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex.
XX
XX Example 4; Page 109; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
XX
XX Query Match 57.1%; Score 4; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 KLOP 6
XX ||||
XX Db 3 KLOP 6
XX
XX RESULT 40
XX AAM46067
XX ID AAM46067 standard; Peptide; 7 AA.
XX
XX AC AAM46067;
XX
XX DT 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #2338.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;

```

KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 XX 08-DEC-1999; 99CA-2290722.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX  
 XX WPI; 2001-425937/46.  
 XX  
 XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 XX  
 PS Example 4; Page 109; 154pp; English.  
 XX  
 XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KLQP 6  
 DB 3 KLQP 6  
 RESULT 41  
 AAM46235.  
 ID AAM46235 standard; Peptide; 7 AA.  
 XX  
 AC AAM46235;  
 XX  
 XX 25-OCT-2001 (first entry).  
 DT  
 XX H11 binding site consensus conforming peptide (CCP) #2506.  
 DE  
 DE Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.

OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 XX 08-DEC-1999; 99CA-2290722.  
 XX  
 PF 08-DEC-1999; 99CA-2290722.  
 XX  
 PR 08-DEC-1999; 99CA-2290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, MacDonald GC;  
 XX  
 XX WPI; 2001-425937/46.  
 XX  
 XX Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated  
 PT antigen-binding fragments of an antibody that binds specifically to the  
 PT complex -  
 XX  
 PS Example 4; Page 109; 154pp; English.  
 XX  
 XX The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 57.1%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KLQP 6  
 DB 3 KLQP 6  
 RESULT 42  
 ABG60340  
 ID ABG60340 standard; Peptide; 7 AA.  
 XX  
 AC ABG60340;  
 XX  
 XX 30-JUL-2002 (first entry)  
 DT  
 XX Selective targeting peptide #15.  
 DE  
 XX Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;  
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;  
 KW viral infection; cardiovascular disease; degenerative disease; ischaemia;  
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;  
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;  
 KW gene therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200220769-A1.  
 XX

PD 14-MAR-2002.  
 XX  
 PF 07-SEP-2001; 2001WO-US27692.  
 XX  
 PR 08-SEP-2000; 2000US-231266P.  
 PR 17-JAN-2001; 2001US-0765101.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Arap W, Pasqualini R;  
 XX  
 DR WPI; 2002-415731/44.  
 XX  
 PT Targeting peptides identified by phage display, useful for targeting  
 PT delivery to an organ or tissue, particularly for treating a disease,  
 PT e.g. cancer, inflammatory or autoimmune diseases, infections or  
 PT cardiovascular disease -  
 XX  
 PS Claim 22; Page 56; 317pp; English.  
 XX  
 CC The invention relates to an isolated peptide of 100 amino acids or less  
 CC in size useful for targeting delivery to an organ or tissue, particularly  
 CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory  
 CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral  
 CC infection, cardiovascular disease or degenerative disease. The peptide is  
 CC also useful for inducing apoptosis, particularly to a subject with  
 CC leukaemia, cancer, arthritis, diabetes, cardiovascular disease,  
 CC inflammation or macular degeneration. Furthermore, the peptide is useful  
 CC for diagnosing the diseases cited above. Targeting peptides of the  
 CC invention can also be used to deliver an agent to a foetus, by attaching  
 CC a peptide to the agent and administering the peptide to a pregnant  
 CC subject. Sequences ABG60326-ABG60574 represent selective targeting  
 CC peptides of the invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 57.1%; Score 4; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YKIQ 5  
 DB 4 YKIQ 7  
 RESULT 43  
 AAR10631  
 ID AAR10631 standard; Protein; 8 AA.  
 XX  
 AC AAR10631;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 18-APR-1991 (first entry)  
 XX  
 DE Human Papilloma Virus-16 "[Gln27]-E7-(20-27)-AMIDE" peptide.  
 XX  
 KW Papilloma virus; retinoblastoma gene-binding protein; genital warts;  
 KW cervical cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN EP412762-A.  
 XX  
 PD 13-FEB-1991.  
 XX  
 PF 06-AUG-1990; 90BP-0308652.  
 XX  
 PR 09-APR-1990; 90US-0506981.  
 PR 07-AUG-1989; 89US-0390569.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 PA (OLIF/) OLIFF A I.  
 XX

PI Oliff AI, Riemen MW;  
 XX  
 DR WPI; 1991-045887/07.  
 XX  
 PT Papilloma virus and retinoblastoma gene-binding protein  
 PT inhibitors - involves a specified aminoacid sequence contg. 13  
 PT residues for treatment of genital warts and cervical cancer  
 XX  
 PS Claim 12; Page 11; 11pp; English.  
 XX  
 CC The peptide carries an amide group at the C-terminus. The sequence  
 CC comprises residues 20 to 27 of the deduced HPV-16 E7 protein  
 CC sequence (N.Salzman and P.Howley, "The Papovaviridae", Vol 2,p.379,  
 CC Plenum Press, N.Y. 1987) but with Gln replacing Asp at position 27.  
 CC The peptides are used as screening tools and in the prevention,  
 CC therapy, prophylaxis and treatment of HPV-induced diseases. They  
 CC can also be used to raise antibodies either as vaccines or to  
 CC heighten the immune response to an HPV infection all ready present.  
 CC See also AAR10628-R10630, AAR10632-7.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 8 AA;  
 Query Match 57.1%; Score 4; DB 12; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LOPE 7  
 DB 2 LOPE 5  
 RESULT 44  
 AAR33158  
 ID AAR33158 standard; peptide; 8 AA.  
 XX  
 AC AAR33158;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 25-JUN-1993 (first entry)  
 XX  
 DE HPV E7 protein - RBG protein binding inhibitor peptide.  
 XX  
 KW Human papilloma virus; retinoblastoma gene; genital warts;  
 KW cervical cancer; treatment.  
 XX  
 OS Synthetic.  
 XX  
 PN EP531080-A2.  
 XX  
 PD 10-MAR-1993.  
 XX  
 PF 01-SEP-1992; 92EP-0307905.  
 XX  
 PR 04-SEP-1991; 91US-0754829.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Oliff AI, Riemen MW;  
 XX  
 DR WPI; 1993-078581/10.  
 XX  
 PT New polypeptide(s) which inhibit human papilloma virus binding to  
 PT RBG protein - useful for treating genital warts and cervical cancer  
 XX  
 PS Claim 7; Page 15; 15pp; English.  
 XX  
 CC The sequence is that of a peptide which inhibits binding of human  
 CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)  
 CC protein. It can be used in the treatment of conditions caused by HPV,  
 CC esp. genital warts and cervical cancer.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

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SQ Sequence 8 AA;
Query Match 57.1%; Score 4; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
DB 2 LOPE 5
|||||
|||||

RESULT 45
AAV10184
ID AAY10184 standard; Peptide; 8 AA.
AC AAY10184;
XX
DT 12-MAY-1999 (first entry)
XX
DE T cell epitope/MHC ligand SEQ ID NO:114.
XX
KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
KW immunisation; tumour; infectious disease; immunotherapy; cancer;
KW malignant melanoma; viral disease; hepatitis; AIDS.
XX
OS Synthetic.
XX Human immunodeficiency virus type 1.
XX WO9902183-A2.
XX
XX 21-JAN-1999.
XX
XX 10-JUL-1998; 98WO-US14289.
XX
XX 10-DEC-1997; 97US-0988320.
XX 10-JUL-1997; 97CA-2209815.
XX (CTL-) CTL IMMUNOTHERAPIES CORP.
XX
XX Kuendig TM, Simard JUL;
XX WPI; 1999-120514/10.
XX
XX Inducing a cytotoxic T lymphocyte response - by maintaining a level
XX of antigen in the lymphatic system of a mammal so as to provide a
XX sustained CTL response, used to treat, e.g. AIDS
XX
XX Disclosure; Page 27; 199pp; English.
XX
XX The present invention describes a method of inducing and/or sustaining
XX an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
XX method comprises: (a) delivering an antigen to the mammal at a level to
XX induce an immunological CTL response in the mammal; and (b) maintaining
XX the level of the antigen in the mammal's lymphatic system to maintain
XX the immunologic CTL response. The method can be used for the delivery of
XX e.g. a differentiation antigen, a tumour-specific multilineage antigen,
XX an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
XX gene antigen, or a viral antigen. They can be used for the treatment of
XX disease such as cancer, e.g. malignant melanoma or infectious disease,
XX e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
XX to the lymphatic system provides for potent CTL stimulation that takes
XX place in the milieu of the lymphoid organ, and it sustains stimulation
XX that is necessary to keep CTL active, cytotoxic and recirculating
XX through the body. AAY10071 to AAY10639 represent examples of peptide
XX antigens given in the present invention.
XX
SQ Sequence 8 AA;
Query Match 57.1%; Score 4; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4
DB 5 KYKL 8
|||||
|||||

RESULT 46
AAV83922
ID AAY83922 standard; peptide; 8 AA.
XX
AC AAY83922;
XX
DT 05-JUL-2000 (first entry)
XX
DE HIV-1 gag p17 B8-restricted CTL epitope.
XX
KW Immunogen; particulate composition; immune response; assessment;
KW target skin site; skin immune reaction; HIV-1; immunocompetence;
KW antibody; cell mediated immunity; antigen exposure; allergy.
XX
OS Human immunodeficiency virus type 1.
XX
XX WO200014547-A1.
XX
XX 16-MAR-2000.
XX
XX 03-SEP-1999; 99WO-GB02915.
XX
XX 04-SEP-1998; 98US-0099261.
XX 10-JUN-1999; 99US-0139045.
XX (POWD-) POWDERJECT RES LTD.
XX
XX Sarphie DF, Roberts LK, Fuller DL;
XX WPI; 2000-257072/22.
XX
XX Assessing an immune response against a selected agent in an individual
XX comprises accelerating a particulate composition, containing an
XX immunogenic compound from a selected agent, into the target skin site
XX of the individual -
XX
XX Disclosure; Page 23; 41pp; English.
XX
XX The invention relates to a method of using an immunogenic compound from
XX a selected agent in the manufacture of a particulate composition for
XX assessing an immune response against the selected agent in an
XX individual. The method comprises: (a) accelerating the particulate
XX composition into a target skin site in the individual; and (b) assessing
XX the target site to determine the presence or absence of a localized skin
XX immune reaction, where the presence of the immune reaction is indicative
XX of an immune response against the selected agent. Peptides
XX AAY83916-Y83925 represent examples of peptides that could be used if the
XX method is used to detect human immunodeficiency virus type 1 (HIV-1). The
XX method is useful for assessing immunocompetence, antibody and cell
XX mediated immunity, antigen exposure, or allergic conditions in an
XX individual.
XX
XX Sequence 8 AA;
Query Match 57.1%; Score 4; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4
DB 5 KYKL 8
|||||
|||||

RESULT 47
AAU12533
ID AAU12533 standard; Peptide; 8 AA.
XX
AC AAU12533;
XX

```

DT 27-SEP-2001 (first entry)  
 XX Human HIV-1 Th-CTL overlapping epitope #40.  
 DE XX  
 XX Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;  
 KW human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;  
 KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;  
 KW Vaccinia ankara.  
 XX  
 XX Homo sapiens.  
 OS Human immunodeficiency virus type 1.  
 OS  
 XX WO200156355-A2.  
 PN  
 XX 09-AUG-2001.  
 XX  
 XX 05-FEB-2001; 2001WO-US03540.  
 XX  
 XX 04-FEB-2000; 2000US-0497497.  
 PR (UYDU-) UNIV DUKE.  
 PA  
 XX Haynes BF, Liao H;  
 PI  
 XX WPI; 2001-488827/53.  
 XX  
 XX Vaccine for immunizing against human immunodeficiency virus has mixture  
 PT or linear array of peptides comprising immunodominant T-helper epitopes  
 PT and major histocompatibility complex cytotoxic T-lymphocyte epitopes -  
 XX  
 XX Disclosure; Page 27; 33pp; English.  
 PS  
 XX The present invention relates to human immunodeficiency virus (HIV)  
 CC and in particular to a human leukocyte antigen (HLA)-based HIV vaccine.  
 CC The vaccine comprises a mixture or linear array of peptides, or its  
 CC variants, where the peptides contain immunodominant T-helper (Th)  
 CC epitopes and major histocompatibility complex (MHC) cytotoxic T-  
 CC lymphocyte (CTL) epitopes and the linear array of peptides are  
 CC preferably expressed in modified Vaccinia ankara. The vaccine is useful  
 CC for immunising a patient against HIV and focuses immune response on many  
 CC dominant and subdominant CTL epitopes of HIV. DNA or live vectors with  
 CC linear arrays of CTL epitopes can be used as either primes or boosts of  
 CC peptides or of each other to optimally give CTL anti-HIV responses. The  
 CC vaccine induces salutary anti-HIV immune responses. AAU12447-AAU12558  
 CC represent the amino acid sequences of the Th-CTL epitopes and HIV  
 CC immunogenic peptides used in the invention.  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 57.1%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KYKL 4  
 Db |||||  
 5 KYKL 8  
 RESULT 48  
 AAG62330  
 ID AAG62330 standard; peptide; 8 AA.  
 XX  
 XX AAG62330;  
 AC  
 XX 24-AUG-2001 (first entry)  
 DT  
 XX Casein-related peptide SEQ ID 29.  
 DE  
 XX Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.  
 KW  
 XX Synthetic.  
 OS  
 XX WO200134828-A1.  
 PN

XX 17-MAY-2001.  
 PD  
 XX 10-NOV-2000; 2000WO-JP07930.  
 PF  
 XX 11-NOV-1999; 99JP-0321084.  
 PR  
 XX (CALV ) CALPIS CO LTD.  
 PA  
 XX Yamamoto N, Ueno K, Ejiri M;  
 PI  
 XX WPI; 2001-343606/36.  
 DR  
 XX Production of tripeptides for treating hypertension and stress by  
 PT processing casein with proteinase and peptidase  
 XX  
 XX Example 4; Page 13; 32pp; Japanese.  
 PS  
 XX This invention relates to a method for the production of tripeptides. The  
 CC method comprises treating material containing milk casein with a  
 CC proteinase to produce intermediate peptide containing ValProPro or  
 CC IleProPro with no proline residue any where else in the peptide. Use of  
 CC the peptides may result in hypotensive and tranquiliser activity. The  
 CC peptide can be used in treatments to lower blood pressure and in the  
 CC treatment of stress. The present sequence represents a peptide used in an  
 CC example illustrating the method of the invention.  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 57.1%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LQPE 7  
 Db |||||  
 5 LQPE 8  
 RESULT 49  
 ABUS7482  
 ID ABUS7482 standard; Peptide; 8 AA.  
 XX  
 XX ABUS7482;  
 AC  
 XX 08-APR-2003 (first entry)  
 DT  
 XX HIV cytotoxic lymphocyte epitope #46.  
 DE  
 XX  
 XX MHC; major histocompatibility complex; human; cytostatic; anti-HIV;  
 KW antiinflammatory; dermatological; antiasthmatic; antidiabetic; virucide;  
 KW antiarteriosclerotic; antiulcer; antirheumatic; antiarthritic; AIDS;  
 KW antipsoriatic; immunosuppressive; inflammatory bowel disease; measles;  
 KW Crohn's disease; ulcerative colitis; sclerositis; type I diabetes; pox;  
 KW rheumatoid arthritis; psoriasis; atopic dermatitis; asthma; chicken pox;  
 KW malignant melanoma; carcinoma; cancer; leukaemia; lymphoma; hepatitis;  
 KW rubella; herpes; human immunodeficiency virus.  
 XX  
 XX Human immunodeficiency virus.  
 OS  
 XX WO200272631-A2.  
 PN  
 XX 19-SEP-2002.  
 PD  
 XX  
 XX 13-MAR-2002; 2002WO-DK00169.  
 PF  
 XX 14-MAR-2001; 2001DK-0000435.  
 PR  
 XX 14-MAR-2001; 2001DK-0000436.  
 PR  
 XX 14-MAR-2001; 2001DK-0000441.  
 PR  
 XX 14-MAR-2001; 2001US-275447P.  
 PR  
 XX 14-MAR-2001; 2001US-275448P.  
 PR  
 XX 14-MAR-2001; 2001US-275470P.  
 PR  
 XX (DAKO-) DAKOCYTOMATION DENMARK AS.  
 PA

PA (DYNA-) DYNAL BIOTECH ASA.  
 XX Winther L, Petersen LO, Buus S, Schoeller J, Ruub E, Aamellem O;  
 XX WPI; 2002-759837/82.  
 DR  
 XX New Major Histocompatibility Complex (MHC) molecule construct, useful  
 PT for treating, preventing, stabilizing or alleviating a disease  
 PT involving MHC recognizing cells e.g., cancer  
 XX  
 PS Disclosure; Figure 37; 304pp; English.  
 XX  
 CC This invention relates to a new Major Histocompatibility Complex (MHC)  
 CC molecule construct comprising a carrier molecule to which one or more  
 CC MHC molecules are attached either directly or via one or more entities.  
 CC The construct of the invention may have cytostatic, antiinflammatory,  
 CC dermatological, antitumor, antidiabetic, anti-HIV, virucide,  
 CC antiparasitic, antitumor, antirheumatic, antiarthritic,  
 CC antipsoriatic and immunosuppressive activities and may be used in gene  
 CC therapy. The MHC molecule construct is useful as a therapeutic  
 CC composition in vivo or ex vivo therapy, for treating, preventing,  
 CC stabilising or alleviating a disease involving MHC recognising cells,  
 CC for monitoring MHC recognising cells or establishing a prognosis of a  
 CC disease or diagnosing a disease, or determining the status of a disease  
 CC or the effectiveness of a medicament against a disease, involving MHC  
 CC recognising cells, e.g., chronic inflammatory bowel disease such as  
 CC Crohn's disease or ulcerative colitis, scleroderma, type I diabetes,  
 CC rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant  
 CC melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the  
 CC uterus, cervical cancer, prostate cancer, brain cancer, head and neck  
 CC cancer, leukaemia, cutaneous lymphoma, hepatic carcinoma, colorectal  
 CC cancer, bladder cancer, rejection-related disease, Graft-versus-host-  
 CC related disease, or a viral disease associated with hepatitis, Acquired  
 CC Immunodeficiency Syndrome (AIDS), measles, pox, chicken pox, rubella or  
 CC herpes. The MHC molecule construct is also useful for flow cytometry,  
 CC histology or cytology. The present sequence represents a peptide  
 CC used to create the MHC molecule construct of the invention.  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 57.1%; Score 4; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KYKL 4  
 DB 5 KYKL 8  
 RESULT 50  
 ABG79866  
 ID ABG79866 standard; Peptide; 8 AA.  
 AC  
 XX ABG79866;  
 XX  
 XX 15-NOV-2002 (first entry)  
 XX  
 DE MHC class I molecule, viral epitope #114.  
 XX  
 XX Major histocompatibility complex; MHC; MHC class I molecule; virus;  
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
 KW antigen; immunogenic; malignant tumor; carcinoma; melanoma; leukaemia;  
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
 KW acquired immune deficiency syndrome; AIDS.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 XX WO200262368-A2.  
 XX  
 XX 15-AUG-2002.  
 PD  
 XX 22-JAN-2002; 2002WO-US02033.  
 XX  
 PR 02-FEB-2001; 2001US-0776232.  
 XX  
 PA (CTL-) CTL IMMUNOTHERAPIES CORP.  
 XX  
 PI Kundig TM, Simard JUL;  
 XX  
 XX WPI; 2002-657506/70.  
 DR  
 XX Inducing or sustaining immunological cytotoxic T lymphocyte response in  
 PT a mammal, useful for treating a mammal with malignant tumour or  
 PT infectious disease, by directly administering an antigen to the  
 PT lymphatic system of the mammal  
 XX  
 XX Disclosure; Page 21; 73pp; English.  
 PS  
 XX The invention relates to a method of inducing and/or sustaining an  
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal  
 CC comprising administering directly to the lymphatic system of the mammal:  
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a  
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The  
 CC method is useful for inducing and/or sustaining CTL response in a mammal.  
 CC This is particularly useful for treating a mammal having a malignant  
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious  
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),  
 CC malaria, measles or tuberculosis), or in an animal having a  
 CC predisposition to these diseases. The mammal may be dogs, cats, mice,  
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans.  
 CC ABG79753-ABG80319 represent viral epitopes on major histocompatibility  
 CC complex (MHC) class I molecules, used in the method of the invention.  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 57.1%; Score 4; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KYKL 4  
 DB 5 KYKL 8  
 RESULT 51  
 AAR10635  
 ID AAR10635 standard; Protein; 9 AA.  
 XX  
 XX AAR10635;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 18-APR-1991 (first entry)  
 XX  
 DE Human Papilloma Virus-16 "[Gln26]-E7-(20-28)-AMIDE" peptide.  
 XX  
 XX Papilloma virus; retinoblastoma gene-binding protein; genital warts;  
 KW cervical cancer.  
 KW  
 XX Synthetic.  
 XX  
 XX EP412762-A.  
 XX  
 XX 13-FEB-1991.  
 PD  
 XX 06-AUG-1990; 90EP-0308652.  
 PF  
 XX 09-APR-1990; 90US-0506981.  
 PR 07-AUG-1989; 89US-0390569.  
 XX  
 XX (MERI ) MERCK & CO INC.  
 PA (OLIF/) OLIFF A I.  
 XX  
 XX Oliff AI, Riemen MW;  
 XX WPI; 1991-045887/07.  
 XX



PT Papilloma virus and retinoblastoma gene-binding protein  
 PT inhibitors - involves a specified aminoacid sequence contg. 13  
 PT residues for treatment of genital warts and cervical cancer  
 XX  
 PS Claim 12; Page 11; 11pp; English.  
 XX  
 CC The peptide carries an amide group at the C-terminus. The sequence  
 CC comprises residues 20 to 28 of the deduced HPV-16 E7 protein  
 CC sequence (N.Salzman and P.Howley, "The Papovaviridae", Vol 2,p.379,  
 CC Plenum Press, N.Y. 1987) but with Gln replacing Thr at position 26.  
 CC The peptides are used as screening tools and in the prevention,  
 CC therapy, prophylaxis and treatment of HPV-induced diseases. They  
 CC can also be used to raise antibodies either as vaccines or to  
 CC heighten the immune response to an HPV infection all ready present.  
 CC See also AAR10628-R10634, AAR10636-7.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 CC  
 SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
 ||||  
 DB 2 LQPE 5

RESULT 52  
 AAR25420  
 ID AAR25420 standard; peptide; 9 AA.  
 AC AAR25420;  
 XX  
 DT 11-DEC-1992 (first entry)  
 XX  
 DE Non-homologous auto-immune peptide 1.  
 XX  
 KW 75 kD antigen; infectious agent antigen; vaccination.  
 XX  
 OS Plasmodium falciparum.  
 XX  
 PN GB2251186-A.  
 XX  
 PD 01-JUL-1992.  
 XX  
 PF 04-DEC-1990; 90GB-0026278.  
 XX  
 PR 04-DEC-1990; 90GB-0026278.  
 XX  
 PA (BROW/) BROWLEY P A.  
 PA (GATZ/) GATZ R N.  
 XX  
 PI Bromley PA, Gatz RN;  
 XX  
 DR WPI; 1992-219635/27.  
 XX  
 PT Treatment of auto-immune diseases using polypeptide vaccines -  
 PT derived from heat shock or stress proteins of bacterial or other  
 PT pathogens  
 XX  
 PS Disclosure; Page 9; 32pp; English.  
 XX  
 CC The sequences given in AAR25420-1 are peptides which are non-  
 CC homologous to known stress proteins and related antigen sequences.  
 CC They are homologous to part of the P. falciparum 75 kD antigen. These  
 CC peptides are examples of the polypeptides used in the vaccine of the  
 CC invention, which are all derived from stress proteins from infectious  
 CC agent antigens which are related to human stress proteins, but have  
 CC little or no sequence homology within such human stress proteins.  
 CC It has been shown that certain infectious agent antigens are  
 CC closely related in amino acid sequence to human stress proteins,  
 CC and that immune reactions against such antigens can cross react

CC with the human proteins, leading to the possibility of developing  
 CC autoimmune disease. The injection of non-homologous peptides into  
 CC human beings would provide a route of effective vaccination against  
 CC subsequent autoimmune disease induction. The antibodies raised  
 CC through vaccination with these non-homologous peptides are specific  
 CC to the selected infectious agent antigen from which the vaccinating  
 CC peptide was derived.  
 XX  
 SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 13; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
 ||||  
 DB 1 KLQP 4

RESULT 53  
 AAR33157  
 ID AAR33157 standard; peptide; 9 AA.  
 XX  
 AC AAR33157;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 25-JUN-1993 (first entry)  
 XX  
 DE HPV E7 protein - RBG protein binding inhibitor peptide.  
 XX  
 KW Human papilloma virus; retinoblastoma gene; genital warts;  
 KW cervical cancer; treatment.  
 XX  
 OS Synthetic.  
 XX  
 PN EP531080-A2.  
 XX  
 PD 10-MAR-1993.  
 XX  
 PF 01-SEP-1992; 92EP-0307905.  
 XX  
 PR 04-SEP-1991; 91US-0754829.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Oliff AI, Riemen MW;  
 XX  
 DR WPI; 1993-078581/10.  
 XX  
 PT New polypeptide(s) which inhibit human papilloma virus binding to  
 PT RBG protein - useful for treating genital warts and cervical cancer  
 XX  
 PS Claim 7; Page 15; 15pp; English.  
 XX  
 CC The sequence is that of a peptide which inhibits binding of human  
 CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)  
 CC protein. It can be used in the treatment of conditions caused by HPV,  
 CC esp. genital warts and cervical cancer.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 14; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
 ||||  
 DB 2 LQPE 5

RESULT 54  
 AAR33163

ID AAR33163 standard; peptide; 9 AA.

XX AAR33163;

XX 25-MAR-2003 (updated)

DT 25-JUN-1993 (first entry)

XX HPV E7 protein - RBG protein binding inhibitor peptide.

XX Human papilloma virus; retinoblastoma gene; genital warts;

KW cervical cancer; treatment.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

/note= "N-acetyl-Leu"

XX EP531080-A2.

XX 10-MAR-1993.

XX 01-SEP-1992; 92EP-0307905.

XX 04-SEP-1991; 91US-0754829.

XX (MERI ) MERCK & CO INC.

XX Oliff AI, Riemen MW;

XX WPI; 1993-078581/10.

XX New polypeptide(s) which inhibit human papilloma virus binding to  
PT RBG protein - useful for treating genital warts and cervical cancer

XX Claim 7; Page 15; 15pp; English.

XX The sequence is that of a peptide which inhibits binding of human  
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)  
CC protein. It can be used in the treatment of conditions caused by HPV,  
CC esp. genital warts and cervical cancer.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 57.1%; Score 4; DB 14; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7

Db 1 LOPE 4

RESULT 55

AAR33170

ID AAR33170 standard; peptide; 9 AA.

XX AAR33170;

XX 25-MAR-2003 (updated)

DT 25-JUN-1993 (first entry)

XX HPV E7 protein - RBG protein binding inhibitor peptide.

XX Human papilloma virus; retinoblastoma gene; genital warts;

KW cervical cancer; treatment.

XX Synthetic.

XX EP531080-A2.

PD 10-MAR-1993.

XX 01-SEP-1992; 92EP-0307905.

XX 04-SEP-1991; 91US-0754829.

XX (MERI ) MERCK & CO INC.

XX Oliff AI, Riemen MW;

XX WPI; 1993-078581/10.

XX New polypeptide(s) which inhibit human papilloma virus binding to  
PT RBG protein - useful for treating genital warts and cervical cancer

XX Claim 7; Page 15; 15pp; English.

XX The sequence is that of a peptide which inhibits binding of human  
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)  
CC protein. It can be used in the treatment of conditions caused by HPV,  
CC esp. genital warts and cervical cancer.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 57.1%; Score 4; DB 14; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7

Db 2 LOPE 5

RESULT 56

AAR43741

ID AAR43741 standard; peptide; 9 AA.

XX AAR43741;

XX 25-MAR-2003 (updated)

DT 19-MAY-1994 (first entry)

XX MHC Class I allele HLA-A2.1 binding HPV16 E7 peptide.

XX Human papilloma virus; major histocompatibility complex; prevention;  
KW treatment; virus-related diseases; T cell response; cervical; human;  
KW carcinoma; adenoma; screening tools; diagnostics; diagnosis.

XX Synthetic.

XX WO9322338-A1.

XX 11-NOV-1993.

XX 04-MAY-1993; 93WO-NL00093.

XX 05-MAY-1992; 92EP-0201252.

PR 10-DEC-1992; 92EP-0203870.

PR 01-FEB-1993; 93EP-0200243.

PR 05-MAR-1993; 93EP-0200621.

XX (UYLE-) RIJKSUNIV LEIDEN.

XX Kast WM, Melief CJM, Sette AD, Sidney JC;

XX WPI; 1993-368718/46.

XX Peptide(s) derived from human papilloma virus - which bind to a  
PT human major histocompatibility complex Class I molecule, used for  
PT prevention and treatment of virus-related diseases

XX Claim 5; Page 51; 64pp; English.

XX The sequence is that of a peptide, derived from the E7 protein of  
 CC human papilloma virus (HPV) (residues 11-19), which is able to bind  
 CC to human MHC Class I allele HLA-A2.1. It is able to induce a T cell  
 CC response effective against HPV, in partic. a HLA class I-restricted  
 CC CD8+ cytotoxic T cell response. It can be used for prevention and  
 CC treatment of cervical carcinoma and/or adenoma and other HPV-related  
 CC diseases. It can also be used as a screening tool and in diagnostic  
 CC applications.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 9 AA;

SQ Sequence 9 AA;  
 Query Match 57.1%; Score 4; DB 14; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
 ||||  
 Db 5 LOPE 8

RESULT 57  
 AAR43742  
 ID AAR43742 standard; peptide; 9 AA.

XX AAR43742;

XX AC  
 XX 25-MAR-2003 (updated)  
 DT 19-MAY-1994 (first entry)

XX MHC Class I allele HLA-A2.1 binding HPV16 E7 peptide.

XX Human papilloma virus; major histocompatibility complex; prevention;  
 KW treatment; virus-related diseases; T cell response; cervical; human;  
 KW carcinoma; adenoma; screening tools; diagnostics; diagnosis.

XX Synthetic.

XX WO9322338-A1.

XX PD 11-NOV-1993.

XX PF 04-MAY-1993; 93WO-NL00093.

XX PR 05-MAY-1992; 92EP-0201252.

XX PR 10-DEC-1992; 92EP-0203870.

XX PR 01-FEB-1993; 93EP-0200243.

XX PR 05-MAR-1993; 93EP-0200621.

XX (UYLE-) RIJKSUNIV LEIDEN.

XX Kast WM, Melief CJM, Sette AD, Sidney JC;

XX WPI; 1993-368718/46.

XX Peptide(s) derived from human papilloma virus - which bind to a

PT human major histocompatibility complex Class I molecule, used for

PT prevention and treatment of virus-related diseases

XX Claim 5; Page 51; 64pp; English.

XX The sequence is that of a peptide, derived from the E7 protein of  
 CC human papilloma virus (HPV) (residues 12-20), which is able to bind  
 CC to human MHC Class I allele HLA-A2.1. It is able to induce a T cell  
 CC response effective against HPV, in partic. a HLA class I-restricted  
 CC CD8+ cytotoxic T cell response. It can be used for prevention and  
 CC treatment of cervical carcinoma and/or adenoma and other HPV-related  
 CC diseases. It can also be used as a screening tool and in diagnostic  
 CC applications.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

XX Sequence 9'AA;

Query Match 57.1%; Score 4; DB 14; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
 ||||  
 Db 4 LOPE 7

RESULT 58

AAR59257

ID AAR59257 standard; peptide; 9 AA.

XX AAR59257;

XX 25-MAR-2003 (updated)

DT 10-MAY-1995 (first entry)

XX Peptide fragment (1.0229) of HPV binds HLA-A2.1.

XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;  
 KW HIV; core antigen; surface antigen; pharmaceutical composition;  
 KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;  
 KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;

XX human leukocyte antigen.

XX Human papilloma virus.

XX PN WO9420127-A1.

XX PD 15-SEP-1994.

XX PF 04-MAR-1994; 94WO-US02353.

XX PR 05-MAR-1993; 93US-0027146.

XX PR 04-JUN-1993; 93US-0073205.

XX PR 29-NOV-1993; 93US-0159184.

XX (CYTE-) CYTEL CORP.

XX Grey HM, Kast WM, Sette A, Sidney J;

XX WPI; 1994-302678/37.

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 for treatment or prophylaxis of cancer, virus infection or  
 autoimmune diseases.

XX Example 5; Page 106; 138pp; English.

XX AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1  
 CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity  
 CC of at least 1% as compared to a reference peptide (AAR71293). AAR59257  
 CC has an IC50 of <0.003 and the sequence occurs at position 14 in the HPV  
 CC E7 protein. The peptides of the invention can induce cytotoxic T  
 CC lymphocytes which can react with target cells. They can be used for the  
 CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,  
 CC etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
 ||||  
 Db 2 LOPE 5

RESULT 59

```

AAR59246
ID AAR59246 standard; peptide; 9 AA.
XX
AC AAR59246;
XX
DT 25-MAR-2003 (updated)
DT 04-MAY-1995 (first entry)
XX
DE Peptide fragment (1.0316) of c-ERB2 binds HLA-A2.1.
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; core antigen; surface antigen; pharmaceutical composition;
KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO9420127-A1.
XX
PD 15-SEP-1994.
XX
PF 04-MAR-1994; 94WO-US02353.
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
DR WPI; 1994-302678/37.
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX Example 5; Page 105; 138pp; English.
XX
AA AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59246
CC has an IC50 of <0.0002 and the sequence occurs at position 391 in the
CC c-ERB2 protein. The peptides of the invention can induce cytotoxic T
CC lymphocytes which can react with target cells. They can be used for the
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
CC etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA;
Query Match 57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
DB 2 LOPE 5

RESULT 60
AAR73799
ID AAR73799 standard; peptide; 9 AA.
XX
AC AAR73799;
XX
DT 25-MAR-2003 (updated)
DT 19-JUN-1995 (first entry)
XX
DE Antigen fragment 115, from HPV(a) has binding affinity for HLA-A2.1.
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;

AAR59246
ID AAR59246 standard; peptide; 9 AA.
XX
AC AAR59246;
XX
DT 25-MAR-2003 (updated)
DT 04-MAY-1995 (first entry)
XX
DE Peptide fragment (1.0316) of c-ERB2 binds HLA-A2.1.
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; core antigen; surface antigen; pharmaceutical composition;
KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO9420127-A1.
XX
PD 15-SEP-1994.
XX
PF 04-MAR-1994; 94WO-US02353.
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
DR WPI; 1994-302678/37.
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX Example 5; Page 105; 138pp; English.
XX
AA AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59246
CC has an IC50 of <0.0002 and the sequence occurs at position 391 in the
CC c-ERB2 protein. The peptides of the invention can induce cytotoxic T
CC lymphocytes which can react with target cells. They can be used for the
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
CC etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA;
Query Match 57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
DB 2 LOPE 5

RESULT 61
AAR73800
ID AAR73800 standard; peptide; 9 AA.
XX
AC AAR73800;
XX
DT 25-MAR-2003 (updated)
DT 19-JUN-1995 (first entry)
XX
DE Antigen fragment 116, from HPV has binding affinity for HLA-A2.1.
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
KW diagnostic; MHC class I molecule; major histocompatibility complex;
KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; P1P; 8mer;

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KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
KW herpes simplex virus; influenza A; M1.
XX
OS Human papilloma virus strain 16.
XX
PN WO9420127-A1.
XX
PD 15-SEP-1994.
XX
PF 04-MAR-1994; 94WO-US02353.
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
PA (CYTE-) CYTEL CORP.
XX
XX Grey HM, Kast WM, Sette A, Sidney J;
PI WPI; 1994-302678/37.
XX
DR Disclosure; Page 84; 138pp; English.
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX Disclosure; Page 84; 138pp; English.
XX
CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
CC motifs disclosed in the invention, these peptides were screened for
CC further motifs. Only peptides with binding affinity of at least 1%
CC (binding affinity is expressed as an IC50 value) as compared to the
CC standard peptide (AAR71293) in assays. This peptide from HPV E7
CC antigen has a binding value of 1.4000. The peptides of the invention can
CC induce cytotoxic T lymphocytes which can react with target cells. They
CC can be used for the treatment or prophylaxis of cancer, eg. prostate
CC cancer or lymphoma, etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA;
Query Match 57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
Db 5 LOPE 8

RESULT 63
AAR80939
ID AAR80939 standard; peptide; 9 AA.
XX
AC AAR80939;
XX
XX 03-MAY-1996 (first entry)
XX
DE Peptide for increasing HLA-A2.1 cell expression.
XX
KW Human melanoma-associated protein; MAGE-2; tumour rejection antigen;
KW precursor; major histocompatibility complex; MHC; class I; HLA-A2.1;
KW binding motif; cytolytic T cell; CTL; induction; peptide loading;
KW primary immune response.
XX
XX Synthetic.
XX
XX WO9525530-A1.
PN
XX 28-SEP-1995.
PD
XX 21-MAR-1995; 95WO-US03535.
PF
XX 24-MAR-1994; 94US-0217188.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
XX Boon-Falleur T, Kast WM, Melief CJM, Van Der Bruggen P;
PI Visseren NW;

KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
KW herpes simplex virus; influenza A; M1.
XX
OS Human papilloma virus strain 16.
XX
PN WO9420127-A1.
XX
PD 15-SEP-1994.
XX
PF 04-MAR-1994; 94WO-US02353.
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
PA (CYTE-) CYTEL CORP.
XX
XX Grey HM, Kast WM, Sette A, Sidney J;
PI WPI; 1994-302678/37.
XX
DR Disclosure; Page 84; 138pp; English.
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX Disclosure; Page 84; 138pp; English.
XX
CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
CC motifs disclosed in the invention, these peptides were screened for
CC further motifs. Only peptides with binding affinity of at least 1%
CC (binding affinity is expressed as an IC50 value) as compared to the
CC standard peptide (AAR71293) in assays. This peptide from HPV E7
CC antigen has a binding value of 0.0130. The peptides of the invention can
CC induce cytotoxic T lymphocytes which can react with target cells. They
CC can be used for the treatment or prophylaxis of cancer, eg. prostate
CC cancer or lymphoma, etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA;
Query Match 57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
Db 4 LOPE 7

RESULT 62
AAR73796
ID AAR73796 standard; peptide; 9 AA.
XX
AC AAR73796;
XX
XX 25-MAR-2003 (updated)
XX 19-JUN-1995 (first entry)
XX
DE Antigen fragment 112, from HPV has binding affinity for HLA-2.1.
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
KW diagnostic; MHC class I molecule; major histocompatibility complex;
KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
KW herpes simplex virus; influenza A; M1.
XX
XX Human papilloma virus strain 16.
OS
XX WO9420127-A1.
PN

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XX WPI; 1995-344456/44.  
 XX New peptide(s) based on tumour rejection antigen precursor MAGE-2 -  
 PT which bind HLA-A2 molecules to provoke cytolytic T cell prodn., used  
 PT partic. for treating cancers  
 XX  
 XX Example 3; Page 37; 44pp; English.  
 XX  
 CC Expression of HLA-A2.1 (T2) cells is increased by incubating T2  
 CC cells in medium containing the present peptide. T2 cells will  
 CC present the peptide bound to HLA-A2.1 in high amount and are good  
 CC antigen presenting cells. The claimed MAGE-2 peptides (see AAR80878-  
 CC AAR80888) can induce a similar primary immune response.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 57.1%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LOPE 7  
 DB ||||  
 4 LOPE 7

RESULT 64  
 AAR78889  
 ID AAR78889 standard; peptide; 9 AA.  
 XX  
 AC AAR78889;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 27-MAR-1996 (first entry)  
 XX  
 DE HPV16 E7 11-19 cytotoxic T lymphocyte epitope.  
 XX  
 KW HPV16 E7 11-19; cytotoxic T; CTL; epitope; helper T; HTL; cell;  
 KW lymphocyte; antigens; treatment; disease prevention;  
 XX  
 OS Human papillomavirus.  
 XX  
 PN WO9522317-A1.  
 XX  
 PD 24-AUG-1995.  
 XX  
 PF 16-FEB-1995; 95WO-US02121.  
 XX  
 PR 16-FEB-1994; 94US-0197484.  
 XX  
 XX (CYTE-) CYTEL CORP.  
 PA  
 PI Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;  
 XX  
 DR WPI; 1995-302545/39.  
 XX  
 XX 24-AUG-1995.  
 XX  
 PF 16-FEB-1995; 95WO-US02121.  
 XX  
 PR 16-FEB-1994; 94US-0197484.  
 XX  
 XX (CYTE-) CYTEL CORP.  
 PA  
 PI Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;  
 XX  
 DR WPI; 1995-302545/39.  
 XX  
 XX Compn. inducing cytotoxic T lymphocyte response to pref. viral,  
 PT bacterial, parasitic or tumour antigens - useful in the treatment  
 PT and prevention of diseases associated with the antigen e.g.  
 PT hepatitis B  
 XX  
 XX Example 14; Page 72; 109pp; English.  
 XX  
 CC A compn. which induces a cytotoxic T lymphocyte (CTL) response to  
 CC a human papillomavirus (HPV) antigen (Ag) in a mammal comprises, a  
 CC HPV CTL Ag response inducing peptide (i.e. AAR78888-R78895) and a  
 CC lipid conjugated helper T cell inducing peptide. The compn. is  
 CC useful in the treatment and prevention of HPV associated diseases.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 57.1%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LOPE 7  
 DB ||||  
 4 LOPE 7

RESULT 66  
 AAR78853  
 ID AAR78853 standard; peptide; 9 AA.  
 XX  
 AC AAR78853;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 27-MAR-1996 (first entry)  
 XX  
 DE HIV gap p17.3 cytotoxic T lymphocyte epitope.  
 XX

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LOPE 7  
 DB ||||  
 5 LOPE 8

RESULT 65  
 AAR78894  
 ID AAR78894 standard; peptide; 9 AA.  
 XX  
 AC AAR78894;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 27-MAR-1996 (first entry)  
 XX  
 DE HPV16 E7 12-20 cytotoxic T lymphocyte epitope.  
 XX  
 KW HPV16 E7 12-20; cytotoxic T; CTL; epitope; helper T; HTL; cell;  
 KW lymphocyte; antigens; treatment; disease prevention;  
 XX  
 OS Human papillomavirus.  
 XX  
 PN WO9522317-A1.  
 XX  
 PD 24-AUG-1995.  
 XX  
 PF 16-FEB-1995; 95WO-US02121.  
 XX  
 PR 16-FEB-1994; 94US-0197484.  
 XX  
 XX (CYTE-) CYTEL CORP.  
 PA  
 PI Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;  
 XX  
 DR WPI; 1995-302545/39.  
 XX  
 XX Compn. inducing cytotoxic T lymphocyte response to pref. viral,  
 PT bacterial, parasitic or tumour antigens - useful in the treatment  
 PT and prevention of diseases associated with the antigen e.g.  
 PT hepatitis B  
 XX  
 XX Example 14; Page 72; 109pp; English.  
 XX  
 CC A compn. which induces a cytotoxic T lymphocyte (CTL) response to  
 CC a human papillomavirus (HPV) antigen (Ag) in a mammal comprises, a  
 CC HPV CTL Ag response inducing peptide (i.e. AAR78888-R78895) and a  
 CC lipid conjugated helper T cell inducing peptide. The compn. is  
 CC useful in the treatment and prevention of HPV associated diseases.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 57.1%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LOPE 7  
 DB ||||  
 4 LOPE 7

RESULT 66  
 AAR78853  
 ID AAR78853 standard; peptide; 9 AA.  
 XX  
 AC AAR78853;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 27-MAR-1996 (first entry)  
 XX  
 DE HIV gap p17.3 cytotoxic T lymphocyte epitope.  
 XX

XX HIV gap p17.3; cytotoxic T; CTL; epitope; helper T; HTL; cell;  
 KW lymphocyte; viruses; parasites; tumours; antigens; treatment;  
 KW disease prevention.  
 XX Human immunodeficiency virus.  
 OS  
 XX WO9522317-A1.  
 PN  
 XX 24-AUG-1995.  
 PD  
 XX 16-FEB-1995; 95WO-US02121.  
 PP  
 XX 16-FEB-1994; 94US-0197484.  
 PR  
 XX (CYTE-) CYTEL CORP.  
 PA  
 XX Vitello MA, Chesnut RW, Sette AD, Celis E, Grey H;  
 PI WPI; 1995-302545/39.  
 XX  
 DR Compn. inducing cytotoxic T lymphocyte response to pref. viral,  
 XX bacterial, parasitic or tumour antigens - useful in the treatment  
 PT and prevention of diseases associated with the antigen e.g.  
 PT hepatitis B  
 PT  
 XX Disclosure; Page 17; 109pp; English.  
 PS  
 XX A compn. which induces a cytotoxic T lymphocyte (CTL) response to  
 CC an antigen (Ag) in a mammal comprises, a CTL Ag response inducing  
 CC peptide (i.e. AAR78824-R78853) and a lipid conjugated helper T cell  
 CC inducing peptide. The compn. induces a CTL response to bacterial,  
 CC viral or tumour Ags, and is therefore useful in the treatment and  
 CC prevention of diseases associated with the Ag.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 CC  
 XX Sequence 9 AA;  
 SQ

Query Match 57.1%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
 DB 5 KYKL 8  
 ||||  
 ||||

RESULT 67  
 AAW39661  
 ID AAW39661 standard; peptide; 9 AA.  
 XX  
 XX AAW39661;  
 AC  
 XX 11-JUN-1998 (first entry)  
 DT  
 XX HPV16/18 E7 peptide (pos. 11-19).  
 DE  
 XX T cell epitope; immune response; human leukocyte antigen; HLA Class I;  
 KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;  
 KW disease; anti-tumour; anti-viral.  
 XX  
 OS Human papillomavirus.  
 XX  
 PN WO9741440-A1.  
 PD  
 XX 06-NOV-1997.  
 PP  
 XX 28-APR-1997; 97WO-NL00229.  
 PF  
 XX 23-DEC-1996; 96EP-0203670.  
 PR  
 XX 26-APR-1996; 96EP-0201145.  
 XX  
 OS Human papillomavirus.  
 XX  
 PN WO9741440-A1.  
 PD  
 XX 06-NOV-1997.  
 PP  
 XX 28-APR-1997; 97WO-NL00229.  
 PF  
 XX 23-DEC-1996; 96EP-0203670.  
 PR  
 XX 26-APR-1996; 96EP-0201145.  
 XX  
 OS (UYLE-) RIJKSUNIV LEIDEN.  
 XX  
 PN (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.  
 PD  
 XX Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;  
 PP WPI; 1997-549891/50.  
 PF  
 XX Method of selecting T cell peptide epitope(s) - by measuring the  
 PR stability of HLA class I-peptide complexes on intact B cells  
 XX  
 OS Example 3; Page 78; 109pp; English.

PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.  
 XX Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;  
 PI WPI; 1997-549891/50.  
 DR  
 XX Method of selecting T cell peptide epitope(s) - by measuring the  
 PT stability of HLA class I-peptide complexes on intact B cells  
 PT  
 XX Example 3; Page 78; 109pp; English.  
 PS  
 XX Peptides AAW39430-W39734 are used in a novel method for the selection of  
 CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The  
 CC method involves the identification of peptide sequences capable of  
 CC binding to an HLA (human leukocyte antigen) class I molecule and  
 CC measuring the binding of this epitope peptide to the HLA class I  
 CC peptide. The stability of binding of the peptide and MHC (major  
 CC histocompatibility complex) class I molecule is measured on intact human  
 CC B cells carrying the MHC molecule at their cell surfaces. The method can  
 CC be used to select peptide epitopes for generating vaccines against a  
 CC disease associated with the polypeptide, e.g. cancers or AIDS. The  
 CC peptide epitopes are especially T-cell peptide epitopes with strong  
 CC anti-tumour and anti-viral immune responses. Peptide AAW39661 is derived  
 CC from the human papillomavirus E7 protein and is capable of binding to the  
 CC human MHC Class I allele HLA-A2.1.  
 CC  
 XX Sequence 9 AA;  
 SQ

Query Match 57.1%; Score 4; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
 DB 5 LQPE 8  
 ||||  
 ||||

RESULT 68  
 AAW39662  
 ID AAW39662 standard; peptide; 9 AA.  
 XX  
 XX AAW39662;  
 AC  
 XX 11-JUN-1998 (first entry)  
 DT  
 XX HPV16/18 E7 peptide (pos. 12-20).  
 DE  
 XX T cell epitope; immune response; human leukocyte antigen; HLA Class I;  
 KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;  
 KW disease; anti-tumour; anti-viral.  
 XX  
 OS Human papillomavirus.  
 XX  
 PN WO9741440-A1.  
 PD  
 XX 06-NOV-1997.  
 PP  
 XX 28-APR-1997; 97WO-NL00229.  
 PF  
 XX 23-DEC-1996; 96EP-0203670.  
 PR  
 XX 26-APR-1996; 96EP-0201145.  
 XX  
 OS (UYLE-) RIJKSUNIV LEIDEN.  
 XX  
 PN (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.  
 PD  
 XX Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;  
 PP WPI; 1997-549891/50.  
 PF  
 XX Method of selecting T cell peptide epitope(s) - by measuring the  
 PR stability of HLA class I-peptide complexes on intact B cells  
 XX  
 OS Example 3; Page 78; 109pp; English.

XX Peptides AAW39430-W39734 are used in a novel method for the selection of  
CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The  
CC method involves the identification of peptide sequences capable of  
CC binding to an HLA (human leukocyte antigen) class I molecule and  
CC measuring the binding of this epitope peptide to the HLA class I  
CC peptide. The stability of binding of the peptide and MHC (major  
CC histocompatibility complex) class I molecule is measured on intact human  
CC B cells carrying the MHC molecule at their cell surfaces. The method can  
CC be used to select peptide epitopes for generating vaccines against a  
CC disease associated with the polypeptide, e.g. cancers or AIDS. The  
CC peptide epitopes are especially T-cell peptide epitopes with strong  
CC anti-tumour and anti-viral immune responses. Peptide AAW39662 is derived  
CC from the human papillomavirus E7 protein and is capable of binding to the  
CC human MHC Class I allele HLA-A2.1.  
XX  
SQ Sequence 9 AA;  
Query Match 57.1%; Score 4; DB 18; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;  
QY 4 LOPE 7  
| | | |  
DB 4 LOPE 7  
| | | |  
RESULT 69  
AAW36590  
ID AAW36590 standard; peptide; 9 AA.  
XX  
AC AAW36590;  
XX  
XX  
DT 25-MAR-2003 (updated)  
DT 09-MAR-1998 (first entry)  
XX  
DE Hepatitis B virus bulk antigen.  
XX  
XX Melanoma protein; MAGE-2; tumour rejection antigen precursor; HBV;  
KW binding motif; human leukocyte antigen; HLA-A2.1; cytolytic T cell;  
KW CTL; induce; production; Hepatitis B virus.  
XX  
XX Hepatitis B virus.  
XX  
XX US5686068-A.  
PN  
XX  
PD 11-NOV-1997.  
XX  
XX 25-JUL-1996; 96US-0687226.  
PF  
XX 25-JUL-1996; 96US-0687226.  
PR  
PR 24-MAR-1994; 94US-0217188.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
XX  
XX Boon-Falleur T, Melief CJM, Van Der Bruggen P, Van Der Burg S;  
PI Visseren MW;  
PI  
XX WPI; 1997-558084/51.  
XX  
XX Induction of cytolytic T cell production in vivo - by administering  
PT MAGE-2 peptide(s)  
PT  
XX  
XX Example 3; Column 9; 24pp; English.  
XX  
XX This peptide sequence represents a hepatitis B virus reference peptide  
CC used in determining the primary induction of the immune response against  
CC MAGE-2 (a tumour rejection antigen precursor) peptides. Only peptides  
CC AAW36529-39 have the ability to bind to human leukocyte antigen (HLA)  
CC A2.1 molecule with high affinity and are therefore the only candidates of  
CC the MAGE-2 protein to be recognised by human cytolytic T cells (CTL),  
CC because CTL recognise peptides only when bound to HLA molecules.

CC Production of CTL in a subject can be induced by administering a MAGE-2  
CC peptide (particularly AAW36531, AAW36533 and AAW36537) to a subject who  
CC presents HLA-A2 molecules on cells. The method can be used to treat  
CC subjects in need of additional CTL.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 9 AA;  
Query Match 57.1%; Score 4; DB 18; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;  
QY 4 LOPE 7  
| | | |  
DB 4 LOPE 7  
| | | |  
RESULT 70  
AAW78893  
ID AAW78893 standard; peptide; 9 AA.  
XX  
AC AAW78893;  
XX  
XX 17-NOV-1998 (first entry)  
XX  
XX Human papillomavirus 16 E7 protein fragment 11-19.  
DE  
XX  
KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;  
KW class II associated peptide; pathogen; gene therapy; genetic disease;  
KW infection; downregulation; immune response.  
XX  
XX Human papillomavirus.  
OS  
OS Synthetic.  
XX  
XX WO9831398-A1.  
PN  
XX 23-JUL-1998.  
PD  
XX 22-JAN-1998; 98WO-US01499.  
PF  
XX 06-JAN-1998; 98US-0003253.  
PR  
PR 22-JAN-1997; 97US-0787547.  
XX  
XX (PANG-) PANGAEA PHARM INC.  
XX  
XX Curley JM, Hedley ML, Langer RS, Lunsford LB;  
PI  
XX WPI; 1998-427556/36.  
XX  
XX New preparations of microparticles - comprising a synthetic polymer  
PT matrix and nucleic acid comprising an expression vector for use in  
PT gene therapy  
XX  
XX Disclosure; Page 10; 101pp; English.  
XX  
XX A microparticle preparation (MP) has been developed, consisting of  
CC microparticles having a diameter of less than 100 nm. The MP  
CC comprises: (a) a polymeric matrix (PM) consisting of one or more  
CC synthetic polymers having a solubility in water of less than 1 mg/l; and  
CC (b) an expression vector selected from RNA molecules (at least 50% of  
CC which are closed circles) or circular plasmid DNA (at least 50% of which  
CC are supercoiled). Also described is a MP of at most 20 microns in  
CC diameter, comprising: (a) a PM; and (b) a NAM comprising an expression  
CC control sequence operatively linked to a coding sequence, where the  
CC coding sequence encodes an expression product selected from: (1) a  
CC polypeptide at least 7 amino acids in length, having a sequence identical  
CC to the sequence of: (i) a fragment of a naturally-occurring mammalian  
CC protein; or (ii) a fragment of a naturally-occurring protein from an  
CC infectious agent which infects a mammal; (2) a peptide having a length  
CC and sequence which permits it to bind to an MHC class I or II molecule;  
CC and (3) the polypeptide or the peptide linked to a trafficking sequence.  
CC AAW69763 to AAW69765, and AAW78793 to AAW78897 are peptide fragments for  
CC use in the present invention. The MPs are highly effective vehicles for



CC the delivery of polynucleotides into phagocytic cells. They can be used  
 CC for gene therapy, e.g. for treating genetic diseases, infections or  
 CC tumours or for downregulating an immune response.

XX Sequence 9 AA;

Query Match 57.1%; Score 4; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
 ||||  
 Db 5 LQPE 8

#### RESULT 71

AAW54766  
 ID AAW54766 standard; peptide; 9 AA.

XX AC AAW54766;

XX DT 25-SEP-1998 (first entry)

XX DE Peptide from HPV 16 E7 (11-19).

XX KW Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;  
 KW vaccine; treatment.

XX OS Synthetic.

XX PN WO9813378-A1.

XX PD 02-APR-1998.

XX PF 25-SEP-1997; 97WO-NL00536.

XX PR 26-SEP-1996; 96EP-0202701.

XX PA (UYLE-) RIJKSUNIV LEIDEN.

XX PI Drijfhout JW, Koning F;

XX DR WPI; 1998-230631/20.

XX Increasing uptake and presentation of antigen(s) - by adding mannose  
 PT residue(s) to antigen for increasing T cell response, useful in,  
 PT e.g. vaccines against viral infection(s)

XX PS Disclosure; Page 37; 47pp; English.

XX The peptides AAW5459-W54809 are examples of peptides to which at least  
 CC 1 (preferably 2) mannose can be attached to increase their uptake as  
 CC antigens by antigen-presenting cells. Uptake of agonist mannosylated  
 CC peptides will increase the T cell response, whereas uptake of antagonist  
 CC peptides blocks the T cell response. Blocking binding of immunogenic  
 CC autoantigens can be used in treatment of type I diabetes, rheumatoid  
 CC arthritis, graft rejection etc., also to induce T-cell non-  
 CC responsiveness. Vaccines containing mannosylated antigen are used to  
 CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths  
 CC and parasites.

XX Sequence 9 AA;

Query Match 57.1%; Score 4; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
 ||||  
 Db 5 LQPE 8

#### RESULT 72

AAW54767

ID AAW54767 standard; peptide; 9 AA.

XX AC AAW54767;

XX DT 25-SEP-1998 (first entry)

XX DE Peptide from HPV 16 E7 (12-20).

XX KW Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;  
 KW vaccine; treatment.

XX OS Synthetic.

XX PN WO9813378-A1.

XX PD 02-APR-1998.

XX PF 25-SEP-1997; 97WO-NL00536.

XX PR 26-SEP-1996; 96EP-0202701.

XX PA (UYLE-) RIJKSUNIV LEIDEN.

XX PI Drijfhout JW, Koning F;

XX DR WPI; 1998-230631/20.

XX Increasing uptake and presentation of antigen(s) - by adding mannose  
 PT residue(s) to antigen for increasing T cell response, useful in,  
 PT e.g. vaccines against viral infection(s)

XX PS Disclosure; Page 37; 47pp; English.

XX The peptides AAW5459-W54809 are examples of peptides to which at least  
 CC 1 (preferably 2) mannose can be attached to increase their uptake as  
 CC antigens by antigen-presenting cells. Uptake of agonist mannosylated  
 CC peptides will increase the T cell response, whereas uptake of antagonist  
 CC peptides blocks the T cell response. Blocking binding of immunogenic  
 CC autoantigens can be used in treatment of type I diabetes, rheumatoid  
 CC arthritis, graft rejection etc., also to induce T-cell non-  
 CC responsiveness. Vaccines containing mannosylated antigen are used to  
 CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths  
 CC and parasites.

XX Sequence 9 AA;

Query Match 57.1%; Score 4; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
 ||||  
 Db 4 LOPE 7

#### RESULT 73

AAW53459

ID AAW53459 standard; Protein; 9 AA.

XX AC AAW53459;

XX DT 18-JAN-2000 (first entry)

XX DE HIV-1 P17 protein (aa 24-32) binds HLA-B8.

XX KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;  
 KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;  
 KW human immunodeficiency virus; hepatitis B virus; papilloma virus;  
 KW melanoma; malaria; parasite.

XX OS Synthetic.

OS Human immunodeficiency virus type 1.

XX FR2776926-A1.  
 PN  
 PD 08-OCT-1999.  
 PD  
 PF 07-APR-1998; 98FR-0004323.  
 XX  
 PR 07-APR-1998; 98FR-0004323.  
 XX  
 XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (INSP ) INST PASTEUR LILLE.  
 XX  
 PI Le Gal FA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;  
 XX  
 XX WPI; 1999-583113/50.  
 XX  
 XX New lipopeptide containing lipid regions and two epitopes, all  
 PT separated by peptide spacers that impart hydrophilicity, useful in  
 PT vaccines  
 XX  
 PS Disclosure; Page 21; 35pp; French.  
 XX  
 CC The invention relates to the generation of a lipopeptide comprising at  
 CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)  
 CC epitope and at least one lipid residue with (i) the epitopes and lipid  
 CC portion and (ii) the epitopes, being separated independently by peptide  
 CC spacers. These spacers comprise sequences of amino acids which carry an  
 CC overall electrical charge in neutral media to ensure that the  
 CC lipopeptide is hydrophilic. The peptides AAY53301-Y53549 represents  
 CC examples of peptide epitopes used to generate the lipopeptides. These are  
 CC used in therapeutic or prophylactic compositions and vaccines to induce  
 CC specific immune responses against human immunodeficiency, hepatitis B or  
 CC papilloma viruses; p53 of melanoma or the malaria parasite.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 57.1%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 KYKL 4  
 DB 5 KYKL 8  
 RESULT 74  
 AAY55432  
 ID AAY55432 standard; peptide; 9 AA.  
 XX  
 AC AAY55432;  
 XX  
 DT 17-JAN-2000 (first entry)  
 XX  
 DE HLA binding plu-1 peptide.  
 XX  
 KW Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;  
 KW breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;  
 KW therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9949034-A1.  
 PN  
 PD 30-SEP-1999.  
 XX  
 XX 19-MAR-1999; 99WO-GB00866.  
 PF  
 XX 20-MAR-1998; 98GB-0005877.  
 PR  
 XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
 PA  
 XX

PI Taylor-papadimitriou J;  
 XX  
 DR WPI; 1999-591090/50.  
 XX  
 PT New nucleic acid encoding the cancer-associated polypeptide plu-1, for  
 PT diagnosis, treatment and prevention of cancer, especially of breast and  
 PT ovary  
 XX  
 PS Example 2; Fig 12; 173pp; English.  
 XX  
 CC The invention relates to a human cancer-associated polypeptide plu-1.  
 CC The plu-1 polypeptide can be recombinantly expressed by standard  
 CC recombinant methodology. Detection of the plu-1 nucleic acid or the  
 CC polypeptide is used for the following: (i) diagnosis (including imaging)  
 CC and prognosis of, and determination of susceptibility to, cancer,  
 CC specifically ovarian or breast cancer; and (ii) treating cancer (by  
 CC inducing an immune response against cancer cells, e.g. as a vaccine, or  
 CC by antisense inhibition). Antigens derived from the polypeptide are used  
 CC to generate activated cytotoxic T lymphocytes, or dendritic cells, for  
 CC subsequent return to the patient for treatment of cancer. The polypeptide  
 CC may also be used to identify inhibitors of plu-1 activity. Fragments of  
 CC the polypeptide, and antibodies raised against plu-1, are useful as assay  
 CC and imaging agents, also therapeutically (to induce an anti-idiotype  
 CC response or where conjugated to cytotoxic agents). The plu-1 antigen is  
 CC expressed more commonly in breast tumors than some known tumor antigens.  
 CC Sequences AAY55320-629 represent predicted peptides from the plu-1  
 CC polypeptide which may bind to the human class I alleles B27, A2, A3 and  
 CC All.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 57.1%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 LOPE 7  
 DB 2 LOPE 5  
 RESULT 75  
 AAY46565  
 ID AAY46565 standard; Peptide; 9 AA.  
 XX  
 AC AAY46565;  
 XX  
 DT 01-DEC-1999 (first entry)  
 XX  
 DE Immunogenic peptide having a human leukocyte antigen binding motif #1176.  
 XX  
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KW immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KW vaccine; immunisation.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9945954-A1.  
 PN  
 PD 16-SEP-1999.  
 XX  
 XX 13-MAR-1998; 98WO-US05039.  
 PF  
 XX 13-MAR-1998; 98WO-US05039.  
 PR  
 XX (EPIM-) EPIMUNE INC.  
 PA  
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;  
 PI WPI; 1999-551214/46.  
 XX  
 DR  
 XX

PT New immunogenic peptides with HLA binding motif, useful in treatment  
XX and diagnosis of cancers and viral diseases  
PS Claim 1; Page 76; 150pp; English.  
XX  
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
CC having a human major histocompatibility complex (MHC) Class I (also  
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
CC response against the antigen from which the peptide is derived.  
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
CC normally induced by an antigen in the form of a peptide fragment bound  
CC to a HLA molecule, rather than the intact foreign antigen itself, and  
CC are particularly important in tumour rejection and in fighting viral  
CC infections. The peptides are therefore useful therapeutically to treat  
CC or prevent viral infections and cancers in mammals (especially humans)  
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
CC They can be administered as vaccines to elicit an immune response in  
CC individuals susceptible or otherwise at risk of viral infection or  
CC cancer, or used to treat chronic or acute conditions. They are also  
CC useful diagnostically, and can be used to induce a cytotoxic T cell  
CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
CC produce CTLs ex vivo for infusion back into a patient. The  
CC polynucleotides encoding the immunogenic peptides are also useful  
CC therapeutically and for immunisation as above.  
XX  
SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 20; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
|||  
Db 1 KYKL 4

Search completed: November 25, 2003, 18:16:01  
Job time : 23.6755 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 13.9255 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-16

Perfect score: 7

Sequence: 1 KYKLOPE 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

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Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications\_AA.\*

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- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	15 US-10-281-652-16	Sequence 16, Appl
2	4	57.1	7	15 US-10-211-088-280	Sequence 280, Appl
3	4	57.1	8	10 US-09-380-323-4	Sequence 4, Appl
4	4	57.1	9	7 US-08-344-824-35	Sequence 35, Appl
5	4	57.1	9	9 US-09-759-960-17	Sequence 17, Appl
6	4	57.1	9	10 US-09-894-018-246	Sequence 246, Appl
7	4	57.1	9	10 US-09-909-460-104	Sequence 104, Appl
8	4	57.1	9	12 US-09-942-052-33	Sequence 33, Appl
9	4	57.1	9	12 US-09-942-052-39	Sequence 39, Appl
10	4	57.1	9	12 US-09-942-052-104	Sequence 104, Appl
11	4	57.1	9	12 US-09-942-052-218	Sequence 218, Appl
12	4	57.1	9	12 US-09-942-052-235	Sequence 235, Appl
13	4	57.1	9	12 US-09-942-052-236	Sequence 236, Appl
14	4	57.1	9	12 US-09-942-052-312	Sequence 312, Appl
15	4	57.1	9	12 US-09-942-052-339	Sequence 339, Appl

Sequence 424, App	9	12	US-09-942-052-424	4	57.1	16
Sequence 548, App	9	12	US-09-942-052-548	4	57.1	17
Sequence 619, App	9	12	US-09-942-052-619	4	57.1	18
Sequence 3, Appli	9	12	US-10-365-908-3	4	57.1	19
Sequence 26, Appl	9	12	US-10-365-908-26	4	57.1	20
Sequence 134, App	9	12	US-10-353-929-134	4	57.1	21
Sequence 455, App	9	12	US-10-371-069-455	4	57.1	22
Sequence 455, App	9	12	US-10-371-645-455	4	57.1	23
Sequence 12, Appl	9	15	US-10-001-546-12	4	57.1	24
Sequence 30, Appl	9	15	US-10-128-711-30	4	57.1	25
Sequence 66, Appl	9	15	US-10-128-711-66	4	57.1	26
Sequence 71, Appl	9	15	US-10-128-711-71	4	57.1	27
Sequence 263, App	9	15	US-10-133-210-263	4	57.1	28
Sequence 284, App	9	15	US-10-211-088-284	4	57.1	29
Sequence 19, Appl	10	9	US-09-847-185-19	4	57.1	30
Sequence 22, Appl	10	10	US-09-835-853-22	4	57.1	31
Sequence 2, Appli	10	10	US-09-902-556-2	4	57.1	32
Sequence 33, Appl	10	12	US-10-177-390-33	4	57.1	33
Sequence 54, Appl	10	12	US-09-942-052-54	4	57.1	34
Sequence 74, Appl	10	12	US-09-942-052-74	4	57.1	35
Sequence 256, App	10	12	US-09-942-052-256	4	57.1	36
Sequence 257, App	10	12	US-09-942-052-257	4	57.1	37
Sequence 360, App	10	12	US-09-942-052-360	4	57.1	38
Sequence 476, App	10	12	US-09-942-052-476	4	57.1	39
Sequence 573, App	10	12	US-09-942-052-573	4	57.1	40
Sequence 669, App	10	12	US-09-942-052-669	4	57.1	41
Sequence 688, App	10	12	US-09-942-052-688	4	57.1	42
Sequence 228, App	10	15	US-10-062-710-228	4	57.1	43
Sequence 271, App	10	15	US-10-133-210-271	4	57.1	44
Sequence 19, Appl	10	15	US-10-224-286-19	4	57.1	45
Sequence 206, App	11	15	US-10-062-710-206	4	57.1	46
Sequence 468, App	12	12	US-10-137-867-468	4	57.1	47
Sequence 3, Appli	13	12	US-10-300-215-3	4	57.1	48
Sequence 7, Appli	13	12	US-10-300-215-7	4	57.1	49
Sequence 29, Appl	13	12	US-10-300-215-29	4	57.1	50
Sequence 36, Appl	13	12	US-10-300-215-36	4	57.1	51
Sequence 36, Appl	13	15	US-10-001-546-36	4	57.1	52
Sequence 50, Appli	14	9	US-09-765-527-50	4	57.1	53
Sequence 4, Appli	14	10	US-09-902-556-4	4	57.1	54
Sequence 151, App	14	12	US-10-239-313A-151	4	57.1	55
Sequence 43, Appl	14	15	US-10-033-741-43	4	57.1	56
Sequence 51, Appl	15	9	US-09-765-527-51	4	57.1	57
Sequence 280, App	15	10	US-09-894-018-280	4	57.1	58
Sequence 9, Appli	15	12	US-09-569-197-9	4	57.1	59
Sequence 415, App	15	12	US-10-371-069-415	4	57.1	60
Sequence 415, App	15	12	US-10-371-645-415	4	57.1	61
Sequence 52, Appl	16	9	US-09-765-527-52	4	57.1	62
Sequence 65, Appl	16	9	US-09-765-527-65	4	57.1	63
Sequence 6, Appli	16	12	US-10-387-645-6	4	57.1	64
Sequence 7, Appli	16	12	US-10-387-645-7	4	57.1	65
Sequence 2, Appli	16	15	US-10-062-710-2	4	57.1	66
Sequence 53, Appl	17	9	US-09-765-527-53	4	57.1	67
Sequence 54, Appl	18	9	US-09-765-527-54	4	57.1	68
Sequence 8, Appli	18	12	US-09-569-197-8	4	57.1	69
Sequence 21, Appl	18	15	US-10-281-652-21	4	57.1	70
Sequence 44869, A	19	9	US-09-864-761-44869	4	57.1	71
Sequence 21, Appl	20	9	US-09-466-320-21	4	57.1	72
Sequence 45874, A	20	9	US-09-864-761-45874	4	57.1	73
Sequence 34, Appl	20	15	US-10-001-546-34	4	57.1	74
Sequence 15, Appl	3	15	US-10-119-417-15	3	42.9	75
Sequence 7, Appli	4	12	US-10-305-238-7	3	42.9	76
Sequence 2, Appli	4	12	US-10-150-654A-2	3	42.9	77
Sequence 3, Appli	4	12	US-10-150-654A-3	3	42.9	78
Sequence 4, Appli	4	12	US-10-150-654A-4	3	42.9	79
Sequence 5, Appli	4	12	US-10-150-654A-5	3	42.9	80
Sequence 6, Appli	4	12	US-10-150-654A-6	3	42.9	81
Sequence 7, Appli	4	12	US-10-150-654A-7	3	42.9	82
Sequence 11, Appl	4	12	US-10-150-654A-11	3	42.9	83
Sequence 101, App	4	14	US-10-101-487-101	3	42.9	84
Sequence 14, Appl	4	15	US-10-119-417-14	3	42.9	85
Sequence 7, Appli	4	15	US-10-142-049-7	3	42.9	86
Sequence 5, Appli	4	15	US-10-305-268-5	3	42.9	87
Sequence 12, Appl	4	15	US-10-305-268-12	3	42.9	88

89 3 42.9 5 11 US-09-788-006-57 Sequence 57, Appl  
90 3 42.9 5 11 US-09-788-006-58 Sequence 58, Appl  
91 3 42.9 5 11 US-09-788-006-59 Sequence 59, Appl  
92 3 42.9 5 12 US-10-027-038-18 Sequence 18, Appl  
93 3 42.9 5 12 US-10-315-920-17 Sequence 17, Appl  
94 3 42.9 5 12 US-10-020-354-89 Sequence 89, Appl  
95 3 42.9 5 12 US-10-150-654A-1 Sequence 1, Appl  
96 3 42.9 5 12 US-10-168-758-11 Sequence 11, Appl  
97 3 42.9 5 12 US-10-168-758-16 Sequence 16, Appl  
98 3 42.9 5 13 US-10-014-774-21 Sequence 21, Appl  
99 3 42.9 5 14 US-10-101-487-105 Sequence 105, App  
100 3 42.9 5 15 US-10-028-075B-69 Sequence 69, Appl

## ALIGNMENTS

RESULT 1  
US-10-281-652-16  
; Sequence 16, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265-00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-16

Query Match 100.0%; Score 7; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKLOPE 7  
Db 1 KYKLOPE 7

RESULT 2  
US-10-211-088-280  
; Sequence 280, Application US/10211088  
; Publication No. US2003010479A1  
; GENERAL INFORMATION:  
; APPLICANT: Premkumar, D. David  
; APPLICANT: Chen, Yih-Tai  
; TITLE OF INVENTION: No. US2003010479A1 Fusion Proteins And Assays For Molecular Bi  
; FILE REFERENCE: 01-1022-US  
; CURRENT APPLICATION NUMBER: US/10/211,088  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/309,395  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/341,589  
; PRIOR FILING DATE: 2001-12-13  
; NUMBER OF SEQ ID NOS: 366  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 280

; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Nuclear localization signal  
US-10-211-088-280

Query Match 57.1%; Score 4; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
Db 3 KYKL 6

RESULT 3  
US-09-380-323-4  
; Sequence 4, Application US/09380323  
; Patent No. US20020123471A1  
; GENERAL INFORMATION:  
; APPLICANT: Bavarian No. US20020123471A1dlic Research Institute A/S  
; APPLICANT: Uberia, Klaus  
; TITLE OF INVENTION: LENTIVIRUS BASED VECTOR AND VECTOR  
; TITLE OF INVENTION: SYSTEM  
; FILE REFERENCE: 20239-705  
; CURRENT APPLICATION NUMBER: US/09/380,323  
; CURRENT FILING DATE: 1999-11-22  
; PRIOR APPLICATION NUMBER: PCT/EP98/01191  
; PRIOR FILING DATE: 1998-03-23  
; PRIOR APPLICATION NUMBER: DK 0238/97  
; PRIOR FILING DATE: 1997-03-06  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Vector mutant  
US-09-380-323-4

Query Match 57.1%; Score 4; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
Db 4 KYKL 7

RESULT 4  
US-08-344-824-35  
; Sequence 35, Application US/08344824  
; Publication No. US20030152580A1  
; GENERAL INFORMATION:  
; APPLICANT: SETTE, Alessandro  
; APPLICANT: SIDNEY, John  
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
; NUMBER OF SEQUENCES: 399  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: One Market Plaza, Steuart Street Tower, 20th  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/344,824

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; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-35

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Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KYKL 4
Db 5 KYKL 8

RESULT 5
US-09-759-960-17
; Sequence 17, Application US/09759960
; Patent No. US20010006639A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORGANISM: Human papilloma virus

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; MOLECULE TYPE: peptide
US-09-759-960-17

Query Match 57.1%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 LQPE 7
Db 5 LQPE 8

RESULT 6
US-09-894-018-246
; Sequence 246, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 9
; TYPE: PRT
; ORGANISM: P. falciparum
US-09-894-018-246

Query Match 57.1%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KYKL 4
Db 1 KYKL 4

RESULT 7
US-09-909-460-104
; Sequence 104, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Junsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
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US-09-909-460-104

Query Match 57.1%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
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Db 5 LOPE 8

## RESULT 8

US-09-942-052-33  
; Sequence 33, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-33

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
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Db 2 LOPE 5

## RESULT 9

US-09-942-052-39  
; Sequence 39, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-39

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 5 LOPE 8

## RESULT 10

US-09-942-052-104  
; Sequence 104, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 104  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-104

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 2 LOPE 5

## RESULT 11

US-09-942-052-218  
; Sequence 218, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 218  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:



; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-218

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LQPE 7  
| | | |  
Db 2 LQPE 5

RESULT 12  
US-09-942-052-235  
; Sequence 235, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 235  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-235

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LQPE 7  
| | | |  
Db 1 LQPE 4

RESULT 13  
US-09-942-052-236  
; Sequence 236, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 236  
; LENGTH: 9  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-236

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LQPE 7  
| | | |  
Db 6 LQPE 9

RESULT 14  
US-09-942-052-312  
; Sequence 312, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 312  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-312

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LQPE 7  
| | | |  
Db 5 LQPE 8

RESULT 15  
US-09-942-052-339  
; Sequence 339, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 339  
; LENGTH: 9

;  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-339

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 1 LOPE 4

RESULT 16  
US-09-942-052-424  
; Sequence 424, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 424  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-424

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 1 LOPE 4

RESULT 17  
US-09-942-052-548  
; Sequence 548, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 548

;  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-548

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 2 LOPE 5

RESULT 18  
US-09-942-052-619  
; Sequence 619, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 619  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-619

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 1 LOPE 4

RESULT 19  
US-10-365-908-3  
; Sequence 3, Application US/10365908  
; Publication No. US20030170268A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/214,202  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-3

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LOPE 7
DB      5 LOPE 8

RESULT 20
US-10-365-908-26
; Sequence 26, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-26

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LOPE 7
DB      1 LOPE 4

US-10-353-929-134
; Sequence 134, Application US/10353929
; Publication No. US20030175288A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Tumor antigen
; FILE REFERENCE: GP01-1024
; CURRENT APPLICATION NUMBER: US/10/353,929
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: JP P2000-231814
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide based on the amino acid sequence of SEQ ID NO.50
US-10-353-929-134

Query Match      57.1%; Score 4; DB 12; Length 9;

US-10-371-069-455
; Sequence 455, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pf EXP1 73 (peptide 1167.53)
US-10-371-069-455

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYKL 4
DB      1 KYKL 4

US-10-371-645-455
; Sequence 455, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 455  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Pf EXP1 73 (peptide 1167.53)  
US-10-371-645-455

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
|||  
Db 1 KYKL 4

## RESULT 24

US-10-001-546-12  
; Sequence 12, Application US/10001546  
; Publication No. US20030027766A1  
; GENERAL INFORMATION:  
; APPLICANT: IOANNIDES, CONSTANTIN G.  
; APPLICANT: FISK, BRYAN A.  
; APPLICANT: IOANNIDES, MARIA G.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
; FILE REFERENCE: UTSC:390USC2  
; CURRENT APPLICATION NUMBER: US/10/001,546  
; CURRENT FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 08/403,459  
; PRIOR FILING DATE: 1995-03-14  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-001-546-12

Query Match 57.1%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 2 LOPE 5

## RESULT 25

US-10-128-711-30  
; Sequence 30, Application US/10128711  
; Publication No. US2003009634A1  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, Maria A.  
; APPLICANT: CHESTNUT, Robert W.  
; APPLICANT: SETTE, Alessandro D.  
; APPLICANT: CELIS, Esteban  
; APPLICANT: GRAY, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
CTL IMMUNITY  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/10/128,711  
FILING DATE: 22-Apr-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,484  
FILING DATE: 16-FEB-1994  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-10-128-711-30

Query Match 57.1%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
|||  
Db 5 KYKL 8

## RESULT 26

US-10-128-711-66  
; Sequence 66, Application US/10128711  
; Publication No. US2003009634A1  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, Maria A.  
; APPLICANT: CHESTNUT, Robert W.  
; APPLICANT: SETTE, Alessandro D.  
; APPLICANT: CELIS, Esteban  
; APPLICANT: GRAY, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
CTL IMMUNITY  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/10/128,711  
FILING DATE: 22-Apr-2002

```

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-128-711-66

Query Match          57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LOPE 7
Db      5 LOPE 8

RESULT 27
US-10-128-711-71
; Sequence 71, Application US/10128711
; Publication No. US2003099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491

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; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-128-711-71

Query Match          57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LOPE 7
Db      4 LOPE 7

RESULT 28
US-10-133-210-263
; Sequence 263, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 263
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-263

Query Match          57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYKL 4
Db      1 KYKL 4

RESULT 29
US-10-211-088-284
; Sequence 284, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David

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; CURRENT APPLICATION NUMBER: US/09/902,556
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/220,178
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An Artificial Sequence which is a synthetic variation of known G
; OTHER INFORMATION: peptides which were isolated in the stomach by a distinct cell ty
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)...(3)
; OTHER INFORMATION: Octanoyl ester attached to serine residue
US-09-902-556-2

Query Match          57.1%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KLOP 6
DB      6 KLOP 9

RESULT 33
US-10-177-390-33
; Sequence 33, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Influenza virus
US-10-177-390-33

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LQPE 7
DB      5 LQPE 8

RESULT 34
US-09-942-052-54
; Sequence 54, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
```

```
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-54

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LQPE 7
DB      2 LQPE 5

RESULT 35
US-09-942-052-74
; Sequence 74, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-74

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LQPE 7
DB      6 LQPE 9

RESULT 36
US-09-942-052-256
; Sequence 256, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
```

; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 256  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-256

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 6 LOPE 9

## RESULT 37

US-09-942-052-257  
; Sequence 257, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 257  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-257

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 2 LOPE 5

## RESULT 38

US-09-942-052-360  
; Sequence 360, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 257  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-257

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 2 LOPE 5

## RESULT 39

US-09-942-052-476  
; Sequence 476, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 476  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-476

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 2 LOPE 5

## RESULT 40

US-09-942-052-573  
; Sequence 573, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 476  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-476

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 2 LOPE 5

## RESULT 40

US-09-942-052-573  
; Sequence 573, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 476  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-476



; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 573  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-573

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|||  
Db 5 LQPE 8

RESULT 41  
US-09-942-052-669  
; Sequence 669, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 669  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-669

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|||  
Db 5 LQPE 8

RESULT 42  
US-09-942-052-688  
; Sequence 688, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 688  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-688

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|||  
Db 2 LQPE 5

RESULT 43  
US-10-062-710-228  
; Sequence 228, Application US/10062710  
; Publication No. US20030049253A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Frank Q.  
; APPLICANT: Chu, Yong-Liang  
; APPLICANT: Qiu, Jian-Tai  
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of  
; TITLE OF INVENTION: MHC-Recognized Epitopes  
; FILE REFERENCE: 3781-001-27  
; CURRENT APPLICATION NUMBER: US/10/062,710  
; PRIOR FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: US 60/310,498  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 228  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Epstein-Barr Virus  
US-10-062-710-228

Query Match 57.1%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|||  
Db 5 LQPE 8

RESULT 44  
US-10-133-210-271  
; Sequence 271, Application US/10133210  
; Publication No. US20030103964A1  
; GENERAL INFORMATION:  
; APPLICANT: Delisi, Charles  
; APPLICANT: Berzofsky, Jay  
; APPLICANT: Gulukota, Kamalakara  
; APPLICANT: Vaccaro, Dennis  
; APPLICANT: Weng, Zhiping  
; APPLICANT: Zhang, Chao  
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND  
; FILE REFERENCE: BU-035AX

```

; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 271
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-271

Query Match          57.1%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LOPE 7
Db      5 LOPE 8

RESULT 45
US-10-224-286-19
; Sequence 19, Application US/10224286
; Publication No. US20030108517A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/224,286
; FILING DATE: 19-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-224-286-19

Query Match          57.1%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LOPE 7
Db      5 LOPE 8
```

```

RESULT 46
US-10-062-710-206
; Sequence 206, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T Cell epitopes
US-10-062-710-206

Query Match          57.1%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LOPE 7
Db      6 LOPE 9

RESULT 47
US-10-137-867-468
; Sequence 468, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 468
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-468

Query Match          57.1%; Score 4; DB 12; Length 12;
```

Best Local Similarity 100.0%; Pred. No. 2.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKQ 5  
|  
|  
|  
|  
Db 1 YKQ 4

## RESULT 48

US-10-300-215-3  
; Sequence 3, Application US/10300215  
; Publication No. US20030153043A1  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne  
; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
; FILE REFERENCE: MER-104-Con.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; CURRENT FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: GB 9710480.6  
; PRIOR FILING DATE: 1997-05-21  
; PRIOR APPLICATION NUMBER: GB 9716197.0  
; PRIOR FILING DATE: 1997-07-31  
; PRIOR APPLICATION NUMBER: GB 9725270.4  
; PRIOR FILING DATE: 1997-11-28  
; PRIOR APPLICATION NUMBER: GB 9807751.4  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/067,235  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized monoclonal antibody fragments

US-10-300-215-3

Query Match 57.1%; Score 4; DB 12; Length 13;

Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|  
|  
|  
|  
Db 6 LQPE 9

## RESULT 49

US-10-300-215-7  
; Sequence 7, Application US/10300215  
; Publication No. US20030153043A1  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne  
; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
; FILE REFERENCE: MER-104-Con.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; CURRENT FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21

US-10-300-215-3

Query Match 57.1%; Score 4; DB 12; Length 13;

Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|  
|  
|  
|  
Db 6 LQPE 9

## RESULT 50

US-10-300-215-29  
; Sequence 29, Application US/10300215  
; Publication No. US20030153043A1  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne  
; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
; FILE REFERENCE: MER-104-Con.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; CURRENT FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: GB 9710480.6  
; PRIOR FILING DATE: 1997-05-21  
; PRIOR APPLICATION NUMBER: GB 9716197.0  
; PRIOR FILING DATE: 1997-07-31  
; PRIOR APPLICATION NUMBER: GB 9725270.4  
; PRIOR FILING DATE: 1997-11-28  
; PRIOR APPLICATION NUMBER: GB 9807751.4  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/067,235  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized monoclonal antibody fragments

US-10-300-215-3

Query Match 57.1%; Score 4; DB 12; Length 13;

Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|  
|  
|  
|  
Db 6 LQPE 9

## RESULT 51

US-10-300-215-29  
; Sequence 29, Application US/10300215  
; Publication No. US20030153043A1  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne  
; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
; FILE REFERENCE: MER-104-Con.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; CURRENT FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21

US-10-300-215-3

Query Match 57.1%; Score 4; DB 12; Length 13;

Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|  
|  
|  
|  
Db 6 LQPE 9

US-10-300-215-7  
; Sequence 29, Application US/10300215  
; Publication No. US20030153043A1  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne  
; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
; FILE REFERENCE: MER-104-Con.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; CURRENT FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: GB 9710480.6  
; PRIOR FILING DATE: 1997-05-21  
; PRIOR APPLICATION NUMBER: GB 9716197.0  
; PRIOR FILING DATE: 1997-07-31  
; PRIOR APPLICATION NUMBER: GB 9725270.4  
; PRIOR FILING DATE: 1997-11-28  
; PRIOR APPLICATION NUMBER: GB 9807751.4  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/067,235  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized monoclonal antibody fragments

US-10-300-215-7

Query Match 57.1%; Score 4; DB 12; Length 13;

Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|  
|  
|  
|  
Db 3 LQPE 6

## RESULT 52

US-10-300-215-29  
; Sequence 29, Application US/10300215  
; Publication No. US20030153043A1  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne  
; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
; FILE REFERENCE: MER-104-Con.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; CURRENT FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: GB 9710480.6  
; PRIOR FILING DATE: 1997-05-21  
; PRIOR APPLICATION NUMBER: GB 9716197.0  
; PRIOR FILING DATE: 1997-07-31  
; PRIOR APPLICATION NUMBER: GB 9725270.4  
; PRIOR FILING DATE: 1997-11-28  
; PRIOR APPLICATION NUMBER: GB 9807751.4  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/067,235  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized monoclonal antibody fragments

US-10-300-215-3

Query Match 57.1%; Score 4; DB 12; Length 13;

Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|  
|  
|  
|  
Db 3 LQPE 6

Db 6 LOPE 9

RESULT 51  
US-10-300-215-36  
; Sequence 36, Application US/10300215  
; Publication No. US20030153043A1  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne  
; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
; FILE REFERENCE: MER-104-CON.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; CURRENT FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: GB 9710480.6  
; PRIOR FILING DATE: 1997-05-21  
; PRIOR APPLICATION NUMBER: GB 9716197.0  
; PRIOR FILING DATE: 1997-07-31  
; PRIOR APPLICATION NUMBER: GB 9725270.4  
; PRIOR FILING DATE: 1997-11-28  
; PRIOR APPLICATION NUMBER: GB 9807751.4  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/067,235  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized monoclonal antibody fragments  
US-10-300-215-36

Query Match 57.1%; Score 4; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LOPE 7  
|||  
Db 3 LOPE 6

RESULT 52  
US-10-001-546-36  
; Sequence 36, Application US/10001546  
; Publication No. US20030027766A1  
; GENERAL INFORMATION:  
; APPLICANT: IOANNIDES, CONSTANTIN G.  
; APPLICANT: FISK, BRYAN A.  
; APPLICANT: IOANNIDES, MARIA G.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
; TITLE OF INVENTION: T-LYMPHOCYTES  
; FILE REFERENCE: UTSC:390USC2  
; CURRENT APPLICATION NUMBER: US/10/001,546  
; CURRENT FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 08/403,459  
; PRIOR FILING DATE: 1995-03-14  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide  
US-10-001-546-36

Query Match 57.1%; Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LOPE 7  
|||  
Db 1 LOPE 4

RESULT 53  
US-09-765-527-50  
; Sequence 50, Application US/09765527  
; Patent No. US20020006638A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/765,527  
; FILING DATE: 18-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: <unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: "XMP.49"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: C-Terminus  
; OTHER INFORMATION: /label= Amidation  
; /note= "The C-Terminus is Amidated."  
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-09-765-527-50

Query Match 57.1%; Score 4; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KLOP 6  
|||  
Db 8 KLOP 11

## RESULT 54

US-09-902-556-4  
; Sequence 4, Application US/09902556  
; Publication No. US20020187938A1  
; GENERAL INFORMATION:  
; APPLICANT: Dsghenghi, Romano  
; TITLE OF INVENTION: GHRELIN ANTAGONISTS  
; FILE REFERENCE: 87264-200  
; CURRENT APPLICATION NUMBER: US/09/902,556  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/220,178  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: An Artificial Sequence which is a synthetic variation of known GH  
; OTHER INFORMATION: peptides which were isolated in the stomach by a distinct cell ty  
; OTHER INFORMATION: humans.  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: An octanoyl ester is attached to the serine residue  
US-09-902-556-4

## Query Match

Best Local Similarity 57.1%; Score 4; DB 10; Length 14;  
100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6  
|||  
DB 10 KLOP 13

## RESULT 55

US-10-239-313A-151  
; Sequence 151, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 151  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-151

## Query Match

Best Local Similarity 57.1%; Score 4; DB 12; Length 14;  
100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6  
|||  
DB 10 KLOP 13

## RESULT 56

US-10-033-741-43  
; Sequence 43, Application US/10033741  
; Publication No. US20030049640A1  
; GENERAL INFORMATION:  
; APPLICANT: Herman, et al.  
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Vas  
; FILE REFERENCE: 9195-079  
; CURRENT APPLICATION NUMBER: US/10/033,741  
; CURRENT FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 43  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-033-741-43

## Query Match

Best Local Similarity 57.1%; Score 4; DB 15; Length 14;  
100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
|||  
DB 8 LQPE 11

## RESULT 57

US-09-765-527-51  
; Sequence 51, Application US/09765527  
; Patent No. US20020006638A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; FUSION PROTEINS AND BPI-DERIVED PEPTIDES  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/765,527  
; FILING DATE: 18-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: "XMP.50"  
; FEATURE:

```
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note="The C-terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-765-527-51

Query Match      57.1%; Score 4; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KLQP 6
Db      8 KLQP 11

RESULT 58
US-09-894-018-280
; Sequence 280, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Deniaw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 15
; TYPE: PRT
; ORGANISM: P. falciparum
US-09-894-018-280

Query Match      57.1%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYKL 4
Db      3 KYKL 6

RESULT 59
US-09-569-197-9
; Sequence 9, Application US/09569197
; Publication No. US20030170751A1
; GENERAL INFORMATION:
; APPLICANT: Frost & Jacobs LLP
; APPLICANT: Sherman, Lawrence
; APPLICANT: Ratner, Nancy
; TITLE OF INVENTION: Immunohistochemical Assay for RAS Activity
; FILE REFERENCE: 91830/642
; CURRENT APPLICATION NUMBER: US/09/569,197
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/133,811
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
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; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-197-9

Query Match      57.1%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LOPE 7
Db      1 LOPE 4

RESULT 60
US-10-371-069-415
; Sequence 415, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 415
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pf EXP1 71 (peptidel188.16)
US-10-371-069-415

Query Match      57.1%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYKL 4
Db      3 KYKL 6

RESULT 61
US-10-371-645-415
; Sequence 415, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
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PRIOR APPLICATION NUMBER: US 09/078,904  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: US 60/085,751  
PRIOR FILING DATE: 1998-05-15  
NUMBER OF SEQ ID NOS: 463  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 415  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Pf EXP1 71 (peptidell88.16)  
US-10-371-645-415

Query Match 57.1%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
DB 3 KYKL 6

RESULT 62  
US-09-765-527-52  
Sequence 52, Application US/09765527  
Patent No. US20020006638A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "XMP.51"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: C-Terminus  
OTHER INFORMATION: /label= Amidation  
/note= "The C-Terminus is Amidated."  
SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-09-765-527-52  
Query Match 57.1%; Score 4; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
DB 8 KLQP 11

RESULT 63  
US-09-765-527-65  
Sequence 65, Application US/09765527  
Patent No. US20020006638A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "XMP.64"  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-765-527-65

Query Match 57.1%; Score 4; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLQP 6  
DB 8 KLQP 11

RESULT 64  
US-10-387-645-6  
Sequence 6, Application US/10387645  
Publication No. US20030175845A1  
GENERAL INFORMATION:  
APPLICANT: GENENTECH, INC.

; APPLICANT: KALBAG, Suresh M.  
; APPLICANT: KARUNATILAKE, Chulani  
; TITLE OF INVENTION: USE OF SULFITYLYSIS IN HIGH PERFORMANCE  
; FILE REFERENCE: 39766-0102A  
; CURRENT APPLICATION NUMBER: US/10/387,645  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/364,992  
; PRIOR FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-387-645-6

Query Match 57.1%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 2 LOPE 5

RESULT 65  
US-10-387-645-7  
; Sequence 7, Application US/10387645  
; Publication No. US20030175845A1  
; GENERAL INFORMATION:  
; APPLICANT: GENENTECH, INC.  
; APPLICANT: KALBAG, Suresh M.  
; APPLICANT: KARUNATILAKE, Chulani  
; TITLE OF INVENTION: USE OF SULFITYLYSIS IN HIGH PERFORMANCE  
; FILE REFERENCE: 39766-0102A  
; CURRENT APPLICATION NUMBER: US/10/387,645  
; CURRENT FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/364,992.  
; PRIOR FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-387-645-7

Query Match 57.1%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 2 LOPE 5

RESULT 66  
US-10-062-710-2  
; Sequence 2, Application US/10062710  
; Publication No. US20030049253A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Frank Q.  
; APPLICANT: Chu, Yong-Liang  
; APPLICANT: Qiu, Jian-Tai  
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of  
; TITLE OF INVENTION: MHC-Recognized Epitopes  
; TITLE OF INVENTION: Via Peptide Vaccines  
; FILE REFERENCE: 3781-001-27  
; CURRENT APPLICATION NUMBER: US/10/062,710  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: US 60/310,498

; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV Helper-T Cell Epitopes  
US-10-062-710-2

Query Match 57.1%; Score 4; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
Db 9 KYKL 12

RESULT 67  
US-09-765-527-53  
; Sequence 53, Application US/09765527  
; Patent No. US2002006638A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/765,527  
; FILING DATE: 18-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: "XMP.52"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: C-Terminus  
; OTHER INFORMATION: /label= Amidation  
; /note= The C-Terminus is Amidated."  
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:  
US-09-765-527-53

Query Match 57.1%; Score 4; DB 9; Length 17;



Best Local Similarity 100.0%; Pred. No. 3.7e+02; Indels 0; Gaps 0; Mismatches 0;  
Matches 4; Conservative 0;

QY 3 KLOP 6  
Db 8 KLOP 11

RESULT 68  
US-09-765-527-54  
; Sequence 54, Application US/09765527  
; Patent No. US2002006638A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-8402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/765,527  
; FILING DATE: 18-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: "XMP.53"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: C-Terminus  
; OTHER INFORMATION: /label= Amidation  
; /note="The C-Terminus is Amidated."  
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:  
US-09-765-527-54

Query Match 57.1%; Score 4; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6  
Db 8 KLOP 11

RESULT 69  
US-09-569-197-8  
; Sequence 8, Application US/09569197  
; Publication No. US20030170751A1

GENERAL INFORMATION:  
; APPLICANT: Frost & Jacobs LLP  
; APPLICANT: Sherman, Lawrence  
; APPLICANT: Ratner, Nancy  
; TITLE OF INVENTION: Immunohistochemical Assay for RAS Activity  
; FILE REFERENCE: 91830/642  
; CURRENT APPLICATION NUMBER: US/09/569,197  
; CURRENT FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: 60/133,811  
; PRIOR FILING DATE: 1999-05-11  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 8  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-569-197-8

Query Match 57.1%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
Db 4 LQPE 7

RESULT 70  
US-10-281-652-21  
; Sequence 21, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265, 00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-21

Query Match 57.1%; Score 4; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7  
Db 1 LQPE 4

RESULT 71  
US-09-864-761-44869  
; Sequence 44869, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng

;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
;; FILE REFERENCE: Aecmice-X-1  
;; CURRENT APPLICATION NUMBER: US/09/864,761  
;; CURRENT FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/180,312  
;; PRIOR FILING DATE: 2000-02-04  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: US 09/632,366  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: GB 24263.6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00662  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00661  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 09/608,408  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: US 09/774,203  
;; PRIOR FILING DATE: 2001-01-29  
;; NUMBER OF SEQ ID NOS: 49117  
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
;; SEQ ID NO 44869  
;; LENGTH: 19  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: MAP TO AL121944.10  
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.6  
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.52  
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.54  
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.59  
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61  
US-09-864-761-44869

Query Match 57.1%; Score 4; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6  
|||  
Db 7 KLOP 10

RESULT 72

US-09-466-320-21  
;; Sequence 21, Application US/09466320  
;; Patent No. US2002025939A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Iversen, Patrick  
;; TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and  
;; TITLE OF INVENTION: Methods

;; FILE REFERENCE: 0450-0026.30  
;; CURRENT APPLICATION NUMBER: US/09/466,320  
;; CURRENT FILING DATE: 1999-12-17  
;; EARLIER APPLICATION NUMBER: US 60/112,910  
;; EARLIER FILING DATE: 1998-12-18  
;; NUMBER OF SEQ ID NOS: 25  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 21  
;; LENGTH: 20  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: peptide  
US-09-466-320-21

Query Match 57.1%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 17 LOPE 20

RESULT 73

US-09-864-761-45874  
;; Sequence 45874, Application US/09864761  
;; Patent No. US20020048763A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Penn, Sharon G.  
;; APPLICANT: Rank, David R.  
;; APPLICANT: Hanzel, David K.  
;; APPLICANT: Chen, Wensheng  
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
;; FILE REFERENCE: Aecmice-X-1  
;; CURRENT APPLICATION NUMBER: US/09/864,761  
;; CURRENT FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/180,312  
;; PRIOR FILING DATE: 2000-02-04  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: US 09/632,366  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: GB 24263.6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00662  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00661  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 09/608,408  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 45874  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC011941.4  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.82  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.63  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.65  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.6  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.67  
US-09-864-761-45874

Query Match 57.1%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0

QY 1 KYKL 4  
|||  
Db 2 KYKL 5

## RESULT 74

US-10-001-546-34  
; Sequence 34, Application US/10001546  
; Publication No. US20030027766A1  
; GENERAL INFORMATION:

; APPLICANT: IOANNIDES, CONSTANTIN G.  
; APPLICANT: FISK, BRYAN A.  
; APPLICANT: IOANNIDES, MARIA G.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
; FILE OF INVENTION: T-LYMPHOCYTES  
; FILE REFERENCE: UTSC:390USC2  
; CURRENT APPLICATION NUMBER: US/10/001,546  
; CURRENT FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 08/403,459  
; PRIOR FILING DATE: 1995-03-14  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-001-546-34

Query Match 57.1%; Score 4; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0

QY 4 LQPE 7  
|||  
Db 1 LQPE 4

## RESULT 75

US-10-119-417-15  
; Sequence 15, Application US/10119417  
; Publication No. US20030035804A1  
; GENERAL INFORMATION:

; APPLICANT: D'Amico, Anthony  
; APPLICANT: Buble, Glenn J.  
; APPLICANT: Jebaratnam, David J.  
; APPLICANT: Weinberg, James S.  
; TITLE OF INVENTION: Drug Complex for Treatment of Metastatic  
; TITLE OF INVENTION: Prostate Cancer  
; FILE REFERENCE: JCRT96-01A2  
; CURRENT APPLICATION NUMBER: US/10/119,417

; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: US/09/110,822  
; PRIOR FILING DATE: 1998-07-06  
; PRIOR APPLICATION NUMBER: US 09/003,838  
; PRIOR FILING DATE: 1998-01-07  
; PRIOR APPLICATION NUMBER: US 08/713,114  
; PRIOR FILING DATE: 1996-09-16  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-119-417-15

Query Match 42.9%; Score 3; DB 15; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0

QY 3 KLQ 5  
|||  
Db 1 KLQ 3

Search completed: November 25, 2003, 20:25:42  
Job time : 14.9255 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 7.63298 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-16

Perfect score: 7  
Sequence: 1 KYKLOPE 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued\_Patents\_AA.\*

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	4	US-09-641-803-16
2	5	71.4	8	3	US-08-779-814-2
3	4	57.1	8	4	US-09-389-390-7
4	4	57.1	9	1	US-08-217-188A-62
5	4	57.1	9	1	US-08-687-226-62
6	4	57.1	9	1	US-08-467-083-2
7	4	57.1	9	1	US-08-787-547-104
8	4	57.1	9	1	US-08-414-417B-2
9	4	57.1	9	2	US-08-486-348A-2
10	4	57.1	9	2	US-08-468-545B-2
11	4	57.1	9	3	US-08-948-378A-17
12	4	57.1	9	3	US-08-667-725B-62
13	4	57.1	9	3	US-08-466-680B-2
14	4	57.1	9	3	US-09-007-748-62
15	4	57.1	9	3	US-09-169-425C-17
16	4	57.1	9	4	US-08-197-484-30
17	4	57.1	9	4	US-08-197-484-66
18	4	57.1	9	4	US-08-197-484-71
19	4	57.1	9	4	US-08-403-459-12
20	4	57.1	9	4	US-09-311-784A-455
21	4	57.1	9	4	US-09-759-960-17
22	4	57.1	9	5	PCT-US95-02121-30
23	4	57.1	9	5	PCT-US95-02121-66
24	4	57.1	9	5	PCT-US95-02121-71
25	4	57.1	10	2	US-08-902-516-19
26	4	57.1	10	3	US-08-704-344-22
27	4	57.1	10	4	US-09-019-346A-5

28	4	57.1	10	4	US-09-847-185-19	Sequence 19, Appl
29	4	57.1	12	3	US-08-747-599A-22	Sequence 22, Appl
30	4	57.1	12	4	US-09-019-346A-6	Sequence 6, Appl
31	4	57.1	13	4	US-08-403-459-36	Sequence 36, Appl
32	4	57.1	14	2	US-08-621-803-50	Sequence 50, Appl
33	4	57.1	14	3	US-09-217-352-50	Sequence 50, Appl
34	4	57.1	15	1	US-07-854-629-11	Sequence 11, Appl
35	4	57.1	15	1	US-08-474-008-11	Sequence 11, Appl
36	4	57.1	15	1	US-08-259-672-11	Sequence 11, Appl
37	4	57.1	15	1	US-08-459-351-11	Sequence 11, Appl
38	4	57.1	15	1	US-08-460-533-11	Sequence 11, Appl
39	4	57.1	15	2	US-08-621-803-51	Sequence 51, Appl
40	4	57.1	15	3	US-09-217-352-51	Sequence 51, Appl
41	4	57.1	15	4	US-09-009-953-10	Sequence 10, Appl
42	4	57.1	15	4	US-09-009-953-11	Sequence 11, Appl
43	4	57.1	15	4	US-09-009-953-42	Sequence 42, Appl
44	4	57.1	15	4	US-09-009-953-43	Sequence 43, Appl
45	4	57.1	15	4	US-09-311-784A-415	Sequence 415, App
46	4	57.1	15	5	PCT-US94-06654-11	Sequence 11, Appl
47	4	57.1	16	1	US-07-854-629-4	Sequence 4, Appl
48	4	57.1	16	1	US-08-474-008-4	Sequence 4, Appl
49	4	57.1	16	2	US-08-621-803-52	Sequence 52, Appl
50	4	57.1	16	2	US-08-621-803-65	Sequence 65, Appl
51	4	57.1	16	3	US-09-217-352-52	Sequence 52, Appl
52	4	57.1	16	3	US-09-217-352-65	Sequence 65, Appl
53	4	57.1	17	2	US-08-621-803-53	Sequence 53, Appl
54	4	57.1	17	3	US-09-217-352-53	Sequence 53, Appl
55	4	57.1	18	1	US-08-259-672-10	Sequence 10, Appl
56	4	57.1	18	1	US-08-459-351-10	Sequence 10, Appl
57	4	57.1	18	1	US-08-460-533-10	Sequence 10, Appl
58	4	57.1	18	2	US-08-621-803-54	Sequence 54, Appl
59	4	57.1	18	3	US-08-075-541D-34	Sequence 34, Appl
60	4	57.1	18	3	US-08-075-541D-35	Sequence 35, Appl
61	4	57.1	18	3	US-08-075-541D-45	Sequence 45, Appl
62	4	57.1	18	3	US-09-217-352-54	Sequence 54, Appl
63	4	57.1	18	4	US-09-641-803-21	Sequence 21, Appl
64	4	57.1	18	5	PCT-US94-06654-10	Sequence 10, Appl
65	4	57.1	19	1	US-08-524-757-26	Sequence 26, Appl
66	4	57.1	20	2	US-08-934-915-46	Sequence 46, Appl
67	4	57.1	20	2	US-08-934-915-152	Sequence 152, App
68	4	57.1	20	3	US-08-075-541D-43	Sequence 43, Appl
69	4	57.1	20	3	US-08-075-541D-44	Sequence 44, Appl
70	4	57.1	20	4	US-08-403-459-34	Sequence 34, Appl
71	3	42.9	3	4	US-09-110-822-15	Sequence 15, Appl
72	3	42.9	4	1	US-08-843-035-3	Sequence 3, Appl
73	3	42.9	4	2	US-08-609-271-1	Sequence 1, Appl
74	3	42.9	4	2	US-08-755-496A-3	Sequence 3, Appl
75	3	42.9	4	2	US-08-441-871-71	Sequence 71, Appl
76	3	42.9	4	3	US-09-306-789-1	Sequence 1, Appl
77	3	42.9	4	3	US-08-188-374-1	Sequence 1, Appl
78	3	42.9	4	3	US-09-081-707-1	Sequence 1, Appl
79	3	42.9	4	4	US-09-110-822-14	Sequence 14, Appl
80	3	42.9	4	4	US-09-588-921-1	Sequence 1, Appl
81	3	42.9	4	4	US-09-588-822-1	Sequence 1, Appl
82	3	42.9	4	4	US-09-627-851B-1	Sequence 1, Appl
83	3	42.9	4	4	US-09-696-169A-7	Sequence 7, Appl
84	3	42.9	5	1	US-08-843-035-4	Sequence 4, Appl
85	3	42.9	5	2	US-08-755-496A-4	Sequence 4, Appl
86	3	42.9	5	2	US-08-464-182A-23	Sequence 23, Appl
87	3	42.9	5	2	US-08-928-958-20	Sequence 20, Appl
88	3	42.9	5	2	US-08-406-271-23	Sequence 23, Appl
89	3	42.9	5	2	US-09-072-429-20	Sequence 20, Appl
90	3	42.9	5	3	US-08-765-856-5	Sequence 5, Appl
91	3	42.9	5	3	US-09-020-880-40	Sequence 40, Appl
92	3	42.9	5	3	US-08-935-009A-7	Sequence 7, Appl
93	3	42.9	5	3	US-09-081-707-4	Sequence 4, Appl
94	3	42.9	5	4	US-09-101-544-40	Sequence 40, Appl
95	3	42.9	5	4	US-09-588-921-4	Sequence 4, Appl
96	3	42.9	5	4	US-09-043-872-21	Sequence 21, Appl
97	3	42.9	5	4	US-09-588-822-4	Sequence 4, Appl
98	3	42.9	5	4	US-09-627-851B-4	Sequence 4, Appl
99	3	42.9	6	1	US-08-843-035-5	Sequence 5, Appl
100	3	42.9	6	2	US-08-755-496A-5	Sequence 5, Appl

## ALIGNMENTS

```
RESULT 1
US-09-641-803-16
Sequence 16, Application US/09641803
Patent No. 6500798
GENERAL INFORMATION:
APPLICANT: STANTON, G. John
APPLICANT: HUGHES, Thomas K.
APPLICANT: BOLDOGH, Istvan
TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
FILE REFERENCE: 265.00220101
CURRENT APPLICATION NUMBER: US/09/641,803
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/149,310
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-09-641-803-16

Query Match          100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYKLOPE 7
        |||||
Db      1 KYKLOPE 7

RESULT 2
US-08-779-814-2
Sequence 2, Application US/08779814
Patent No. 6297361
GENERAL INFORMATION:
APPLICANT: Haak-Frendscho, M.
APPLICANT: Falus, A.
TITLE OF INVENTION: USE OF HISTIDINE DECARBOXYLASE
TITLE OF INVENTION: IMMUNOREACTIVITY TO DETECT CANCER
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth., P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: U.S.A
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,814
FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Embretson, Janet E
REGISTRATION NUMBER: 39,665
REFERENCE/DOCKET NUMBER: 341.003051
```

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
TELEFAX: 612-339-3061
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-779-814-2

Query Match          71.4%; Score 5; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYKLQ 5
        |||||
Db      4 KYKLQ 8

RESULT 3
US-09-389-390-7
Sequence 7, Application US/09389390
Patent No. 6558961
GENERAL INFORMATION:
APPLICANT: SARPHIE
TITLE OF INVENTION: IMMUNODIAGNOSTICS USING PARTICLE DELIVERY METHODS
FILE REFERENCE: OPF1620
CURRENT APPLICATION NUMBER: US/09/389,390
CURRENT FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/099,261
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 60/139,045
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: construct
US-09-389-390-7

Query Match          57.1%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYKL 4
        |||||
Db      5 KYKL 8

RESULT 4
US-08-217-188A-62
Sequence 62, Application US/08217188A
Patent No. 5554724
GENERAL INFORMATION:
APPLICANT: Melief, Cornelis J. M.
APPLICANT: Visseren, M. J. W.
APPLICANT: Kast, W. M.
APPLICANT: van der Bruggen, Pierre
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Tumor Rejection Antigen
TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
```

STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/217,188A  
FILING DATE: 24-MARCH-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5554724man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5340  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acid residues  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-217-188A-62

Query Match 57.1%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 4 LOPE 7

RESULT 5  
US-08-687-226-62  
Sequence 62, Application US/08687226  
Patent No. 5686068  
GENERAL INFORMATION:  
APPLICANT: Meliet, Cornelis J. M.; Visseren, M. W.;  
APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;  
APPLICANT: Boon-Falleur, Thierry  
TITLE OF INVENTION: Isolated Peptides Derived From  
TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of  
TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,226  
FILING DATE: 25-JULY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/217,188  
FILING DATE: 24-MARCH-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5686068man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5447  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acid residues  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-687-226-62

Query Match 57.1%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 4 LOPE 7

RESULT 6  
US-08-467-083-2  
Sequence 2, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836 SEEDANBERRY  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-467-083-2

Query Match 57.1%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 2 LOPE 5

RESULT 7

US-08-787-547-104  
; Sequence 104, Application US/08787547  
; Patent No. 5783567  
; GENERAL INFORMATION:  
; APPLICANT: Hedley, Mary Lynne  
; APPLICANT: Curley, Joanne M.  
; APPLICANT: Langer, Robert S.  
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY  
; TITLE OF INVENTION: OF NUCLEIC ACID  
; NUMBER OF SEQUENCES: 107  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/787,547  
; FILING DATE: 22-JAN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 08191/003001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-787-547-104

Query Match 57.1%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
DB 5 LOPE 8

RESULT 8  
US-08-414-417B-2  
; Sequence 2, Application US/08414417B  
; Patent No. 5801005  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disig, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/414,417B  
; FILING DATE: 31-MAR-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-414-417B-2

Query Match 57.1%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
DB 2 LOPE 5

RESULT 9  
US-08-486-348A-2  
; Sequence 2, Application US/08486348A  
; Patent No. 5846538  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disig, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,348A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-486-348A-2

Query Match 57.1%; Score 4; DB 2; Length 9;



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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
   ||||
Db 2 LOPE 5

RESULT 10
US-08-468-545B-2
; Sequence 2, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disie, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-468-545B-2

Query Match 57.1%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
   ||||
Db 2 LOPE 5

RESULT 11
US-08-948-378A-17
; Sequence 17, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
; TITLE OF INVENTION: THE HPV E7 PROTEIN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street

```

```

; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,378A
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLESCULE TYPE: peptide
US-08-948-378A-17

Query Match 57.1%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
   ||||
Db 5 LOPE 8

RESULT 12
US-08-667-725B-62
; Sequence 62, Application US/08667725B
; Patent No. 6063900
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,725B
; FILING DATE: 21 June 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6063900man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)

```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-667-725B-62

Query Match 57.1%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7
Db 4 LQPE 7

RESULT 13
US-08-466-680B-2
; Sequence 2, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-466-680B-2

Query Match 57.1%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7
Db 2 LQPE 5

RESULT 14
US-09-007-74B-62
; Sequence 62, Application US/0900774B
```

```
; Patent No. 6147187
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,748
; FILING DATE: 15 January 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6147187man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-007-748-62

Query Match 57.1%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7
Db 4 LQPE 7

RESULT 15
US-09-169-425C-17
; Sequence 17, Application US/09169425C
; Patent No. 6183746
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
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;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/169,425C  
;; FILING DATE: 09-OCT-1998  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/061,657  
;; FILING DATE: 09-OCT-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Fraser, Janis K.  
;; REGISTRATION NUMBER: 34,819  
;; REFERENCE/DOCKET NUMBER: 08191/004002  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-542-5070  
;; TELEFAX: 617-543-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-09-169-425C-17

Query Match 57.1%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 KYKL 7  
Db 5 LQPE 8

RESULT 16  
US-08-197-484-30  
; Sequence 30, Application US/08197484  
; Patent No. 6419931  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, Maria A.  
; APPLICANT: CHESTNUT, Robert W.  
; APPLICANT: SETTE, Alessandro D.  
; APPLICANT: CELIS, Esteban  
; APPLICANT: GRAY, Howard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Hourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (206) 623-6793

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Parmelee, Steven W.  
;; REGISTRATION NUMBER: 31,990  
;; REFERENCE/DOCKET NUMBER: 14137-26-4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 467-9600  
;; TELEFAX: (206) 623-6793  
;; INFORMATION FOR SEQ ID NO: 30:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-08-197-484-30

Query Match 57.1%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KYKL 4  
Db 5 KYKL 8

RESULT 17  
US-08-197-484-66  
; Sequence 66, Application US/08197484  
; Patent No. 6419931  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, Maria A.  
; APPLICANT: CHESTNUT, Robert W.  
; APPLICANT: SETTE, Alessandro D.  
; APPLICANT: CELIS, Esteban  
; APPLICANT: GRAY, Howard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Hourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-197-484-66

Query Match 57.1%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 5 LOPE 8

RESULT 18

US-08-197-484-71  
; Sequence 71, Application US/08197484  
; Patent No. 6419931

GENERAL INFORMATION:  
APPLICANT: VITIELLO, Maria A.  
APPLICANT: CHESTNUT, Robert W.  
APPLICANT: SETTE, Alessandro D.  
APPLICANT: CELIS, Estebean  
APPLICANT: GRAY, Howard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: Stuart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484

FILING DATE: 16-FEB-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/935,811

FILING DATE: 26-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,568

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-26-4

TELEPHONE: (206) 467-9600

TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-197-484-71

Query Match 57.1%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 4 LOPE 7

RESULT 19

US-08-403-459-12

; Sequence 12, Application US/08403459

; Patent No. 6514942

GENERAL INFORMATION:

APPLICANT: Ioannides, Constantin G.

APPLICANT: Fisk, Bryan A.

APPLICANT: Ioannides, Maria G.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING

T-LYMPHOCYTES

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/403,459

FILING DATE: Concurrently Herewith

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: UTSC:390/KIT

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-403-459-12

Query Match 57.1%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 2 LOPE 5

RESULT 20

US-09-311-784A-455

; Sequence 455, Application US/09311784A

; Patent No. 6534482

GENERAL INFORMATION:

APPLICANT: Fikes, John D.

APPLICANT: Hermanson, Gary G.

APPLICANT: Sette, Alessandro

APPLICANT: Ishioka, Glenn Y.

```

; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 3963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 455
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pf EXP1 73 (peptide 1167.53)
US-09-311-784A-455

Query Match          57.1%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4
Db 1 KYKL 4

RESULT 21
US-09-759-960-17
; Sequence 17, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICANT:

US-09-759-960-17
Query Match          57.1%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4
Db 1 KYKL 4

RESULT 22
PCT-US95-02121-30
; Sequence 30, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; PCT-US95-02121-30

Query Match          57.1%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4
Db 5 KYKL 8

RESULT 23
PCT-US95-02121-66
; Sequence 66, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
```

```

US-09-759-960-17
Query Match          57.1%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7
Db 5 LOPE 8

RESULT 22
PCT-US95-02121-30
; Sequence 30, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; PCT-US95-02121-30

Query Match          57.1%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4
Db 5 KYKL 8

RESULT 23
PCT-US95-02121-66
; Sequence 66, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
```

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
;; NUMBER OF SEQUENCES: 153  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US95/02121  
;; FILING DATE: 16-FEB-1995  
;; CLASSIFICATION:  
;; APPLICATION NUMBER: US 08/197,484  
;; FILING DATE: 16-FEB-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/935,811  
;; FILING DATE: 26-AUG-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/874,491  
;; FILING DATE: 27-APR-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/827,682  
;; FILING DATE: 29-JAN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/749,568  
;; FILING DATE: 26-AUG-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Parmelee, Steven W.  
;; REGISTRATION NUMBER: 31,990  
;; REFERENCE/DOCKET NUMBER: 14137-26-4PC  
;; TELEPHONE: (206) 467-9600  
;; TELEFAX: (415) 543-5043  
;; INFORMATION FOR SEQ ID NO: 66:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
PCT-US95-02121-66

Query Match 57.1%; Score 4; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 5 LQPE 8

RESULT 24  
PCT-US95-02121-71  
;; Sequence 71, Application PC/TUS9502121  
;; GENERAL INFORMATION:  
;; APPLICANT:  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
;; NUMBER OF SEQUENCES: 153  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US95/02121  
;; FILING DATE: 16-FEB-1995  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/197,484  
;; FILING DATE: 16-FEB-1994  
;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/935,811  
;; FILING DATE: 26-AUG-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/874,491  
;; FILING DATE: 27-APR-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/827,682  
;; FILING DATE: 29-JAN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/749,568  
;; FILING DATE: 26-AUG-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Parmelee, Steven W.  
;; REGISTRATION NUMBER: 31,990  
;; REFERENCE/DOCKET NUMBER: 14137-26-4PC  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 467-9600  
;; TELEFAX: (415) 543-5043  
;; INFORMATION FOR SEQ ID NO: 71:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
PCT-US95-02121-71

Query Match 57.1%; Score 4; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 4 LQPE 7

RESULT 25  
US-08-902-516-19  
;; Sequence 19, Application US/08902516  
;; Patent No. 5891432  
;; GENERAL INFORMATION:  
;; APPLICANT: Soo Hoo, William  
;; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
;; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
;; TITLE OF INVENTION: RESPONSE USING SAME  
;; NUMBER OF SEQUENCES: 50  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CAMPBELL & FLORES, LLP  
;; STREET: 4370 La Jolla Village Drive, Suite 700  
;; CITY: San Diego  
;; STATE: California  
;; COUNTRY: United States  
;; ZIP: 92121  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/902,516  
;; FILING DATE: 29-JUL-1997  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn A.  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-IM 2442  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-902-516-19

Query Match 57.1%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 5 LOPE 8

## RESULT 26

US-08-704-344-22  
; Sequence 22, Application US/08704344  
; Patent No. 6218363

## ; GENERAL INFORMATION:

; APPLICANT: BASERGA, Renato L.

; APPLICANT: RESNICOFF, Mariana

; APPLICANT: HUANG, Ziwei

; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HALE and DORR LLP

; STREET: 1455 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/704,344

; FILING DATE: 28-AUG-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: WIXON, Henry N.

; REGISTRATION NUMBER: 32,073

; REFERENCE/DOCKET NUMBER: 104322.196

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 942-8459

; TELEFAX: (202) 942-8484

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-704-344-22

Query Match 57.1%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||  
Db 5 LOPE 8

## RESULT 27

US-09-019-346A-5

; Sequence 5, Application US/09019346A

; Patent No. 6372720

; GENERAL INFORMATION:

; APPLICANT: Longmuir, Kenneth J.

; APPLICANT: Waring, Alan J.

; APPLICANT: Haynes, Sherry M.  
; TITLE OF INVENTION: Liposome Fusion and Delivery Vehicle  
; FILE REFERENCE: A65189/RFT/DAV  
; CURRENT APPLICATION NUMBER: US/09/019,346A  
; CURRENT FILING DATE: 1998-02-05  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: HIV-1 matrix protein  
US-09-019-346A-5

Query Match 57.1%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
|||  
Db 5 KYKL 8

## RESULT 28

US-09-847-185-19

; Sequence 19, Application US/09847185

; Patent No. 6482407

; GENERAL INFORMATION:

; APPLICANT: Soo Hoo, William

; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS

; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE

; RESPONSE USING SAME

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CAMPBELL & FLORES, LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/847,185

; FILING DATE: 01-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/201,931

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IM 2442

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-847-185-19

Query Match 57.1%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||

Db 5 LQPE 8

## RESULT 29

US-08-747-599A-22

; Sequence 22, Application US/08747599A

; Patent No. 6214795

; GENERAL INFORMATION:

; APPLICANT: Benjamin, Howard et al.

; TITLE OF INVENTION: Peptide Compounds Useful for Modulating

; TITLE OF INVENTION: FGF Receptor Activity

; NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE &amp; COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/747,599A

; FILING DATE: 12-NOV-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Kara, Catherine J.

; REGISTRATION NUMBER: 41,106

; REFERENCE/DOCKET NUMBER: PPI-029

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-747-599A-22

## Query Match

57.1%; Score 4; DB 3; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4

Db 5 KYKL 8

## RESULT 30

US-09-019-346A-6

; Sequence 6, Application US/09019346A

; Patent No. 6372720

; GENERAL INFORMATION:

; APPLICANT: Longmuir, Kenneth J.

; APPLICANT: Waring, Alan J.

; APPLICANT: Haynes, Sherry M.

; TITLE OF INVENTION: Liposome Fusion and Delivery Vehicle

; FILE REFERENCE: A65189/RFT/DAV

; CURRENT APPLICATION NUMBER: US/09/019,346A

; CURRENT FILING DATE: 1998-02-05

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 6

; LENGTH: 12

; TYPE: PPT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-019-346A-6

## Query Match

57.1%; Score 4; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4

Db 7 KYKL 10

## RESULT 31

US-08-403-459-36

; Sequence 36, Application US/08403459

; Patent No. 6514942

; GENERAL INFORMATION:

; APPLICANT: Ioannides, Constantin G.

; APPLICANT: Fisk, Bryan A.

; APPLICANT: Ioannides, Maria G.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING

; TITLE OF INVENTION: T-LYMPHOCYTES

; NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White &amp; Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/403,459

; FILING DATE: Concurrently Herewith

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Kitchell, Barbara S.

; REGISTRATION NUMBER: 33,928

; REFERENCE/DOCKET NUMBER: UTSC:390/KIT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (713) 789-2679

; TELEX: 79-0924

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-403-459-36

## Query Match

57.1%; Score 4; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LQPE 7

Db 1 LQPE 4

## RESULT 32

US-08-621-803-50

; Sequence 50, Application US/08621803

; Patent No. 5851802

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; TITLE OF INVENTION: Methods for Recombinant Microbial Production of

; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides

; NUMBER OF SEQUENCES: 265



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
;; STREET: 6300 Sears Tower, 233 South Wacker Drive  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: United States of America  
;; ZIP: 60606-6402  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/621,803  
;; FILING DATE: 22-MAR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Borun, Michael F.  
;; REGISTRATION NUMBER: 25,447  
;; REFERENCE/DOCKET NUMBER: 27129/33199  
;; TELEPHONE: 312/474-6300  
;; TELEFAX: 312/474-0448  
;; TELEX: 25-3856  
;; INFORMATION FOR SEQ ID NO: 50:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: "XMP.49"  
;; NAME/KEY: Modified-site  
;; LOCATION: C-Terminus  
;; OTHER INFORMATION: /label= Amidation  
;; OTHER INFORMATION: /note= "The C-Terminus is Amidated."  
US-08-621-803-50

Query Match 57.1%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KLOP 6  
|||  
Db 8 KLOP 11

RESULT 33  
US-09-217-352-50  
; Sequence 50, Application US/09217352  
; Patent No. 6274344  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; FUSION PROTEINS AND BPI-DERIVED PEPTIDES  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/217,352  
; FILING DATE:  
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/621,803  
;; FILING DATE: 22-MAR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Borun, Michael F.  
;; REGISTRATION NUMBER: 25,447  
;; REFERENCE/DOCKET NUMBER: 27129/33199  
;; TELEPHONE: 312/474-6300  
;; TELEFAX: 312/474-0448  
;; TELEX: 25-3856  
;; INFORMATION FOR SEQ ID NO: 50:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: "XMP.49"  
;; NAME/KEY: Modified-site  
;; LOCATION: C-Terminus  
;; OTHER INFORMATION: /label= Amidation  
;; OTHER INFORMATION: /note= "The C-Terminus is Amidated."  
US-09-217-352-50  
Query Match 57.1%; Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KLOP 6  
|||  
Db 8 KLOP 11

RESULT 34  
US-07-854-629-11  
; Sequence 11, Application US/07854629  
; Patent No. 5480967  
; GENERAL INFORMATION:  
; APPLICANT: McMICHAE, ANDREW J.  
; APPLICANT: NIXON, DOUGLAS F.  
; APPLICANT: TOWNSEND, ALAIN R. M.  
; APPLICANT: GOTCH, FRANCES M.  
; TITLE OF INVENTION: HIV-1 CORE PROTEIN FRAGMENTS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/854,629  
; FILING DATE: 19920706  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9000287.4  
; FILING DATE: 05-JAN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9003577.5  
; FILING DATE: 16-FEB-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5480967man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 3077-003-0 PCT

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Human immunodeficiency virus  
US-07-854-629-11

Query Match 57.1%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
DB 8 KYKL 11

RESULT 35  
US-08-474-008-11  
Sequence 11, Application US/08474008  
Patent No. 5700469  
GENERAL INFORMATION:  
APPLICANT: MICHAEL, ANDREW J.  
APPLICANT: NIXON DOUGLAS F.  
APPLICANT: TOWNSEND, ALAIN R. M.  
APPLICANT: GOTCH, FRANCES M.  
TITLE OF INVENTION: HIV-1 CORE PROTEIN FRAGMENTS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,008  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/854,629  
FILING DATE: 06-JUL-1992  
APPLICATION NUMBER: GB 9000287.4  
FILING DATE: 05-JAN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9003577.5  
FILING DATE: 16-FEB-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5700469man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 3077-003-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

ORIGINAL SOURCE:  
ORGANISM: Human immunodeficiency virus  
US-08-474-008-11

Query Match 57.1%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
DB 8 KYKL 11

RESULT 36  
US-08-259-672-11  
Sequence 11, Application US/08259672  
Patent No. 5736337  
GENERAL INFORMATION:  
APPLICANT: Joseph Avruch  
APPLICANT: Xian-feng Zhang  
APPLICANT: Mark S. Marchall  
TITLE OF INVENTION: INHIBITING PROTEIN  
TITLE OF INVENTION: INTERACTIONS  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/259,672  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,256  
FILING DATE: June 11, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul T. Clark, Esq.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/234001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-259-672-11

Query Match 57.1%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
DB 1 LOPE 4

RESULT 37  
US-08-459-351-11  
Sequence 11, Application US/08459351  
Patent No. 5763571  
GENERAL INFORMATION:

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; APPLICANT: Joseph Avruch
; APPLICANT: Xian-Feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,351
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,672
; FILING DATE: June 10, 1994
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234003
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-459-351-11

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Query Match 57.1%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 LOPE 7
Db 1 LOPE 4

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RESULT 38
US-08-460-533-11
; Sequence 11, Application US/08460533
; Patent No. 5767075
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-Feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,533
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,672
; FILING DATE: June 10, 1994
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234002
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-460-533-11

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Query Match 57.1%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 LOPE 7
Db 1 LOPE 4

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RESULT 39
US-08-621-803-51
; Sequence 51, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murtagh & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

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NAME/KEY: misc feature  
OTHER INFORMATION: "XMP.50"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: C-Terminus  
OTHER INFORMATION: /label= Amidation  
OTHER INFORMATION: /note= "The C-Terminus is Amidated."  
US-08-621-803-51

Query Match 57.1%; Score 4; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6  
|||  
Db 8 KLOP 11

RESULT 40  
US-09-217-352-51  
; Sequence 51, Application US/09217352  
; Patent No. 6274344  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/217,352  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: 22-MAR-1996

ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: "XMP.50"  
; FEATURE:

NAME/KEY: Modified-site  
LOCATION: C-Terminus  
OTHER INFORMATION: /label= Amidation  
OTHER INFORMATION: /note= "The C-Terminus is Amidated."  
US-09-217-352-51

Query Match 57.1%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6  
|||  
Db 8 KLOP 11

RESULT 41  
US-09-009-953-10  
; Sequence 10, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly  
; TITLE OF INVENTION: Reactive DR Restricted Epitopes  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,953  
; FILING DATE: 21-Jan-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,713  
; FILING DATE: 23-JAN-1997

ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-011520US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-009-953-10

Query Match 57.1%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKL 4  
|||  
Db 3 KYKL 6

RESULT 42  
US-09-009-953-11  
; Sequence 11, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly  
; TITLE OF INVENTION: Reactive DR Restricted Epitopes  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-Jan-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-009-953-11  
Query Match 57.1%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 1 KYKL 4  
DB 1 KYKL 4  
RESULT 43  
US-09-009-953-42  
Sequence 42, Application US/09009953  
Patent No. 6413517  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
TITLE OF INVENTION: Identification of Broadly  
Reactive DR Restricted Epitopes  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-Jan-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-09-009-953-42  
Query Match 57.1%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 1 KYKL 4  
DB 3 KYKL 6  
RESULT 44  
US-09-009-953-43  
Sequence 43, Application US/09009953  
Patent No. 6413517  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
TITLE OF INVENTION: Identification of Broadly  
Reactive DR Restricted Epitopes  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

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;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-009-993-43

Query Match          57.1%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYKL 4
        ||||
Db       1 KYKL 4

RESULT 45
US-09-311-784A-415
; Sequence 415, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 415
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PF EXP1 71 (peptide1188.16)
US-09-311-784A-415

Query Match          57.1%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYKL 4
        ||||
Db       3 KYKL 6

RESULT 46
PCT-US94-06654-11
; Sequence 11, Application PC/TUS9406654
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06654
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US94-06654-11

Query Match          57.1%; Score 4; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LOPE 7
        ||||
Db       1 LOPE 4

RESULT 47
US-07-854-629-4
; Sequence 4, Application US/07854629
; Patent No. 5480967
; GENERAL INFORMATION:
; APPLICANT: McMICHAEL, ANDREW J.
; APPLICANT: NIXON, DOUGLAS F.
; APPLICANT: TOWNSEND, ALAIN R. M.
; APPLICANT: GOTCH, FRANCES M.
; TITLE OF INVENTION: HIV-1 CORE PROTEIN FRAGMENTS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSES: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/854,629
; FILING DATE: 19920706
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9000287.4
; FILING DATE: 05-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9003577.5
; FILING DATE: 16-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5480967man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 3077-003-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
```

TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Human immunodeficiency virus  
US-07-854-629-4

Query Match 57.1%; Score 4; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 KYKL 4  
DB 9 KYKL 12

RESULT 48  
US-08-474-008-4  
Sequence 4, Application US/08474008  
Patent No. 5700469  
GENERAL INFORMATION:  
APPLICANT: MCMICHAEL, ANDREW J.  
APPLICANT: NIXON, DOUGLAS F.  
APPLICANT: TOWNSEND, ALAIN R. M.  
APPLICANT: GOTCH, FRANCES M.  
TITLE OF INVENTION: HIV-1 CORE PROTEIN FRAGMENTS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,008  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/854,629  
FILING DATE: 06-JUL-1992  
APPLICATION NUMBER: GB 9000287.4  
FILING DATE: 05-JAN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9003577.5  
FILING DATE: 16-FEB-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5700469man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 3077-003-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Human immunodeficiency virus  
US-08-474-008-4

Query Match 57.1%; Score 4; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 KYKL 4  
DB 9 KYKL 12

RESULT 49  
US-08-621-803-52  
Sequence 52, Application US/08621803  
Patent No. 5851802  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621,803  
FILING DATE: 22-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "XMP.51"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: C-Terminus  
OTHER INFORMATION: /label= Amidation  
OTHER INFORMATION: /note= "The C-terminus is Amidated."  
US-08-621-803-52

Query Match 57.1%; Score 4; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 KLOP 6  
DB 8 KLOP 11

RESULT 50  
US-08-621-803-65  
Sequence 65, Application US/08621803  
Patent No. 5851802  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.

;; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
;; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides  
;; NUMBER OF SEQUENCES: 265  
;; CORRESPONDENCE ADDRESSES:  
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
;; STREET: 6300 Sears Tower, 233 South Wacker Drive  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: United States of America  
;; ZIP: 60606-6402  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/621,803  
;; FILING DATE: 22-MAR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Borun, Michael F.  
;; REGISTRATION NUMBER: 25,447  
;; REFERENCE/DOCKET NUMBER: 27129/33199  
;; TELEPHONE: 312/474-6300  
;; TELEFAX: 312/474-0448  
;; TELEX: 25-3856  
;; INFORMATION FOR SEQ ID NO: 65:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: "XMP.64"  
;; US-08-621-803-65  
Query Match 57.1%; Score 4; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KLOP 6  
Db 8 KLOP 11  
RESULT 51  
US-09-217-352-52  
; Sequence 52, Application US/09217352  
; Patent No. 6274344  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/217,352  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: 22-MAR-1996

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Borun, Michael F.  
;; REGISTRATION NUMBER: 25,447  
;; REFERENCE/DOCKET NUMBER: 27129/33199  
;; TELEPHONE: 312/474-6300  
;; TELEFAX: 312/474-0448  
;; TELEX: 25-3856  
;; INFORMATION FOR SEQ ID NO: 52:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: "XMP.51"  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: C-Terminus  
;; OTHER INFORMATION: /label= Amidation  
;; OTHER INFORMATION: /note= "The C-Terminus is Amidated."  
;; US-09-217-352-52  
Query Match 57.1%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KLOP 6  
Db 8 KLOP 11  
RESULT 52  
US-09-217-352-65  
; Sequence 65, Application US/09217352  
; Patent No. 6274344  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/217,352  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: 22-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear



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; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.64"
US-09-217-352-65
Query Match 57.1%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KLQP 6
Db 8 KLQP 11
RESULT 53
US-08-621-803-53
; Sequence 53, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.52"
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-53
Query Match 57.1%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KLQP 6
Db 8 KLQP 11
RESULT 54
US-08-621-803-53
; Sequence 53, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.52"
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-53
Query Match 57.1%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KLQP 6
Db 8 KLQP 11
RESULT 55
US-08-259-672-10
; Sequence 10, Application US/08259672
; Patent No. 5736337
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN
; TITLE OF INVENTION: INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
```

;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: U.S.A.  
;; ZIP: 02110-2804  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; COMPUTER: IBM PS/2 Model 50Z or 55SX  
;; OPERATING SYSTEM: MS-DOS (Version 5.0)  
;; SOFTWARE: WordPerfect (Version 5.1)  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/259,672  
;; FILING DATE: Herewith  
;; CLASSIFICATION: 514  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/077,256  
;; FILING DATE: June 11, 1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Paul T. Clark, Esq.  
;; REGISTRATION NUMBER: 30,162  
;; REFERENCE/DOCKET NUMBER: 00786/234001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 542-5070  
;; TELEFAX: (617) 542-8906  
;; TELEX: 200154  
;;  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
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;; US-08-259-672-10

Query Match 57.1%; Score 4; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LOPE 7  
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Db 4 LOPE 7

RESULT 56  
US-08-459-351-10  
;; Sequence 10, Application US/08459351  
;; Patent No. 5763571  
;;  
;; GENERAL INFORMATION:  
;; APPLICANT: Joseph Avruch  
;; APPLICANT: Xian-Feng Zhang  
;; APPLICANT: Mark S. Marshall  
;;  
;; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS  
;; NUMBER OF SEQUENCES: 20  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson P.C.  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: U.S.A.  
;; ZIP: 02110-2804  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; COMPUTER: IBM PS/2 Model 50Z or 55SX  
;; OPERATING SYSTEM: MS-DOS (Version 5.0)  
;; SOFTWARE: WordPerfect (Version 5.1)  
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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/459,351  
;; FILING DATE: June 2, 1995  
;; CLASSIFICATION: 435  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/259,672  
;; FILING DATE: June 10, 1994  
;; APPLICATION NUMBER: 08/077,256  
;; FILING DATE: June 11, 1993  
;; ATTORNEY/AGENT INFORMATION:

;; NAME: Paul T. Clark, Esq.  
;; REGISTRATION NUMBER: 30,162  
;; REFERENCE/DOCKET NUMBER: 00786/234003  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 542-5070  
;; TELEFAX: (617) 542-8906  
;; TELEX: 200154  
;;  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;;  
;; US-08-459-351-10

Query Match 57.1%; Score 4; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LOPE 7  
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Db 4 LOPE 7

RESULT 57  
US-08-460-533-10  
;; Sequence 10, Application US/08460533  
;; Patent No. 5767075  
;;  
;; GENERAL INFORMATION:  
;; APPLICANT: Joseph Avruch  
;; APPLICANT: Xian-Feng Zhang  
;; APPLICANT: Mark S. Marshall  
;;  
;; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS  
;; NUMBER OF SEQUENCES: 20  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson P.C.  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: U.S.A.  
;; ZIP: 02110-2804  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; COMPUTER: IBM PS/2 Model 50Z or 55SX  
;; OPERATING SYSTEM: MS-DOS (Version 5.0)  
;; SOFTWARE: WordPerfect (Version 5.1)  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/460,533  
;; FILING DATE: June 2, 1995  
;; CLASSIFICATION: 435  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/259,672  
;; FILING DATE: June 10, 1994  
;; APPLICATION NUMBER: 08/077,256  
;; FILING DATE: June 11, 1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Paul T. Clark, Esq.  
;; REGISTRATION NUMBER: 30,162  
;; REFERENCE/DOCKET NUMBER: 00786/234002  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 542-5070  
;; TELEFAX: (617) 542-8906  
;; TELEX: 200154  
;;  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;;  
;; US-08-460-533-10

Query Match 57.1%; Score 4; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
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Db 4 LOPE 7

## RESULT 58

US-08-621-803-54  
; Sequence 54, Application US/08621803  
; Patent No. 5851802  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
; FUSION PROTEINS AND BPI-DERIVED PEPTIDES  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/621,803  
; FILING DATE: 22-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: "XMP.53"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: C-Terminus  
; OTHER INFORMATION: /label= Amidation  
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."  
US-08-621-803-54

Query Match 57.1%; Score 4; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6  
|||||  
Db 8 KLOP 11

## RESULT 59

US-08-075-541D-34  
; Sequence 34, Application US/08075541D  
; Patent No. 6183745  
; GENERAL INFORMATION:  
; APPLICANT: TINDLE, ROBERT  
; APPLICANT: FERNANDO, GERMAIN  
; APPLICANT: FRAZER, IAN  
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND

; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: 1601 MARKET STREET, 36TH FLOOR  
; CITY: PHILADELPHIA  
; STATE: PENNSYLVANIA  
; COUNTRY: USA  
; ZIP: 19103-2398  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/075,541D  
; FILING DATE: 10-JUN-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU pk 3876  
; FILING DATE: 12-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: pct/au91/00575  
; FILING DATE: 12-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NADEL, ALAN S  
; REGISTRATION NUMBER: 27,363  
; REFERENCE/DOCKET NUMBER: 8795-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-567-2020  
; TELEFAX: 215-567-2991  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-075-541D-34

Query Match 57.1%; Score 4; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
|||||  
Db 15 LOPE 18

## RESULT 60

US-08-075-541D-35  
; Sequence 35, Application US/08075541D  
; Patent No. 6183745  
; GENERAL INFORMATION:  
; APPLICANT: TINDLE, ROBERT  
; APPLICANT: FERNANDO, GERMAIN  
; APPLICANT: FRAZER, IAN  
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: 1601 MARKET STREET, 36TH FLOOR  
; CITY: PHILADELPHIA  
; STATE: PENNSYLVANIA  
; COUNTRY: USA  
; ZIP: 19103-2398  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/075,541D  
FILING DATE: 10-JUN-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU pk 3876  
FILING DATE: 12-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: pct/au91/00575  
FILING DATE: 12-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NADEL, ALAN S  
REGISTRATION NUMBER: 27,363  
REFERENCE/DOCKET NUMBER: 8795-4  
TELEPHONE: 215-567-2991  
TELEFAX: 215-567-2991  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-075-541D-35

Query Match 57.1%; Score 4; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
DB 7 LOPE 10

RESULT 61  
US-08-075-541D-45  
Sequence 45, Application US/08075541D  
Patent No. 6183745  
GENERAL INFORMATION:  
APPLICANT: TINDLE, ROBERT  
APPLICANT: FERNANDO, GERMAIN  
APPLICANT: FRAZER, IAN  
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND  
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
STREET: 1601 MARKET STREET, 36TH FLOOR  
CITY: PHILADELPHIA  
STATE: PENNSYLVANIA  
COUNTRY: USA  
ZIP: 19103-2398  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/075,541D  
FILING DATE: 10-JUN-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU pk 3876  
FILING DATE: 12-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: pct/au91/00575  
FILING DATE: 12-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NADEL, ALAN S  
REGISTRATION NUMBER: 27,363  
REFERENCE/DOCKET NUMBER: 8795-4  
TELEPHONE: 215-567-2020

TELEFAX: 215-567-2991  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-075-541D-45

Query Match 57.1%; Score 4; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
DB 4 LOPE 7

RESULT 62  
US-09-217-352-54  
Sequence 54, Application US/09217352  
Patent No. 6274344  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/217,352  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: 22-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "XMP.53"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: C-Terminus  
OTHER INFORMATION: /label= Amidation  
OTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-09-217-352-54  
Query Match 57.1%; Score 4; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLOP 6  
Db 8 KLOP 11

RESULT 63  
US-09-641-803-21  
; Sequence 21, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265, 00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-21

Query Match 57.1%; Score 4; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 1 LOPE 4

RESULT 64  
PCT-US94-06654-10  
; Sequence 10, Application PC/TUS9406654  
; GENERAL INFORMATION:  
; APPLICANT: Joseph Avruch  
; APPLICANT: Xian-feng Zhang  
; APPLICANT: Mark S. Marshall  
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/06654  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul T. Clark, Esq.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/234001

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; PCT-US94-06654-10

Query Match 57.1%; Score 4; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LOPE 7  
Db 4 LOPE 7

RESULT 65  
US-08-524-757-26  
; Sequence 26, Application US/08524757  
; Patent No. 5792634  
; GENERAL INFORMATION:  
; APPLICANT: Conaway, Ronald C.  
; APPLICANT: Conaway, Joan W.  
; APPLICANT: Bradsher, John N.  
; TITLE OF INVENTION: RNA Polymerase Transcription Factor  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS  
; STREET: 1201 Elm Street, Suite 4500  
; CITY: Dallas  
; STATE: TX  
; COUNTRY: US  
; ZIP: 75270-2197  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/524,757  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/13621  
; FILING DATE: 29-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/160087  
; FILING DATE: 30-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harre, John A.  
; REGISTRATION NUMBER: 37,345  
; REFERENCE/DOCKET NUMBER: B35006CIPCIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (214) 939-4500  
; TELEFAX: (214) 939-4600  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-524-757-26

Query Match 57.1%; Score 4; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      3 KLOP 6
      ||||
Db      8 KLOP 11

RESULT 66
US-08-934-915-46
; Sequence 46, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-46

Query Match 57.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LQPE 7
      ||||
Db      14 LQPE 17

RESULT 67
US-08-934-915-152
; Sequence 152, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424

QY      4 LQPE 7
      ||||
Db      14 LQPE 17

RESULT 68
US-08-075-541D-43
; Sequence 43, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FRAZER, IAN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424

QY      4 LQPE 7
      ||||
Db      14 LQPE 17

RESULT 69
US-08-934-915-46
; Sequence 46, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-46

Query Match 57.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LQPE 7
      ||||
Db      14 LQPE 17

RESULT 70
US-08-934-915-152
; Sequence 152, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-541D-43

Query Match 57.1%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LOPE 7
Db 15 LOPE 18

RESULT 69
US-08-075-541D-44
; Sequence 44, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-541D-44

Query Match 57.1%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LOPE 7
Db 10 LOPE 13

RESULT 70
US-08-403-459-34
; Sequence 34, Application US/08403459
; Patent No. 6514942
; GENERAL INFORMATION:
; APPLICANT: Ioannides, Constantin G.
; APPLICANT: Fisk, Bryan A.
; APPLICANT: Ioannides, Maria G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITLE OF INVENTION: T-LYMPHOCYTES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,459
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSC:390/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-403-459-34

Query Match 57.1%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LOPE 7
Db 1 LOPE 4

RESULT 71
US-09-110-822-15
; Sequence 15, Application US/09110822A
; Patent No. 6368598
```

;; GENERAL INFORMATION:  
;; APPLICANT: D'Amico, Anthony  
;; APPLICANT: Bubley, Glenn J.  
;; APPLICANT: Jebarathnam, David J.  
;; APPLICANT: Weinberg, James S.  
;; TITLE OF INVENTION: Drug Complex for Treatment of Metastatic  
;; TITLE OF INVENTION: Prostate Cancer  
;; FILE REFERENCE: JCRT96-01A2  
;; CURRENT APPLICATION NUMBER: US/09/110,822A  
;; CURRENT FILING DATE: 1998-07-06  
;; EARLIER APPLICATION NUMBER: US 09/003,838  
;; EARLIER FILING DATE: 1998-01-07  
;; EARLIER APPLICATION NUMBER: US 08/713,114  
;; EARLIER FILING DATE: 1996-09-16  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 15  
;; LENGTH: 3  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic  
US-09-110-822-15

Query Match 42.9%; Score 3; DB 4; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KIQ 5  
Db 1 KIQ 3

RESULT 72  
US-08-843-0335-3  
; Sequence 3, Application US/08843035  
; Patent No. 5783662  
;; GENERAL INFORMATION:  
;; APPLICANT: Janney, Paul A.  
;; APPLICANT: Cunningham, C. Casey  
;; APPLICANT: Hartwig, John H.  
;; APPLICANT: Stossel, Thomas P.  
;; APPLICANT: Vegner, Roland  
;; TITLE OF INVENTION: POLYPHOSPHONOSITIDE BINDING  
;; TITLE OF INVENTION: PEPTIDES FOR INTRACELLULAR DRUG DELIVERY  
;; NUMBER OF SEQUENCES: 36  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
;; STREET: Federal Reserve Plaza, 600 Atlantic Avenue  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02210  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION NUMBER: US/08/843,035  
;; FILING DATE: 11-APR-1997  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/394,027  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Plumer, Elizabeth R.  
;; REGISTRATION NUMBER: 36,637  
;; REFERENCE/DOCKET NUMBER: B0801/7029  
;; TELEPHONE: 617-720-3500  
;; TELEFAX: 617-720-2441  
;; INFORMATION FOR SEQ ID NO: 3:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
US-08-843-035-3

Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYK 3  
Db 1 KYK 3

RESULT 73  
US-08-609-271-1  
; Sequence 1, Application US/08609271  
; Patent No. 5811264  
;; GENERAL INFORMATION:  
;; APPLICANT: Aitken, Jacqueline F.  
;; APPLICANT: Apostol, Izydor Z.  
;; APPLICANT: Lippincott, Julie A.  
;; APPLICANT: Levine, Joseph D.  
;; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylation  
;; NUMBER OF SEQUENCES: 42  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Somatogen, Inc.  
;; STREET: 2545 Central Avenue, Site FD-1  
;; CITY: Boulder  
;; STATE: Colorado  
;; ZIP: 80301  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage  
;; COMPUTER: Apple Macintosh  
;; OPERATING SYSTEM: System 7.0.1  
;; SOFTWARE: Microsoft Word 5.0a  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/609,271  
;; FILING DATE: 28 February 1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/188,374  
;; FILING DATE: 1/27/94  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: No. 5811264elli, Marianne F.  
;; REGISTRATION NUMBER: 38571  
;; NAME: Brown, Theresa A.  
;; REGISTRATION NUMBER: 32547  
;; REFERENCE/DOCKET NUMBER: 170/Div  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 303-541-3324  
;; TELEFAX: 303-444-3013  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: no  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 1  
;; OTHER INFORMATION: /label=Modified-site1  
;; OTHER INFORMATION: /note= "Met(1) is Methylated N terminal Met"  
US-08-609-271-1

Query Match 42.9%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 4 LOP 6  
|||  
Db 2 LOP 4

## RESULT 74

US-08-755-496A-3  
; Sequence 3, Application US/08755496A  
; Patent No. 5846743  
; GENERAL INFORMATION:  
; APPLICANT: Cunningham, Casey  
; APPLICANT: Hartwig, John H.  
; APPLICANT: Janney, Paul A.  
; APPLICANT: Stossel, Thomas P.  
; APPLICANT: Vegners, Roland  
; TITLE OF INVENTION: POLYPHOSPHOSINOTIDE-(PPI-) BINDING  
; TITLE OF INVENTION: PEPTIDE(S) FOR INTRACELLULAR DRUG DELIVERY  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: Federal Reserve Plaza, 600 Atlantic Avenue  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02210

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/755,496A  
; FILING DATE: 22-NOV-1996  
; PRIOR APPLICATION NUMBER: 08/394,027  
; FILING DATE: 22-FEB-1995

ATTORNEY/AGENT INFORMATION:  
; NAME: Plumer, Elizabeth R.  
; REGISTRATION NUMBER: 36,637  
; REFERENCE/DOCKET NUMBER: B0801/7062  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-720-3500  
; TELEFAX: 617-720-2441  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal

US-08-755-496A-3

Query Match 42.9%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3  
|||  
Db 1 KYK 3

## RESULT 75

US-08-441-871-71  
; Sequence 71, Application US/08441871  
; Patent No. 5846765  
; GENERAL INFORMATION:  
; APPLICANT: Matthews, David J.  
; APPLICANT: Wells, James A.  
; APPLICANT: Zoller, Mark J.  
; TITLE OF INVENTION: Identification of No. 5846765el Substrates  
; NUMBER OF SEQUENCES: 152  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,871  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: 08/418928  
; FILING DATE: 05-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/161692  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/864452  
; FILING DATE: 06-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/09133  
; FILING DATE: 03-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/743614  
; FILING DATE: 09-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715300  
; FILING DATE: 14-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/683400  
; FILING DATE: 10-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/621667  
; FILING DATE: 03-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Daryl B.  
; REGISTRATION NUMBER: 32,637  
; REFERENCE/DOCKET NUMBER: 645P5C2D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1249  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-441-871-71

Query Match 42.9%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3  
|||  
Db 2 KYK 4

Search completed: November 25, 2003, 20:16:12  
Job time : 8.63298 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 6.44149 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-17

Perfect score: 7  
Sequence: 1 VLPPNVG 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	57.1	10	A37268	Ig heavy chain C r
2	4	57.1	14	C33098	223K exoantigen -
3	4	57.1	15	B61457	alpha-glucosidase
4	3	42.9	8	S16324	hypothetical prote
5	3	42.9	8	S10783	enamelin f - bovin
6	3	42.9	10	PC2171	triacylglycerol li
7	3	42.9	10	S18396	probable glucose-6
8	3	42.9	10	A44646	neurotoxin-associa
9	3	42.9	10	I44644	neurotoxin-associa
10	3	42.9	11	XASNBA	bradykinin-potenti
11	3	42.9	11	I33098	173K exoantigen -
12	3	42.9	12	PA0037	plastocyanin 2 - A
13	3	42.9	12	PN0663	lebetin 1 isoform
14	3	42.9	12	S711380	protein kinase (EC
15	3	42.9	15	S60341	ribosomal protein
16	3	42.9	15	T09463	protein QA300024 -
17	3	42.9	15	PA0034	recycling receptor
18	3	42.9	15	A36315	alpha-conotoxin Pn
19	3	42.9	16	A54877	alpha-conotoxin Pn
20	3	42.9	16	B54877	superoxide dismuta
21	3	42.9	16	E58503	Ig heavy chain DJ
22	3	42.9	16	PH1302	hypothetical 1.9K
23	3	42.9	17	JQ2030	hydroxyproline-ric
24	3	42.9	17	S59481	thyroid hormone re
25	3	42.9	17	I55612	steroid receptor c
26	3	42.9	18	A43576	shikimate 5-dehydr
27	3	42.9	18	I40062	2-aminobenzoate-Co
28	3	42.9	18	S39845	arsenite oxidase I
29	3	42.9	18	B45138	

alpha-macroglobulin  
Ig heavy chain CDR  
superoxide dismuta  
genome polypeptide  
shikimate 5-dehydr  
small granule S2 c  
translation elonga  
ribulose-bisphosph  
probable trypsin i  
hemagglutinin - In  
carbon-monoxide de  
tumor-derived adhe  
acidic fibroblast  
phenol 2-monooxyge  
proctolin - Americ  
peptidyl-di-peptida  
flagellar protein  
zinc-binding prote  
acid proteinase II  
proctolin - Atlant  
cocoanase (EC 3.4.  
Ig heavy chain CRD  
27.5 kda structura  
27.5K structural p  
28.5K structural p  
28K structural pro  
RNA-directed DNA p  
mosquitocidal toxi  
acylaminoacyl-pept  
MHC H2-K-k cell su  
platelet-derived g  
T-cell receptor be  
hypothetical colla  
dermorphin (Trp-4,  
tryptophyllin, bas  
membrane protein -  
RNA-directed DNA p  
choline oxidase (E  
hypothetical prote  
endospasm protein,  
ICL2 protein - Par  
gene C-rel protein  
Ig heavy chain CRD  
Ig heavy chain CRD  
Ig kappa chain V-I  
caldesquestrin, fas  
glutathione S-tran  
Na+-transporting A  
polyposphate-gluc  
hypertrehalosemic  
hypertrehalosemic  
adipokinetic hormo  
adipokinetic hormo  
neuropeptide Led-C  
neuropeptide Led-C  
hypertrehalosemic  
hypertrehalosemic  
sperm-activating p  
sperm-activating p  
2-hydroxyglutaryl-  
glycine reductase  
endoglycosylcerami  
lectin - potato (f  
variant surface gl  
neuropeptide M-I -  
neuropeptide calla  
acetylcholinestera  
Ig heavy chain CRD  
Ig heavy chain CRD  
fibroblast growth

## ALIGNMENTS

## RESULT 1

A37268  
 Ig heavy chain C region (129) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
 C:Accession: A37268  
 R:Kuff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A:Title: Heavy and light chain variable region sequences and antibody properties of anti-  
 A:Reference number: A38740; MUID:91177923; PMID:1706720  
 A:Accession: A37268  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-10 <RUF>

Query Match 57.1%; Score 4; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PNVP 7  
 ||||  
 Db 6 PNVP 9

## RESULT 2

C33098  
 223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
 C:Species: Plasmodium falciparum  
 C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: C33098  
 R:Nichols, J.H.; Hager, L.P.  
 submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: C33098  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <NIC>

Query Match 57.1%; Score 4; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
 ||||  
 Db 1 VLPP 4

## RESULT 3

B61457  
 alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)  
 C:Species: Tetrahymena pyriformis  
 C>Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-Dec-1999  
 C:Accession: B61457  
 R:Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.  
 J. Protozool. 36, 562-567, 1989  
 A:Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification  
 A:Reference number: A61457; MUID:90095988; PMID:2689637  
 A:Accession: B61457  
 A:Molecule type: protein  
 A:Residues: 1-15 <BAN>  
 C:Genetics:  
 A:Genetic code: SGC5  
 C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monom

Query Match 57.1%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
 ,||||

Db 1 VLPP 4

## RESULT 4

S16324  
 hypothetical protein 2 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000  
 C:Accession: S16324  
 R:Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.  
 EMBO J. 10, 1787-1791, 1991  
 A:Title: A novel class of plant proteins containing a homeodomain with a closely linked  
 A:Reference number: S16323; MUID:91266907; PMID:1675603  
 A:Accession: S16324  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <RUB>  
 A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:G579259

Query Match 42.9%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPP 4  
 ||||  
 Db 6 LPP 8

## RESULT 5

S10783  
 enamelinf - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
 C:Accession: S10783  
 R:Strawich, E.; Glimcher, M.J.  
 Eur. J. Biochem. 191, 47-56, 1990  
 A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu  
 A:Reference number: S10780; MUID:90336641; PMID:2379503  
 A:Accession: S10783  
 A:Molecule type: protein  
 A:Residues: 1-8 <STR>  
 C:Keywords: enamel; phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPP 4  
 ||||  
 Db 3 LPP 5

## RESULT 6

PC2171  
 triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (frag  
 C:Species: Rhizopus niveus  
 C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
 C:Accession: PC2171  
 R:Kohno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.  
 Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994  
 A:Title: Purification, characterization, and crystallization of two types of lipase from  
 A:Reference number: PC2171; MUID:94319059; PMID:7765029  
 A:Accession: PC2171  
 A:Molecule type: protein  
 A:Residues: 1-10 <KOH>  
 C:Comment: This enzyme catalyzes the hydrolysis of the ester bonds.  
 C:Keywords: carboxylic ester hydrolase

Query Match 42.9%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPP 4

Db 5 LPP 7

RESULT 7

S18396

probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Acetobacter hansenii (fragment)

C:Species: Acetobacter hansenii

C>Date: 19-Mar-1997 #sequence\_revision 01-Feb-1999 #text\_change 01-Feb-1999

C:Accession: S18396

R:Levy, H.R.; Cook, C.

Arch. Biochem. Biophys. 291, 161-167, 1991

A:Title: Purification and properties of NADP-linked glucose-6-phosphate dehydrogenase from *Acetobacter hansenii*

A:Reference number: S18396; PMID:92027789; PMID:1929428

A:Accession: S18396

A:Molecule type: protein

A:Residues: 1-10 <LEV>

A:Experimental source: ATCC 23769

C:Function:

A:Description: catalyzes reduction of glucose-6-phosphate to gluconolactone 6-phosphate

A:Pathway: pentose phosphate pathway

C:Keywords: oxidoreductase; homotetramer; NADP; pentose phosphate pathway

Query Match 42.9%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
Db 3 LPP 5

RESULT 8

A44646

neurotoxin-associated protein type A Hn+ 57K chain - Clostridium botulinum (fragment)

C:Species: Clostridium botulinum

C>Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994

C:Accession: A44646

R:Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A:Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinin

A:Reference number: A44644; PMID:92143938; PMID:1781887

A:Contents: type A

A:Accession: A44646

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <SOM>

A>Note: sequence extracted from NCBI backbone (NCBIP:83774)

A>Note: 6-Trp was also found

C:Keywords: hemagglutinin

Query Match 42.9%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
Db 7 VLP 9

RESULT 9

I44644

neurotoxin-associated protein type B Hn+ 57K chain - Clostridium botulinum (fragment)

C:Species: Clostridium botulinum

C>Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994

C:Accession: I44644

R:Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A:Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinin

A:Reference number: A44644; PMID:92143938; PMID:1781887

A:Contents: type B

A:Accession: I44644

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <SOM>

A>Note: sequence extracted from NCBI backbone (NCBIP:83783)

C:Keywords: hemagglutinin

Query Match 42.9%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
Db 7 VLP 9

RESULT 10

XASNBA

bradykinin-potentiating peptide B - mamushi

C:Species: Agkistrodon blomhoffi (mamushi)

C>Date: 13-Jul-1981 #sequence\_revision 13-Jul-1991 #text\_change 08-Dec-1995

C:Accession: A01254

R:Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A:Reference number: A01254

A:Accession: A01254

A:Molecule type: protein

A:Residues: 1-11 <KAT>

A>Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of the peptide

C:Superfamily: bradykinin-potentiating peptide

C:Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venticular fibrillation; pyrrolidone carboxylic acid (Gln) #status experimental

F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
Db 3 LPP 5

RESULT 11

I33098

173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C:Accession: I33098

R:Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: I33098

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <NIC>

Query Match 42.9%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
Db 2 LPP 4

RESULT 12

PA0037

plastocyanin 2 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995

C:Accession: PA0037

R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis

A:Reference number: PA0001

A:Accession: PA0037  
 A:Molecule type: protein  
 A:Residues: 1-12 <KAM>  
 A:Experimental source: stem

Query Match 42.9%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
 |||  
 Db 5 VLP 7

## RESULT 13

PN0663

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C:Accession: PN0663

R.Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained  
 A:Reference number: PN0662; PMID:94156881; PMID:8113213

A:Accession: PN0663

A:Molecule type: protein

A:Residues: 1-12 &lt;YOS&gt;

A:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C:Keywords: glycoprotein; skeletal muscle

Query Match 42.9%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
 |||  
 Db 4 LPP 6

## RESULT 14

S71380

lebetin 1 isoform beta - Vipera lebetina

C:Species: Vipera lebetina

C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C:Accession: S71380

R.Barbouche, R.; Marrakchi, N.; Mansuelle, P.; Krifi, M.; Fenouillet, E.; Rochat, H.; El

FEBS Lett. 392, 6-10, 1996

A:Title: Novel anti-platelet aggregation polypeptides from Vipera lebetina venom: isolat  
 A:Reference number: S71379; PMID:96354866; PMID:8769304

A:Accession: S71380

A:Molecule type: protein

A:Residues: 1-12 &lt;BAR&gt;

A:Experimental source: venom

C:Keywords: anticoagulant; venom

Query Match 42.9%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPN 5  
 |||  
 Db 9 PPN 11

## RESULT 15

S60341

protein kinase (EC 2.7.1.37) raf-1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 31-Oct-1997

A:Accession: S60341

R.Yao, B.; Zhang, Y.; Delikat, S.; Mathias, S.; Basu, S.; Kolesnick, R.

Nature 378, 307-310, 1995

A:Title: Phosphorylation of Raf by ceramide-activated protein kinase.

A:Reference number: S60341; MUID:96069769; PMID:7477354

A:Accession: S60341

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 &lt;YAO&gt;

C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot  
 C:Keywords: phosphotransferase; protein kinase

Query Match 42.9%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6  
 |||  
 Db 5 PNV 7

## RESULT 16

T09463

ribosomal protein S14 - brown alga (Pylaiella littoralis) mitochondrion (fragment)

C:Species: mitochondrion Pylaiella littoralis

C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 13-Aug-1999

C:Accession: T09463

J. Rousvoal, S.; Oudot, M.; Fontaine, J.; Kloareg, B.; Goer, S.L.

J. Mol. Biol. 277, 1047-1057, 1998

A:Title: Witnessing the evolution of transcription in mitochondria: The mitochondrial ge  
 A:Reference number: Z16681; MUID:98239704; PMID:9571021

A:Accession: T09463

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-15 &lt;ROU&gt;

A:Cross-references: EMBL:AF034976; NID:G3243103; PID:G3243104

A:Experimental source: strain Roscoff

C:Genetics:

A:Gene: rps14

A:Genome: mitochondrion

C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 42.9%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
 |||  
 Db 6 VLP 8

## RESULT 17

PA0034

protein QA300024 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997

C:Accession: PA0034

R.Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A:Reference number: PA0001

A:Accession: PA0034

A:Molecule type: protein

A:Residues: 1-15 &lt;KAM&gt;

A:Experimental source: leaf

Query Match 42.9%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6  
 |||  
 Db 5 PNV 7

## RESULT 18

A36315

recycling receptor p180 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 25-Jan-1991 #sequence\_revision 25-Jan-1991 #text\_change 30-Sep-1993  
C:Accession: A36315  
R:Tsacke, C.M.; van der Geer, P.; Hunter, T.; Trowbridge, I.S.  
Mol. Cell. Biol. 10, 2606-2618, 1990  
A:Title: p180, a novel recycling transmembrane glycoprotein with restricted cell type expression  
A:Reference number: A36315; MUID:90258846; PMID:2188094  
A:Accession: A36315  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <ISA>

Query Match 42.9%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6  
DB 10 PNV 12

RESULT 19  
A54877  
alpha-conotoxin pN1A [validated] - cone shell (Conus pennaceus)  
N:Alternate names: alpha-Ctx-PN1A  
C:Species: Conus pennaceus  
C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
C:Accession: A54877  
R:Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlotk  
Biochemistry 33, 9523-9529, 1994  
A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rece  
A:Reference number: A54877; MUID:94347719; PMID:8068627  
A:Accession: A54877  
A:Molecule type: protein  
A:Residues: 1-16 <FAI>  
R:Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.  
submitted to the Brookhaven Protein Data Bank, January 1996  
A:Reference number: A66355; PDB:1PEN  
A:Contents: annotation: X-ray crystallography, 1.1 angstroms; residues 1-16  
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap  
C:Superfamily: alpha-conotoxin  
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
F;2-8,3-16/Disulfide bonds: #status experimental  
F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
DB 5 LPP 7

RESULT 20  
B54877  
alpha-conotoxin pN1B - cone shell (Conus pennaceus)  
C:Species: Conus pennaceus  
C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 23-May-1997  
C:Accession: B54877  
R:Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlotk  
Biochemistry 33, 9523-9529, 1994  
A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rece  
A:Reference number: A54877; MUID:94347719; PMID:8068627  
A:Accession: B54877  
A:Molecule type: protein  
A:Residues: 1-16 <FAI>  
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap  
C:Superfamily: alpha-conotoxin  
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
F;2-8,3-16/Disulfide bonds: #status experimental  
F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
DB 5 LPP 7

RESULT 21  
E58503  
superoxide dismutase (BC 1.15.1.1) - unidentified bacterium (fragment)  
N:Alternate names: 21.3K bladder and kidney stone protein  
C:Species: unidentified bacterium  
C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 05-Mar-1999  
C:Accession: E58503  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A:Description: The proteins of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: E58503  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <BIN>  
A:Experimental source: human bladder and kidney stones  
C:Function:  
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
C:Keywords: metalloprotein; oxidoreductase

Query Match 42.9%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
DB 5 LPP 7

RESULT 22  
PH1302  
Ig heavy chain DJ region (clone C76-105) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1302  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1302  
A:Molecule type: DNA  
A:Residues: 1-16 <WAS>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPN 5  
DB 13 PPN 15

RESULT 23  
JQ2030  
hypothetical 1.9K protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus  
N:Alternate names: ORF2 mini gene protein  
C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 08-Oct-1999  
C:Accession: JQ2030  
R:Russell, R.L.Q.; Rohrmann, G.F.  
J. Gen. Virol. 74, 1191-1195, 1993  
A:Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsuga

A:Reference number: PQ0633; MUID:93286576; PMID:8389803

A:Accession: JQ2030

A:Molecule type: DNA

A:Residues: 1-17 <RUS>

A:Cross-references: DBJ:DJ3375; NID:G222217; PIDN:BAA02640.1; PID:di003144; PID:G222222

Query Match 42.9%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3

Db 2 VLP 4

#### RESULT 24

SS9481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C:Species: Phaseolus vulgaris (kidney bean)

C>Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998

C:Accession: SS9481

R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A:Title: Specificity in the immobilisation of cell wall proteins in response to different

A:Reference number: SS9481; MUID:96011753; PMID:7548825

A:Accession: SS9481

A:Molecule type: protein

A:Residues: 1-17 <WOJ>

A:Keywords: glycoprotein; hydroxyproline

F:6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4

Db 4 LPP 6

#### RESULT 25

IS5612

thyroid hormone receptor beta - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C:Accession: IS5612

R:Adams, M.; Matthews, C.; Collingwood, T.N.; Tane, Y.; Beck-Peccoz, P.; Chatterjee, K.K.

J. Clin. Invest. 94, 506-515, 1994

A:Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to th

A:Reference number: IS5612; MUID:94314950; PMID:8040303

A:Accession: IS5612

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-17 <RES>

A:Cross-references: GB:S72623; NID:G633779; PIDN:AAB31420.1; PID:G633780

C:Genetics:

A:Gene: TRbeta

Query Match 42.9%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4

Db 5 LPP 7

#### RESULT 26

A42576

steroid receptor complex Hsp56 60K component - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Sep-1998

C:Accession: A42576

R:Yem, A.W.; Tomasselli, A.G.; Heinrikson, R.L.; Zurcher-Neely, H.; Ruff, V.A.; Johnson, J. Biol. Chem. 267, 2868-2871, 1992

A:Title: The Hsp56 component of steroid receptor complexes binds to immobilized FK506 an

A:Reference number: A42576; MUID:92147620; PMID:1371107

A:Accession: A42576

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <YEM>

A:Experimental source: thymus

A:Note: sequence extracted from NCBI backbone (NCBIP:80696)

C:Superfamily: human FK506-binding protein FKBP51; BKBP-type peptidylprolyl isomerase h

C:Keywords: steroid hormone receptor

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPN 5

Db 3 PPN 5

#### RESULT 27

I40062

shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)

C:Species: Buchnera aphidicola

C>Date: 02-Aug-1995 #sequence\_revision 02-Aug-1996 #text\_change 08-Oct-1999

C:Accession: I40062

R:Roubhakhsh, D.; Baumann, P.

Gene 155, 107-112, 1995

A:Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endos

A:Reference number: I40061; MUID:95212914; PMID:7535281

A:Accession: I40062

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-18 <RES>

A:Cross-references: EMBL:U10496; NID:G854711; PIDN:AAA79125.1; PID:G854712

C:Genetics:

A:Gene: aroE

C:Keywords: oxidoreductase

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3

Db 8 VLP 10

#### RESULT 28

S39845

2-aminobenzoate-CoA ligase, anaerobic - Pseudomonas sp. (strain KB740) (fragment)

C:Species: Pseudomonas sp.

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995

C:Accession: S39845

R:Altenschmidt, U.; Fuchs, G.

Eur. J. Biochem. 205, 721-727, 1992

A:Title: Novel aerobic 2-aminobenzoate metabolism. Purification and characterization of

from a denitrifying Pseudomonas sp.

A:Reference number: S22402; MUID:92241310; PMID:1315272

A:Accession: S39845

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10,'X',12-14,'X',16-18 <ALT>

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4

Db 12 LPP 14



Db 4 PPN 6

RESULT 32

C56049

superoxide dismutase (EC 1.15.1.1) (Fe/Mn) [similarity] - unidentified organism (fragment)

C:Species: unidentified organism

C>Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 20-Apr-2000

C:Accession: C56049

R:Binette, J.P.; Binette, M.B.

A:Title: Sequencing of proteins extracted from stones.

A:Reference number: A56049; MUID:95215817; PMID:7701298

A:Accession: C56049

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <BIN>

A:Experimental source: urate-calcium oxalate kidney stones

A>Note: The source is designated as Homo sapiens, however the true source probably originates from a different source.

C:Superfamily: superoxide dismutase (Mn)

C:Keywords: metalloprotein; oxidoreductase

Query Match 42.9%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3

Db 4 VLP 6

RESULT 33

B61409

genome polyprotein (clone L3/S2) - Skalka virus (fragment)

C:Species: Skalka virus

C>Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Nov-2000

C:Accession: B61409

R:Guirakho, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Gresikova, M.

A:Title: The relationship between the flaviviruses Skalka and Langat as revealed by molecular biology.

A:Reference number: A61409; MUID:91132129; PMID:1847173

A:Accession: B61409

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: genomic RNA

A:Residues: 1-19 <GUI>

C:Superfamily: yellow fever virus genome polyprotein

Query Match 42.9%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4

Db 1 LPP 3

RESULT 34

I40063

shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)

C:Species: Buchnera aphidicola

C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 08-Oct-1999

C:Accession: I40063

R:Rouhbakheh, D.; Baumann, P.

A:Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endosymbiont) from the pea aphid, Acyrthosiphon pisum.

A:Reference number: I40061; MUID:95212914; PMID:7535281

A:Accession: I40063

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-19 <RES>

A:Cross-references: EMBL:U01497; NID:9854713; PIDN:AAA79126.1; PID:9854714

C:Genetics: aroE

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPN 5

Db 15 PPN 17

RESULT 31

PT0286

Ig heavy chain CDR3 region (clone 4-100B) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0286

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining in the CDR3 region of the human Ig heavy chain CDR3 region.

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0286

A:Molecule type: DNA

A:Residues: 1-18 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPN 5

Db 15 PPN 17

RESULT 30

S23971

alpha-macroglobulin proteinase inhibitor - common octopus

C:Species: Octopus vulgaris (common octopus)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C:Accession: S23971

R:Thogersen, I.B.; Salvesen, G.; Brucato, F.H.; Pizzo, S.V.; Enghild, J.J.

A:Title: Purification and characterization of an alpha-macroglobulin proteinase inhibitor from Octopus vulgaris.

A:Reference number: S23971; MUID:92344633; PMID:1379044

A:Accession: S23971

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <THO>

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4

Db 9 LPP 11

RESULT 29

B45138

arsenite oxidase I - Alcaligenes faecalis (fragment)

C:Species: Alcaligenes faecalis

C>Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Dec-1994

C:Accession: B45138

R:Anderson, G.L.; Williams, J.; Hille, R.

A:Title: The purification and characterization of arsenite oxidase from Alcaligenes faecalis.

A:Reference number: A45138; MUID:93054722; PMID:1331097

A:Accession: B45138

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <AND>

A>Note: sequence extracted from NCBI backbone (NCBI:P118543)

Query Match 42.9%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4

Db 9 LPP 11

C;Keywords: oxidoreductase

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
|||  
DB 8 VLP 10

#### RESULT 35

PC1309  
small granule S2 chain - horseshoe crab (Tachypileus tridentatus) (fragment)  
C;Species: Tachypileus tridentatus  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C;Accession: PC1309  
R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa  
J. Biochem. 114, 307-316, 1993  
A;Title: Separation of large and small granules from horseshoe crab (Tachypileus tridentatus)  
A;Reference number: PC1309; MUID:94110249; PMID:8282718  
A;Accession: PC1309  
A;Molecule type: protein  
A;Residues: 1-19 <SHI>  
C;Comment: This protein contributes to a self-defense system against invaders.

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6  
|||  
DB 17 PNV 19

#### RESULT 36

S43045  
translation elongation factor EF-1 alpha - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 07-May-1999  
C;Accession: S43045  
R;Rosenberry, T.L.; Krall, J.A.; Dever, T.E.; Haas, R.; Louvard, D.; Merrick, W.C.  
J. Biol. Chem. 264, 7096-7099, 1989  
A;Title: Biochemical incorporation of [(3)H]ethanolamine into protein synthesis elongat  
A;Reference number: A33048; MUID:89214136; PMID:2708257  
A;Accession: S43045  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <ROS>

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NVG 7  
|||  
DB 9 NVG 11

#### RESULT 37

A37111  
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - spinach (fragment)  
C;Species: Spinacia oleracea (spinach)  
C;Date: 15-Feb-1991 #sequence\_revision 15-Feb-1991 #text\_change 12-Apr-1995  
C;Accession: A37111  
R;Sato, M.H.; Hisabori, T.; Yoshida, M.  
J. Biol. Chem. 265, 13419-13422, 1990  
A;Title: The 55-kDa polypeptide released from spinach thylakoid membranes with 1 M LiCl  
A;Reference number: A37111; MUID:90337936; PMID:2143183  
A;Accession: A37111  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <SAT>

C;Superfamily: ribulose-bisphosphate carboxylase small chain  
C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 42.9%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
|||  
DB 18 LPP 20

#### RESULT 38

S50741  
probable trypsin inhibitor - potato (fragment)  
N;Alternate names: PKPI major protein  
C;Species: Solanum tuberosum (potato)  
C;Date: 14-Jul-1995 #sequence\_revision 12-Apr-1996 #text\_change 11-Jan-2000  
C;Accession: S50741  
R;Mitsuamori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.  
Plant Mol. Biol. 26, 961-969, 1994  
A;Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibitors  
A;Reference number: S50741; MUID:95093035; PMID:8000008  
A;Accession: S50741  
A;Molecule type: protein  
A;Residues: 1-20 <MIT>  
C;Superfamily: cathepsin D inhibitor

Query Match 42.9%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
|||  
DB 2 VLP 4

#### RESULT 39

PL0161  
hemagglutinin - Influenza H2N2 (fragment)  
C;Species: Influenza H2N2  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-May-1997  
C;Accession: PL0161  
R;Sweetser, M.T.; Braciale, V.L.; Braciale, T.J.  
J. Exp. Med. 170, 1357-1368, 1989  
A;Title: Class I major histocompatibility complex-restricted T lymphocyte recognition of  
A;Reference number: PL0161; MUID:90010790; PMID:2477491  
A;Accession: PL0161  
A;Molecule type: mRNA  
A;Residues: 1-20 <SWE>

Query Match 42.9%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NVG 7  
|||  
DB 6 NVG 8

#### RESULT 40

PL0145  
carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain - Pseudomonas carboxydoflava (f  
C;Species: Pseudomonas carboxydoflava  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 28-Apr-1993  
C;Accession: PL0145  
R;Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.  
Arch. Microbiol. 152, 335-341, 1989

A>Title: Homology and distribution of CO dehydrogenase structural genes in carboxydototrog  
 A:Reference number: PL0138; MUID:90055678; PMID:2818128  
 A:Accession: PL0145  
 A:Molecule type: protein  
 A:Residues: 1-20 <KRA>  
 C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me  
 C:Keywords: oxidoreductase

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 NVG 7  
 Db 9 NVG 11

## RESULT 41

PC2030  
 tumor-derived adhesion factor - human (fragment)  
 N:Alternate names: 30K protein  
 C:Species: Homo sapiens (man)  
 C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 21-Jan-2000  
 A:Accession: PC2030  
 R:Akaogi, K.; Okabe, Y.; Funahashi, K.; Yoshitake, Y.; Nishikawa, K.; Yasumitsu, H.; Ume  
 Biochem. Biophys. Res. Commun. 198, 1046-1053, 1994  
 A>Title: Cell adhesion activity of a 30-kDa major secreted protein from human bladder ca  
 A:Reference number: PC2030; MUID:94161713; PMID:8117260  
 A:Accession: PC2030  
 A:Molecule type: protein  
 A:Residues: 1-20 <AKA>  
 A:Experimental source: cell line EJ-1  
 C:Comment: This protein relates with the aberrant cell adhesion of cancer cells.

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPP 4  
 Db 17 LPP 19

## RESULT 42

S03954  
 acidic fibroblast growth factor - pig (fragment)  
 N:Alternate names: alpha-endothelial cell growth factor  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993  
 A:Accession: S03954  
 R:Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Schape  
 Eur. J. Biochem. 181, 67-73, 1989  
 A>Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea  
 A:Reference number: S03953; MUID:89231704; PMID:2714282  
 A:Accession: S03954  
 A:Molecule type: protein  
 A:Residues: 1-20 <QUI>  
 C:Keywords: growth factor

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPP 4  
 Db 3 LPP 5

## RESULT 43

A37832  
 phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (fragmen  
 C:Species: Pseudomonas sp.  
 C:Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 23-Jun-1993

C:Accession: A37832  
 R:Powlowski, J.; Shingler, V.  
 J. Bacteriol. 172, 6834-6840, 1990  
 A>Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydroxyl  
 A:Reference number: A37832; MUID:91072231; PMID:2254259  
 A:Accession: A37832  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-4 <POW>  
 C:Keywords: oxidoreductase

Query Match 28.6%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 NV 6  
 Db 3 NV 4

## RESULT 44

H0808A  
 proctolin - American cockroach  
 C:Species: Periplaneta americana (American cockroach)  
 C:Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 23-Aug-1996  
 A:Accession: A01644  
 R:Starratt, A.N.; Brown, B.E.  
 Life Sci. 17, 1253-1256, 1975  
 A>Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insect  
 A:Reference number: A93048; MUID:76074708; PMID:576  
 A:Accession: A01644  
 A:Molecule type: protein  
 A:Residues: 1-5 <SPA>  
 A:Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharma  
 R:O'Shea, M.; Adams, M.E.  
 Science 213, 567-569, 1981  
 A>Title: Pentapeptide (proctolin) associated with an identified neuron.  
 A:Reference number: A94260; MUID:81225865; PMID:6113690  
 C:Contents: annotation; biological source  
 C:Comment: This peptide is found in the lateral white neurons, which occur (in the cock  
 innervate the striated hindgut muscles in insects and stimulate contraction of these mu  
 C:Superfamily: proctolin  
 C:Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LP 3  
 Db 3 LP 4

## RESULT 45

JN0860  
 peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito  
 C:Species: Sarda orientalis (striped bonito)  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 A:Accession: JN0860  
 R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
 A>Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe  
 A:Reference number: JN0859; MUID:94080036; PMID:7764272  
 A:Accession: JN0860  
 A:Molecule type: protein  
 A:Residues: 1-5 <MAT>

A:Experimental source: intestine  
 C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotens  
 C:Superfamily: bradykinin-potentiating peptide  
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 28.6%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
||  
Db 2 LP 3

RESULT 46  
E42364  
flagellar protein flir - Salmonella typhimurium (fragment)  
C:Species: Salmonella typhimurium  
C>Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 30-Sep-1993  
C:Accession: E42364  
R:Vogler A.P.; Honma, M.; Irikura, V.M.; Macnab, R.M.  
J. Bacteriol. 173, 3564-3572, 1991  
A:Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion  
A:Reference number: A42364; MUID:91258342; PMID:1646201  
A:Accession: E42364  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <VOG>  
A:Cross-references: GB:M62408

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
||  
Db 4 LP 5

RESULT 47  
S55237  
zinc-binding protein ZBP14 - maize (fragment)  
C:Species: Zea mays (maize)  
C>Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 07-May-1999  
C:Accession: S55237  
R:Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.  
Biochem. J. 307, 267-272, 1995  
A:Title: Expression and characterization of maize ZBP14, a member of a new family of zinc-binding proteins  
A:Reference number: S55237; MUID:95234046; PMID:7717986  
A:Accession: S55237  
A:Molecule type: protein  
A:Residues: 1-5 <ROB>

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
||  
Db 4 VL 5

RESULT 48  
B37988  
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
C:Species: Physarum polycephalum  
C>Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
C:Accession: B37988  
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Ogino, T.  
J. Biol. Chem. 265, 19898-19903, 1990  
A:Title: Purification and characterization of a novel intracellular acid proteinase from Physarum polycephalum  
A:Reference number: A37988; MUID:91060608; PMID:2246266  
A:Accession: B37988  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <MUR>

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
||  
Db 3 PP 4

## RESULT 49

A60411  
proctolin - Atlantic horseshoe crab  
C:Species: Limulus polyphemus (Atlantic horseshoe crab)  
C>Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 17-Mar-1999  
C:Accession: A60411  
R:Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, L.  
Peptides 11, 205-211, 1990  
A:Title: Identification of proctolin in the central nervous system of the horseshoe crab  
A:Reference number: A60411; MUID:90287800; PMID:2356151  
A:Accession: A60411  
A:Molecule type: protein  
A:Residues: 1-5 <GRO>  
C:Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horseshoe crab  
C:Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
||  
Db 3 LP 4

## RESULT 50

B61168  
cocoonase (EC 3.4.21.-) - Chinese oak silkworm (fragment)  
C:Species: Antherea pernyi (Chinese oak silkworm)  
C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C:Accession: B61168  
R:Kramer, K.J.; Felsted, R.L.; Law, J.H.  
J. Biol. Chem. 248, 3021-3028, 1973  
A:Title: Cocoonase. V. Structural studies on an insect serine protease.  
A:Reference number: A61168; MUID:73166540; PMID:4735570  
A:Accession: B61168  
A:Molecule type: protein  
A:Residues: 1-5 <KRA>  
C:Keywords: hydrolase; serine proteinase; zymogen  
C:Product: cocoonase (fragment) #status experimental <MAT>  
F:1-5

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7  
||  
Db 2 VG 3

## RESULT 51

PT0278  
Ig heavy chain CRD3 region (clone 4-88) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0278  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in the generation of the human Ig heavy chain CRD3 region  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0278  
A:Molecule type: DNA  
A:Residues: 1-5 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VL 2  
||  
Db 4 VL 5

## RESULT 52

G44817  
27.5 kda structural protein - Leuconostoc oenos phase P32 (fragment)

C:Species: Leuconostoc oenos phase P32  
C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C:Accession: G44817  
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A:Title: Lysozyme in Leuconostoc oenos  
A:Reference number: A44817; MUID:92085033; PMID:1748868  
A:Accession: G44817  
A:Molecule type: protein  
A:Residues: 1-5 <ARE>  
A>Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VG 7  
||  
Db 3 VG 4

## RESULT 53

I44817  
27.5K structural protein - Leuconostoc oenos phase P37 (fragment)

C:Species: Leuconostoc oenos phase P37  
C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C:Accession: I44817  
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A:Title: Lysozyme in Leuconostoc oenos  
A:Reference number: A44817; MUID:92085033; PMID:1748868  
A:Accession: I44817  
A:Molecule type: protein  
A:Residues: 1-5 <ARE>  
A>Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VG 7  
||  
Db 3 VG 4

## RESULT 54

E44817  
27.5K structural protein - Leuconostoc oenos phase P54 (fragment)

C:Species: Leuconostoc oenos phase P54  
C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C:Accession: E44817  
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A:Title: Lysozyme in Leuconostoc oenos  
A:Reference number: A44817; MUID:92085033; PMID:1748868  
A:Accession: E44817  
A:Molecule type: protein  
A:Residues: 1-5 <ARE>  
A>Note: sequence extracted from NCBI backbone (NCBIP:70336)

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VG 7  
||  
Db 3 VG 4

## RESULT 55

C44817  
28.5K structural protein - Leuconostoc oenos phase PAT5-12 (fragment)

C:Species: Leuconostoc oenos phase PAT5-12  
C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C:Accession: C44817  
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A:Title: Lysozyme in Leuconostoc oenos  
A:Reference number: A44817; MUID:92085033; PMID:1748868  
A:Accession: C44817  
A:Molecule type: protein  
A:Residues: 1-5 <ARE>  
A>Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VG 7  
||  
Db 3 VG 4

## RESULT 56

A44817  
28K structural protein - Leuconostoc oenos phase PZt11-15 (fragment)

C:Species: Leuconostoc oenos phase PZt11-15  
C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C:Accession: A44817  
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A:Title: Lysozyme in Leuconostoc oenos  
A:Reference number: A44817; MUID:92085033; PMID:1748868  
A:Accession: A44817  
A:Molecule type: protein  
A:Residues: 1-5 <ARE>  
A>Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VG 7  
||  
Db 3 VG 4

## RESULT 57

A35890

RNA-directed DNA polymerase (EC 2.7.7.49) 66K chain - human immunodeficiency virus type  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 31-Dec-1993  
C:Accession: A35890  
R:Batchurst, I.C.; Moen, L.K.; Lujan, M.A.; Gibson, H.L.; Feucht, P.H.; Pichuanes, S.;  
Biochem. Biophys. Res. Commun. 171, 589-595, 1990  
A:Title: Characterization of the human immunodeficiency virus type-1 reverse transcriptase  
A:Reference number: A35890; MUID:90386627; PMID:1698361  
A:Accession: A35890  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6 <BAT>  
C:Keywords: nucleotidyltransferase

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
||  
Db 5 VL 6

RESULT 58  
A44916  
mosquitocidal toxin 21 - Bacillus sphaericus (fragment)  
C:Species: Bacillus sphaericus  
C>Date: 01-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995  
C:Accession: A44916  
R:Thanabalu, T.; Hindley, J.; Berry, C.  
J. Bacteriol. 174, 5051-5056, 1992  
A:Title: Proteolytic processing of the mosquitocidal toxin from Bacillus sphaericus SSII-1  
A:Reference number: A44916; MUID:92332441; PMID:1352768  
A:Accession: A44916  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-6 <THA>  
A:Experimental source: SSII-1  
A>Note: sequence extracted from NCBI backbone (NCBIP:108973)

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5  
||  
Db 5 PN 6

RESULT 59  
A49792  
acylaminoacyl-peptidase (EC 3.4.19.1) - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
C:Accession: A49792  
R:Krishna, R.G.; Chin, C.C.Q.; Wold, F.  
Anal. Biochem. 199, 45-50, 1991  
A:Title: N-terminal sequence analysis of N(alpha)-acetylated proteins after unblocking with F:1/Modified site: acetylated amino end (Met) #status experimental  
A:Reference number: A49792; MUID:9222120; PMID:1807161  
A:Accession: A49792  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6 <KRI>  
A:Keywords: acetylated amino end; hydrolase; omega peptidase  
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
||  
Db 5 VL 6

RESULT 60  
I67345  
MHC H2-K-k cell surface glycoprotein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I67345  
R:Archibald, A.L.; Thompson, N.A.; Kvist, S.  
EMBO J. 5, 957-965, 1986  
A:Title: A single nucleotide difference at the 3' end of an intron causes differential splicing of the H2-K-k gene  
A:Reference number: I53243; MUID:86247587; PMID:3013627  
A:Accession: I67345  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>

A:Cross-references: GB:M26859; NID:g199439; PIDN:AAA39612.1; PID:g387458  
C:Genetics:  
A:Introns: 6/1  
C:Keywords: glycoprotein

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
||  
Db 1 LP 2

RESULT 61  
I59142  
platelet-derived growth factor B chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I59142  
R:Pech, M.; Gazit, A.; Arnstein, P.; Aaronson, S.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 2693-2697, 1989  
A:Title: Generation of fibrosarcomas in vivo by a retrovirus that expressed the normal platelet-derived growth factor B chain  
A:Reference number: I59142; MUID:89202393; PMID:2649890  
A:Accession: I59142  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-6 <RES>

A:Cross-references: GB:M26180; NID:g516624; PIDN:AAA39905.1; PID:g516625

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
||  
Db 5 VL 6

RESULT 62  
PT0560  
T-cell receptor beta chain V-D-J region (126-1CE) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0560  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0560  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FEE>  
A:Experimental source: day 18 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
||  
Db 3 VL 4

RESULT 63  
A35039  
hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: A35039  
R:Bennett, V.D.; Adams, S.L.  
J. Biol. Chem. 265, 2223-2230, 1990

A:Title: Identification of a cartilage-specific promoter within intron 2 of the chick alpha 1(I) procollagen gene  
 A:Reference number: A35039; MUID:90130479; PMID:1688851  
 A:Accession: A35039  
 A:Molecule type: mRNA  
 A:Residues: 1-6 <BEN>  
 A:Cross-references: GB:M33382; NID:9211043  
 A:Note: This ORF is not translated in GenBank entry CHKA21CG  
 C:Comment: This sequence is the translation of a cartilage specific alternative transcript  
 C:Keywords: alternative splicing; cartilage

Query Match 28.6%; Score 2; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
 ||  
 DB 4 LP 5

RESULT 64  
 S21230  
 dermorphin (Tirp-4, Asn-7) [validated] - two-colored leaf frog (fragment)  
 C:Species: Phyllomedusa bicolor (two-colored leaf frog)  
 C:Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 18-Aug-2000  
 C:Accession: S21230  
 R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G. FEBS Lett. 302, 151-154, 1992  
 A:Title: Identification and characterization of two dermorphins from skin extracts of the two-colored leaf frog  
 A:Reference number: S21152; MUID:92339502; PMID:1633846  
 A:Accession: S21230  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <MG>  
 C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5  
 ||  
 DB 6 PN 7

RESULT 65  
 A61081  
 tryptophyllin, basic - Rohde's leaf frog  
 C:Species: Phyllomedusa rohdei (Rohde's leaf frog)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000  
 C:Accession: A61081  
 R:Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V. Int. J. Pept. Protein Res. 33, 391-395, 1989  
 A:Title: Isolation, structure determination and synthesis of a novel tryptophan-containing peptide  
 A:Reference number: A61081  
 A:Accession: A61081  
 A:Molecule type: protein  
 A:Residues: 1-7 <MON>  
 C:Comment: The biological activity of this peptide was not determined.  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end; hydroxyproline; skin  
 F:3/Modified site: 4-hydroxyproline (Pro) #status experimental  
 F:7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
 ||  
 DB 2 PP 3

RESULT 66

P00663  
 membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)  
 C:Species: porcine epidemic diarrhea virus  
 C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 08-Oct-1999  
 C:Accession: P00663  
 R:Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M. J. Gen. Virol. 74, 1795-1804, 1993  
 A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic diarrhea virus  
 A:Reference number: JQ2191; MUID:93389433; PMID:8397280  
 A:Accession: P00663  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <BRI>  
 A:Cross-references: GB:Z14976; NID:G311650; PIDN:CAA78699.1; PID:G584083  
 C:Comment: This virus is coronavirus related to human coronavirus 229E.  
 C:Keywords: membrane protein

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
 ||  
 DB 3 VL 4

RESULT 67  
 B35890  
 RNA-directed DNA polymerase (EC 2.7.7.49) 51K chain - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 31-Dec-1993  
 C:Accession: B35890  
 R:Bathurst, I.C.; Moen, L.K.; Lujan, M.A.; Gibson, H.L.; Feucht, P.H.; Pichuantes, S.; Blochem. Biophys. Res. Commun. 171, 589-595, 1990  
 A:Title: Characterization of the human immunodeficiency virus type-1 reverse transcriptase  
 A:Reference number: A35890; MUID:90386627; PMID:1698361  
 A:Accession: B35890  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <BAT>  
 C:Keywords: nucleotidyltransferase

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7  
 ||  
 DB 2 VG 3

RESULT 68  
 A15398  
 choline oxidase (EC 1.1.3.17) - Alcaligenes sp. (tentative sequence) (fragment)  
 C:Species: Alcaligenes sp.  
 C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000  
 C:Accession: A15398  
 R:Ohira-Fukuyama, M.; Miyake, Y.; Emi, S.; Yamano, T. J. Biochem. 88, 197-203, 1980  
 A:Title: Identification and properties of the prosthetic group of choline oxidase from A. chryseus  
 A:Reference number: A15398; MUID:81006769; PMID:6997283  
 A:Accession: A15398  
 A:Molecule type: protein  
 A:Residues: 1-7 <OHT>  
 C:Keywords: oxidoreductase

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5  
 ||  
 DB 3 PN 4

## RESULT 69

I40504

Hypothetical protein 2 (7 aa) - Bacillus stearothermophilus

C:Species: Bacillus stearothermophilus

C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 15-Oct-1999

C:Accession: I40504

R:Waye, M.M.; Winter, G.

Eur. J. Biochem. 158, 505-510, 1986

A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synthetase gene

A:Reference number: I40503; MUID:86274732; PMID:3525162

A:Accession: I40504

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-7 &lt;RES&gt;

A:Cross-references: EMBL:X04193; NID:G40233; PIDN:CAA27782.1; PID:G580943

Query Match 28.6%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NV 6

Db 3 NV 4

## RESULT 70

S70335

Endosperm protein, 40K - rye (fragment)

C:Species: Secale cereale (rye)

C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998

C:Accession: S70335

R:Roche, A.; Calero, M.; Soriano, F.; Mendez, E.

Biochim. Biophys. Acta 1295, 13-22, 1996

A:Title: Identification of major rye secalins as coeliac immunoreactive proteins.

A:Reference number: S70327; MUID:96283789; PMID:8679669

A:Accession: S70335

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 &lt;ROC&gt;

Query Match 28.6%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2

Db 2 VL 3

## RESULT 71

S71299

ICL2 protein - Paramecium tetraurelia (fragment)

C:Species: Paramecium tetraurelia

C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999

C:Accession: S71299

R:Madaddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.

Eur. J. Biochem. 238, 121-128, 1996

A:Title: Characterization of centrin genes in Paramecium.

A:Reference number: S71298; MUID:96248429; PMID:8665928

A:Accession: S71299

A:Molecule type: protein

A:Residues: 1-7 &lt;MAD&gt;

A:Experimental source: strain d4-2

C:Genetics:

A:Genetic code: SGC5

Query Match 28.6%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4

Db 3 PP 4

## RESULT 72

I50210

Gene c-rel protein - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 28-Feb-1997

C:Accession: I50210

R:Kabrun, N.; Bumstead, N.; Hayman, M.J.; Enrietto, P.J.

Mol. Cell. Biol. 10, 4788-4794, 1990

A:Title: Characterization of a novel promoter insertion in the c-rel locus.

A:Reference number: I50210; MUID:90355995; PMID:2167440

A:Accession: I50210

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-7 &lt;KAB&gt;

A:Cross-references: GB:M55577; NID:G555438; PID:G211661

C:Genetics:

A:Gene: c-rel

Query Match 28.6%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5

Db 5 PN 6

## RESULT 73

PT0246

Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0246

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0246

A:Molecule type: DNA

A:Residues: 1-7 &lt;YAM&gt;

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2

Db 3 VL 4

## RESULT 74

PT0283

Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0283

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0283

A:Molecule type: DNA

A:Residues: 1-7 &lt;YAM&gt;

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 7;



Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
||  
Db 6 PP 7

RESULT 75  
E30608  
Ig kappa chain V-III region (Gag) - human (fragment)  
C:Species: Homo sapiens (nan)  
C:Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 16-Aug-1996  
C:Accession: E30608  
R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold  
J. Immunol. 142, 3158-3163, 1989  
A:Title: Structural and idiotypic characterization of the L chains of human IgM autoanti  
A:Reference number: A30601; MCID:89215279; PMID:2496160  
A:Accession: E30608  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <GON>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
||  
Db 3 VL 4

Search completed: November 25, 2003, 18:28:24  
Job time : 6.44149 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 3.3893 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-17

Perfect score: 7

Sequence: 1 VLPPNVG 7

Scoring table: OLIGO 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	42.9	11	1 BPPB AGKHA	P01021 agkistrodon
2	3	42.9	12	1 TMZA METMA	P80852 methanosarc
3	3	42.9	13	1 FIBB RABIT	P14478 oryctolagus
4	3	42.9	13	1 PEDI HYDAT	P80578 hydra atten
5	3	42.9	13	1 TENE RANTE	P56920 rana tempor
6	3	42.9	15	1 CH11 PEPA	P21225 pium sativ
7	3	42.9	15	1 MK1 PALPR	P80408 palomena pr
8	3	42.9	16	1 CXAA CONPE	P50984 conus penna
9	3	42.9	16	1 CXAB CONPE	P50985 conus penna
10	3	42.9	18	1 A2M OCTVU	P30800 octopus vul
11	3	42.9	20	1 BULB NARPS	P80554 narcissus p
12	3	42.9	20	1 EFTU MYCSV	P81407 mycoplasma
13	2	28.6	4	1 EOST HUMAN	P02731 homo sapien
14	2	28.6	5	1 PRCT PERAM	P01373 periplaneta
15	2	28.6	5	1 RE32 LITRU	P82073 litoria rub
16	2	28.6	5	1 TPIS CANFA	P54714 canis famil
17	2	28.6	6	1 ACPI RABIT	P83554 pterodroma
18	2	28.6	6	1 TRPT PSEPU	P36414 pseudomonas
19	2	28.6	7	1 CHOX ALCSP	P16101 alcaligenes
20	2	28.6	7	1 FAR4 PANRE	P41875 panagrellus
21	2	28.6	7	1 PHH2 LYCES	P83379 lycopersico
22	2	28.6	7	1 TPFY PACDA	P83455 pachymedusa
23	2	28.6	7	1 UFO4 MOUSE	P38642 mus musculu
24	2	28.6	7	1 UN06 PINPS	P81575 pinus pinas
25	2	28.6	8	1 ALL5 CALVO	P41841 calliphora
26	2	28.6	8	1 ALLE CYDPO	P82157 cydia pomon
27	2	28.6	8	1 CADI ENTFA	P13268 enterococcu
28	2	28.6	8	1 COM2 CONPU	P58785 conus purpu
29	2	28.6	8	1 FARI PANRE	P41872 panagrellus
30	2	28.6	8	1 FUSS FUSSO	P81010 fusarium so
31	2	28.6	8	1 HTF1 PERAM	P04548 periplaneta
32	2	28.6	8	1 HTF2 PERAM	P04549 periplaneta
33	2	28.6	8	1 HTF TENMO	P25419 tenebrio mo

34	2	28.6	8	1 PPK2 PERAM	P86692 periplaneta
35	2	28.6	8	1 UPA1 HUMAN	P30087 homo sapien
36	2	28.6	9	1 BS43 SERPL	P83375 serratia pl
37	2	28.6	9	1 FAR2 PANRE	P41873 panagrellus
38	2	28.6	9	1 FARA CALVO	P41859 calliphora
39	2	28.6	9	1 FARA CALVO	P41865 calliphora
40	2	28.6	9	1 FIBB ERYPA	P19346 erythrocebu
41	2	28.6	9	1 KNL3 BOMVA	P83058 bomina var
42	2	28.6	9	1 LITO LITAU	P08945 litoria aur
43	2	28.6	9	1 OXYA SCYCA	P42996 scyllorhinu
44	2	28.6	9	1 OXYF SCYCA	P42997 scyllorhinu
45	2	28.6	9	1 OXYV SQUAC	P43000 squalus aca
46	2	28.6	9	1 YBFR AZOVI	P25825 azotobacter
47	2	28.6	10	1 AH3 PRUSE	P29261 prunus sero
48	2	28.6	10	1 BPP2 BOTIN	P30422 bothrops in
49	2	28.6	10	1 BPP2 BOTJA	P30422 bothrops ja
50	2	28.6	10	1 BPP8 BOTIN	P30426 bothrops in
51	2	28.6	10	1 BPP VIPAS	P31351 vipera aspi
52	2	28.6	10	1 BRK ONCMY	P98221 oncorhynch
53	2	28.6	10	1 CATB SHEEP	P83205 ovis aries
54	2	28.6	10	1 ESL LACCA	P81758 lactobacill
55	2	28.6	10	1 GON3 ONCKE	P20167 oncorhynch
56	2	28.6	10	1 GONL SQUAC	P27429 squalus aca
57	2	28.6	10	1 GRP RANRI	P23260 rana ridibu
58	2	28.6	10	1 HTF1 ROMMI	P18110 romalea mic
59	2	28.6	10	1 HTP2 CARMO	P11385 carausius m
60	2	28.6	10	1 ODP2 BOVIN	P11180 bos taurus
61	2	28.6	10	1 TEMK RANTE	P56923 rana tempor
62	2	28.6	10	1 TKNB CHICK	P19851 gallus gall
63	2	28.6	10	1 TKNB ONCMY	P28500 oncorhynch
64	2	28.6	10	1 TKNK PIG	P21292 sus scrofa
65	2	28.6	10	1 TKN PHYBI	P08610 phyllomedus
66	2	28.6	10	1 TKU1 UREUN	P40751 urechis uni
67	2	28.6	10	1 TMOF AEDAE	P19425 aedes aegyp
68	2	28.6	10	1 TPIS NICPL	P19118 nicotiana p
69	2	28.6	10	1 URA3 HUMAN	P40930 homo sapien
70	2	28.6	10	1 UPA2 HUMAN	P30088 homo sapien
71	2	28.6	10	1 UPA4 HUMAN	P30090 homo sapien
72	2	28.6	10	1 UPA5 HUMAN	P30091 homo sapien
73	2	28.6	10	1 UPA8 HUMAN	P30094 homo sapien
74	2	28.6	10	1 URE3 MORMO	P17339 morganella
75	2	28.6	10	1 UXA2 CHLTR	P38003 chlamydia c
76	2	28.6	11	1 BPP3 BOTIN	P30423 bothrops in
77	2	28.6	11	1 BPP4 BOTIN	P30424 bothrops in
78	2	28.6	11	1 BPP AGKHP	P04562 agkistrodon
79	2	28.6	11	1 BRK MEGFL	P12797 megascolia
80	2	28.6	11	1 ESI RAT	P56571 rattus norv
81	2	28.6	11	1 LADD ONCMY	P81018 oncorhynch
82	2	28.6	11	1 LPW THETH	P05624 thermus the
83	2	28.6	11	1 MORN HUMAN	P01163 homo sapien
84	2	28.6	11	1 TIN4 HOPTI	P82654 hoplobatrach
85	2	28.6	11	1 TKC2 CALVO	P41518 calliphora
86	2	28.6	11	1 TKN1 PSEGU	P42986 pseudophryn
87	2	28.6	11	1 TKN1 UPERIN	P82026 uperoleia i
88	2	28.6	11	1 TKN1 UPERU	P08612 uperoleia r
89	2	28.6	11	1 TKN2 PSEGU	P42987 pseudophryn
90	2	28.6	11	1 TKN3 PSEGU	P42988 pseudophryn
91	2	28.6	11	1 TKN4 PSEGU	P42989 pseudophryn
92	2	28.6	11	1 TKN5 PSEGU	P42990 pseudophryn
93	2	28.6	11	1 TKN6 RANRI	P29207 rana ridibu
94	2	28.6	11	1 TKN7 PHYFU	P22691 rana cateab
95	2	28.6	11	1 TKN PHYFU	P08615 physalaemus
96	2	28.6	12	1 FAR7 PENMO	P83322 penaeus mon
97	2	28.6	12	1 FARI CALVO	P41869 calliphora
98	2	28.6	12	1 FIF1 SARBU	P83349 sarcophaga
99	2	28.6	12	1 GRAR RANRU	P40754 rana rugosa
100	2	28.6	12	1 H2AX ONCMY	P83327 oncorhynch

ALIGNMENTS

RESULT 1

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BPPB AGKHA
ID BPPB AGKHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffii (Mamushi) (Gloydus blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii."
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
DB 3 LPP 5

RESULT 2
TW2A METMA STANDARD; PRT; 12 AA.
AC P80652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M
DE methyltransferase 28 kDa subunit) (Fragment).
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE.
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=96370840; PubMed=8774736;
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:
RT coenzyme M methyltransferase from Methanosarcina mazei Go1
RT reconstituted in ether lipid liposomes."
RL Eur. J. Biochem. 239:857-864(1996).
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC TETRAHYDROMETHANOPTERIN.
CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

BPPB AGKHA
ID BPPB AGKHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffii (Mamushi) (Gloydus blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii."
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
DB 3 LPP 5

RESULT 2
TW2A METMA STANDARD; PRT; 12 AA.
AC P80652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M
DE methyltransferase 28 kDa subunit) (Fragment).
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE.
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=96370840; PubMed=8774736;
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:
RT coenzyme M methyltransferase from Methanosarcina mazei Go1
RT reconstituted in ether lipid liposomes."
RL Eur. J. Biochem. 239:857-864(1996).
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC TETRAHYDROMETHANOPTERIN.
CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 42.9%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
DB 7 VLP 9

RESULT 3
FIBB RABIT STANDARD; PRT; 13 AA.
AC P14478;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals."
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro: IPR002181; Fibrinogen C.
DR PROSITE: PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 13 FIBRINOPEPTIDE B.
FT MOD_RES 4 4 SULFATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;

Query Match 42.9%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
DB 8 VLP 10

RESULT 4
PEDI HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE.
RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RT peptides from Hydra vulgaris."
RL Development 122:1941-1948(1996).

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CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT  
 CC DEVELOPMENT.  
 KW Morphogen.  
 SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 42.9%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3

DB 7 VLP 9

#### RESULT 5

ID TME RANTE STANDARD; PRT; 13 AA.  
 AC P56920;

DT 30-MAY-2000 (Rel. 39, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Temporin E.

OS Rana temporaria (European common frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.

OX NCBI\_TaxID=8407;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=97175050; PubMed=9022710;

RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,

RA Barra D.;

RT "Temporins, antimicrobial peptides from the European red frog Rana

temporaria";

RL Eur. J. Biochem. 242:788-792(1996).

CC -!- FUNCTION: Has antibacterial activity against Gram-positive

bacteria.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the brevinin family.

KW Amphibian defense peptide; Antibiotic; Amidation.

FT MOD\_RES 13 13 AMIDATION.

SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match

Best Local Similarity 42.9%; Score 3; DB 1; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3

DB 1 VLP 3

#### RESULT 6

CHIL\_PEA

ID CHIL\_PEA STANDARD; PRT; 15 AA.

AC P21235;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Endochitinase A1 (EC 3.2.1.14) (Fragment).

OS Pisum sativum (Garden pea).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurooids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.

OX NCBI\_TaxID=3888;

RN [1]

RP SEQUENCE.

RC STRAIN=cv. Birte; TISSUE=Leaf;

RA Vad K., Mikelsen J.D., Collinge D.B.;

RT "Induction, purification and characterization of chitinase isolated

from pea leaves inoculated with *Ascochyta blight*,"

RL Planta 184:24-29(1991).

CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN  
 CC CONTAINING FUNGAL PATHOGENS.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-  
 CC acetyl-D-glucosamine polymers of chitin.  
 CC -!- INDUCTION: By infection with the fungal pathogen *Ascochyta blight*.  
 CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO  
 CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL  
 CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL  
 CC HYDROLASES).

DR InterPro: IPR001002; Chitin binding 1.

DR InterPro: IPR000726; Glyco\_Hydro\_19\_1.

DR PROSITE: PS00026; CHITIN\_BINDING; PARTIAL.

DR PROSITE: PS00773; CHITINASE 19\_1; PARTIAL.

DR PROSITE: PS00774; CHITINASE 19\_2; PARTIAL.

KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding;

KW Multigene family.

FT NON\_TER 15 15

SQ SEQUENCE 15 AA; 1438 MW; 23355ED6B11E869 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 9.4e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPN 5

DB 12 PPN 14

#### RESULT 7

MK1\_PALPR

ID MK1\_PALPR STANDARD; PRT; 15 AA.

AC P80408;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Metainikowin I.

OS Palomena prasina (Green shield bug).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;

OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;

OC Palomena.

OX NCBI\_TaxID=55431;

RN [1]

RP SEQUENCE.

RC TISSUE=Hemolymph;

RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;

RT "The inducible antibacterial peptides of the hemipteran insect

Palomena prasina: identification of a unique family of proline-rich

peptides and of a novel insect defensin."

RL J. Insect Physiol. 42:81-89(1996).

CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE

BACTERIA.

CC -!- INDUCTION: By bacterial infection.

KW Antibiotic; Insect immunity.

SQ SEQUENCE 15 AA; 1838 MW; 21407E663CE46299 CRC64;

Query Match

Best Local Similarity 42.9%; Score 3; DB 1; Length 15;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPN 5

DB 12 PPN 14

#### RESULT 8

CXAA\_CONPE

ID CXAA\_CONPE STANDARD; PRT; 16 AA.

AC P50984;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Alpha-conotoxin PnIA.

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OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN (1)
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN (2)
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN (3)
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=96311277; PubMed=8740364;
RA Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
RA Martin J.L.;
RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
RT antagonist, alpha-conotoxin PnIA from Conus pennaceus.";
RL Structure 4:417-423(1996).
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, WHICH ARE
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; A54877; A54877.
DR PDB; 1PEN; 21-APR-97.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT MOD_RES 3 16 SULFATION.
FT MOD_RES 15 15
FT MOD_RES 16 16 AMIDATION.
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
FT TURN 16 16
SQ SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
DB 5 LPP 7

RESULT 9
CXAB CONPE STANDARD; PRT; 16 AA.
ID CXAB CONPE
AC P50985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin PnIB.
OS Conus pennaceus (Feathered cone).

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OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN (1)
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN (2)
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN (3)
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=97444322; PubMed=9298951;
RA Hu S.-H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
RT "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
RT comparison with alpha-conotoxins PnIA and GI.";
RL Biochemistry 36:11323-11330(1997).
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; B54877; B54877.
DR PDB; 1AKG; 20-MAY-98.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16 SULFATION.
FT MOD_RES 15 15
FT MOD_RES 16 16 AMIDATION.
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
FT TURN 16 16
SQ SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
DB 5 LPP 7

RESULT 10
A2M_OCTVU STANDARD; PRT; 18 AA.
ID A2M_OCTVU
AC P30800;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-2-macroglobulin homolog (Alpha-2-M) (Fragment).
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.

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OX NCBI\_TaxID=6645;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92344633; PubMed=1379044;  
RA Thøgersen I.B., Salvessen G., Brucato F.H., Pizzo S.V., Enghild J.J.;  
RT "Purification and characterization of an alpha-macroglobulin  
RL proteinase inhibitor from the mollusc Octopus vulgaris.";  
RL Biochem. J. 285:521-527(1992).  
CC -!- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A  
CC UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,  
CC CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES  
CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT  
CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH  
CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST  
CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR  
CC WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE  
CC BAIT REGION A THIOL-ESTER BOND IS HYDROLYZED AND MEDIATES THE  
CC COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.  
CC -!- SUBUNIT: Homodimer; disulfide-linked.  
CC -!- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,  
CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.  
DR PIR; S23971; S23971.  
DR GO; GO:0016975; F:alpha-2 macroglobulin; NAS.  
DR InterPro; IPR001599; MacroglobinA2.  
DR Pfam; PF00207; A2M; 1.  
DR PROSITE; PS00477; ALPHA\_2\_MACROGLOBULIN; 1.  
KW Serine protease inhibitor; Glycoprotein; Plasma; Bait region;  
KW Thioester bond.  
FT NON\_TER 1  
FT CROSSLINK 5  
FT NON\_TER 18  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2011 MW; D8D61C473D901C9D CRC64;

Query Match 42.9%; Score 3; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PNV 6  
|||  
DB 15 PNV 17

RESULT 11  
BULB NARPS  
ID BULB NARPS STANDARD; PRT; 20 AA.  
AC P80554;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Bulb protein (Fragment).  
OS Narcissus pseudonarcissus (Daffodil).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;  
OC Narcissus.  
OX NCBI\_TaxID=39639;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=cv. Golden Harvest; TISSUE=Bulb;  
RA Paris M.D., Barker P., Thomas B.;  
RL Submitted (FEB-1996) to the SWISS-PROT data bank.  
FT UNSURE 2 2 OR N.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2077 MW; 76212FF3A468AD38 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LPP 4  
|||  
DB 13 LPP 15

RESULT 12  
EFTU MYCSY  
ID EFTU MYCSY STANDARD; PRT; 20 AA.  
AC P81407;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Elongation factor Tu (EF-Tu) (Fragment).  
GN TUF.  
OS Mycoplasma synoviae.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2109;  
RN [1]  
RP SEQUENCE.  
RX STRAIN=ULB 925 / Isolate KF9;  
RX MEDLINE=99237234; PubMed=10220885;  
RA Bencina D., Narat M., Devc P., Drobnic-Valic M., Habe F., Kleven S.H.;  
RT "The characterization of Mycoplasma synoviae EF-Tu protein and  
RT proteins involved in hemadherence and their N-terminal amino acid  
RT sequences.";  
RL PEMS Microbiol. Lett. 173:85-94(1999).  
CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF  
CC AMINOACYL-tRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN  
CC BIOSYNTHESIS.  
CC -!- SUBUNIT: Monomer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
CC EF-TU/EF-1A SUBFAMILY.  
DR HAMAP; MF\_00118; -; 1.  
DR InterPro; IPR000795; EF\_GTPbind.  
DR PROSITE; PS00301; EFACITOR\_GTP; PARTIAL.  
KW Elongation factor; Protein biosynthesis; GTP-binding.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2222 MW; C3C92564B740ACC6 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 NVG 7  
|||  
DB 13 NVG 15

RESULT 13  
EOSI\_HUMAN  
ID EOSI\_HUMAN STANDARD; PRT; 4 AA.  
AC P02731;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last annotation update)  
DE Eosinophilic peptides.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76078412; PubMed=1060093;  
RA Goetzl E.J., Austen K.F.;  
RT "Purification and synthesis of eosinophilic tetrapeptides of  
RT human lung tissue: identification as eosinophil chemotactic factor of  
RT anaphylaxis".  
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).  
CC -!- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG  
CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS  
CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING  
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE  
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.  
DR GO; GO:0030105; P:anaphylaxis; IDA.  
DR GO; GO:0006935; P:chemotaxis; IDA.  
FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).  
FT /FTID=VAR\_005201.

SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 6 VG 7  
DB 1 VG 2

## RESULT 14

PRCT PERAM

ID PRCT PERAM STANDARD; PRT; 5 AA.  
AC P01373;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Proctolin.

OS Periplaneta americana (American cockroach),  
OS Limulus polyphemus (Atlantic horseshoe crab), and  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978, 6850, 6759;  
RN [1]

RN [1]\_TaxID=6978, 6850, 6759;

RP SEQUENCE.

RC SPECIES=P.americana;

RX MEDLINE=76074708; PubMed=576;

RA Starratt A.N., Brown B.E.;

RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter

in insects.";

RL Life Sci. 17:1253-1256(1975).

RN [2]

RP BIOLOGICAL SOURCE.

RC SPECIES=P.americana;

RX MEDLINE=81225865; PubMed=6113690;

RA O'Shea M., Adams M.E.;

RT "Pentapeptide (proctolin) associated with an identified neuron.";

Science 213:567-569(1981).

RN [3]

RP SEQUENCE.

RC SPECIES=L.polyphemus;

RX MEDLINE=90287800; PubMed=2356151;

RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,

RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,

RA Shabanowitz J.;

RT "Identification of proctolin in the central nervous system of the

horseshoe crab, Limulus polyphemus.";

Peptides 11:205-211(1990).

RL [4]

RN SEQUENCE.

RC SPECIES=C.maenas;

RX MEDLINE=86232789; PubMed=2872661;

RA Stangier J., Dirksen H., Keller R.;

RT "Identification and immunocytochemical localization of proctolin in

pericardial organs of the shore crab, Carcinus maenas.";

Peptides 7:67-72(1986).

CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,

MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.

CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN

THE CRAB PERICARDIAL ORGANS.

CC PIR; A01644; HOROHA.

DR PIR; A60411; A60411.

KW Neuropeptide.

SQ SEQUENCE 5 AA; 649 MW; 71B7673B46000000 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 5;

Matches 2; Conservative 0; Mismatches 0;

QY 2 LP 3

DB 3 LP 4

## RESULT 15

RE32\_LITRU

ID RE32\_LITRU STANDARD; PRT; 5 AA.

AC P82073;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Rubellidin 3.2.

OS Litoria rubella (Desert tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

OC Pelodyadinae; Litoria.

OX NCBI\_TaxID=104895;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;

RT "Peptides from the skin glands of the Australian buzzing tree frog

Litoria electrica. Comparison with the skin peptides from Litoria

rubella.";

RL Aust. J. Chem. 52:639-645(1999).

CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic

activity.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

KW Amphibian defense peptide.

SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0;

QY 6 VG 7

DB 1 VG 2

## RESULT 16

TPIS CANFA

ID TPIS CANFA STANDARD; PRT; 5 AA.

AC P54714;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).

GN TP11.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE.

RC TISSUE=Heart;

RX MEDLINE=98163340; PubMed=9504812;

RA Dunn M.J., Corbett J.M., Wheeler C.H.;

RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of

dog heart proteins.";

Electrophoresis 18:2795-2802(1997).

CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glyceralone

phosphate.

CC -1- PATHWAY: Plays an important role in several metabolic pathways.

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.

HSC-2DPAGE; P54714; DOG.

DR InterPro; IPR000652; Triophos.ismrse.

DR PROSITE; PS00171; TIM; PARTIAL.

KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;

Pentose shunt.

FT NON\_TER 1



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FT NON_TER 5 5
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7
DB 2 VG 3

RESULT 17
ACPH_RABIT
ID ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wolf F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RT unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50(1991)
CC -|- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -|- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -|- SUBUNIT: Homotetramer.
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro: IPR002471; ProI endopep ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
DB 5 VL 6

RESULT 18
TRPI_PSEPU
ID TRPI_PSEPU STANDARD; PRT; 6 AA.
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TrpBA operon transcriptional activator (fragment).
GN TRPI.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PPG1 C1S;
RX MEDLINE=89335826; PubMed=2503057;
RA Eberly L., Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
RT putida.";
RL Biochimie 71:521-531(1989).
CC -|- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
CC TRPBA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -|- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X13299; CAA31660.1; -.
DR InterPro; IPR000847; HTH_LySR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.
KW Tryptophan biosynthesis; Transcription regulation; Activator;
KW DNA-binding.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3
DB 5 LP 6

RESULT 19
CHOX_ALCSP
ID CHOX_ALCSP STANDARD; PRT; 7 AA.
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
RT oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1980).
CC -|- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR; A15398; A15398.
KW Oxidoreductase.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5
DB 3 PN 4

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RESULT 20  
 FARA\_PANRE STANDARD; PRT; 7 AA.  
 AC P41875;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE FMRamide-like neuropeptide PF4 (KPNFIRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95232026; PubMed=7716079;  
 RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,  
 RA Thim L., Kubiak T.M., Martin R.A., Geary T.G.;  
 RT "Isolation and preliminary biological characterization of  
 RT KPNFIRamide, a novel FMRamide-related peptide from the free-living  
 RT nematode, Panagrellus redivivus.";  
 RL Peptides 16:87-93(1995).  
 CC -!- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT  
 CC MUSCLE TENSION INCREASE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRamide RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7  
 SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PN 5  
 DB 2 PN 3  
 RESULT 21  
 PPH2\_LYCES STANDARD; PRT; 7 AA.  
 AC P83379;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Purple acid phosphatase isozyme LeSAP2 (EC 3.1.3.2) (Fragment).  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND  
 RP GLYCOSYLATION.  
 RC STRAIN=cv. Moneymaker; TISSUE=Seed;  
 RX MEDLINE=22361242; PubMed=12473124;  
 RA Bozzo G.G., Reghochama K.G., Plaxton W.C.;  
 RT "Purification and characterization of two secreted purple acid  
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon  
 RT esculentum) cell cultures.";  
 RL Eur. J. Biochem. 269:6278-6286(2002).  
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an  
 CC alcohol + phosphate.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Glycosylated.  
 CC -!- MISCELLANEOUS: In L. esculentum there are at least two isoforms of  
 CC purple acid phosphatase.  
 KW Hydrolyase; Glycoprotein.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VG 7  
 DB 4 VG 5  
 RESULT 22  
 TPFY\_PACDA STANDARD; PRT; 7 AA.  
 AC P83455;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Trytophyllin-1 (PdT-1).  
 OS Pachymedusa dactinolor (Giant mexican leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Phyllomedusinae; Pachymedusa.  
 OX NCBI\_TaxID=75988;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
 RP PRO-7.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Shaw C.;  
 RT "Pachymedusa dactinolor tryptophyllin-1 (PdT-1): structural  
 RT characterization, pharmacological activity and cloning of precursor  
 RT cDNA.";  
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
 CC smooth muscle.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.  
 KW Amphibian defense peptide; Amidation; Hydroxylation.  
 FT MOD\_RES 3 3  
 FT MOD\_RES 7 7  
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PP 4  
 DB 2 PP 3  
 RESULT 23  
 UF04\_MOUSE STANDARD; PRT; 7 AA.  
 AC P3842;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=75231108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.

FT NON TER 7  
 SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
 ||  
 Db 3 PP 4

## RESULT 24

ID UN06 PINFS STANDARD; PRT; 7 AA.  
 AC P81675;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DE Unknown protein from 2D-page of needles (N141) (Fragment).  
 OS Pinus pinaster (Maritime pine)  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.  
 FT NON TER 1 1  
 FT NON TER 7 7  
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
 ||  
 Db 5 LP 6

## RESULT 25

ID ALL5 CALVO STANDARD; PRT; 8 AA.  
 AC P41841;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).  
 OS Calliphora vomitoria (Blue blowfly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 CC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN (1)  
 RP SEQUENCE.

RX MEDLINE=93211980; PubMed=8460157;  
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
 RA Thorpe A.;  
 RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria  
 RT with sequence homology to cockroach allatostatins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
 RN (2)  
 RP CHARACTERIZATION, AND HYDROXYLATION.

RC TISSUE=Head;  
 RX MEDLINE=94342269; PubMed=8063725;  
 RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;  
 RT "[Hyp3]Met-callatostatin. Identification and biological properties of  
 RT a novel neuropeptide from the blowfly Calliphora vomitoria.";  
 RL J. Biol. Chem. 269:21059-21066(1994).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTROPHIC FACTOR OR NEUROMODULATOR AND PLAY  
 CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
 CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
 CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
 CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
 CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 DR PIR; E47393; E47393.  
 KW Neuropeptide; Amidation; Hydroxylation.  
 FT MOD\_RES 3 3 HYDROXYLATION (20%).  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
 ||  
 Db 2 PP 3

## RESULT 26

ALL6 CYDPO STANDARD; PRT; 8 AA.  
 AC P82157;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE Cydia pomonella (Codling moth).  
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN (1)  
 RP SEQUENCE.

RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
 ||  
 Db 1 LP 2

## RESULT 27

CADI\_ENTFA STANDARD; PRT; 8 AA.  
 AC P13268;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DE Sex pheromone CADI.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

```

OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE
RX MEDLINE=85051889; PubMed=6437872;
RA Mori M., Sagakami Y., Narita M., Isegai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the bacterial sex pheromone, CAD1, that
RT induces plasmid transfer in Streptococcus faecalis.";
RL FEBS Lett. 178:97-100(1984).
CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC PHEROMONE.
KW HEMOLYSIN PLASMID PAD1.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
DB 5 VL 6

RESULT 28
COM2_CONPU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=clipperton Island; TISSUE=Venom;
RX MEDLINE=99388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD RES 4 4
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
DB 3 VL 4

RESULT 29
FAR1_PANRE STANDARD; PRT; 8 AA.
AC P41872;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide PF1 (SDPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE
RX MEDLINE=85051889; PubMed=6437872;
RA Mori M., Sagakami Y., Narita M., Isegai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the bacterial sex pheromone, CAD1, that
RT induces plasmid transfer in Streptococcus faecalis.";
RL FEBS Lett. 178:97-100(1984).
CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC PHEROMONE.
KW HEMOLYSIN PLASMID PAD1.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
DB 5 VL 6

RESULT 28
COM2_CONPU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=clipperton Island; TISSUE=Venom;
RX MEDLINE=99388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD RES 4 4
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
DB 3 VL 4

RESULT 29
FAR1_PANRE STANDARD; PRT; 8 AA.
AC P41872;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide PF1 (SDPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

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OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE
RX MEDLINE=93027559; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Wintertrowd C.A., Mackenzie C.D.,
RA Garrison R.D., Williams J.F., Friedman A.R.;
RT "Two FMRFamide-like peptides from the free-living nematode
RT Panagrellus redivivus.";
RL Peptides 13:209-214(1992).
CC -!- FUNCTION: MYOACTIVE.
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
CC CAUDALLY TO THE BASE OF THE PHARYNX.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5
DB 3 PN 4

RESULT 30
FUSS_FUSSO STANDARD; PRT; 8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Allergen Fus s I3596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RL Submitted (JUL-1997) to the SWISS-PROT data bank.
KW Allergen.
FT NON TER 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NV 6
DB 6 NV 7

RESULT 31
HTF1_PERAM STANDARD; PRT; 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
DE (Pea-CAH-I) (LeD-CC-I) (Hypertrehalosaemic neuropeptide I).
OS Periplaneta americana (American cockroach), and
OS Lepinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.

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OX NCBI\_TaxID=6978, 7539, 6976;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=85046530; PubMed=6548628;  
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,  
RA Rinehart K.L. Jr.;  
RT "Structures of two cockroach neuropeptides assigned by fast atom  
RT bombardment mass spectrometry.";  
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=84298179; PubMed=6591205;  
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,  
RA Miller C.A., Schooley D.A.;  
RT "Isolation and primary structure of two peptides with  
RT cardioacceleratory and hyperglycemic activity from the corpora  
RT cardiaca of Periplaneta americana.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;  
RX MEDLINE=90160053; PubMed=2576128;  
RA Gaede G., Kellner R.;  
RT "The metabolic neuropeptides of the corpus cardiaca from the potato  
RT beetle and the American cockroach are identical.";  
RL Peptides 10:1287-1289(1989).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;  
RX MEDLINE=90253659; PubMed=2340112;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from  
RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
RT atom bombardment mass spectrometry.";  
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT  
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR; A44960; A44960.  
DR Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5  
DB 6 PN 7

RESULT 32  
HTF2\_PERAM STANDARD; PRT; 8 AA.  
AC P04549;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)  
DE (Pea-CAH-II) (Leu-CC-II) (Hypertrehalosaemic neuropeptide II).  
OS Periplaneta americana (American cockroach),  
OS Leptinotarsa decemlineata (Colorado potato beetle), and

OS Blatta orientalis (Oriental cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978, 7539, 6976;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=85046530; PubMed=6548628;  
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,  
RA Rinehart K.L. Jr.;  
RT "Structures of two cockroach neuropeptides assigned by fast atom  
RT bombardment mass spectrometry.";  
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=84298179; PubMed=6591205;  
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,  
RA Miller C.A., Schooley D.A.;  
RT "Isolation and primary structure of two peptides with  
RT cardioacceleratory and hyperglycemic activity from the corpora  
RT cardiaca of Periplaneta americana.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;  
RX MEDLINE=90160053; PubMed=2576128;  
RA Gaede G., Kellner R.;  
RT "The metabolic neuropeptides of the corpus cardiaca from the potato  
RT beetle and the American cockroach are identical.";  
RL Peptides 10:1287-1289(1989).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;  
RX MEDLINE=90253659; PubMed=2340112;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from  
RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
RT atom bombardment mass spectrometry.";  
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT  
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR; B44960; B44960.  
DR PIR; B49823; B49823.  
DR PIR; S08996; S08996.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5  
DB 6 PN 7

RESULT 33  
HTF\_TENMO STANDARD; PRT; 8 AA.  
ID HTF\_TENMO  
AC P25419;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Hypertrehalosemic factor (HOTH) (Hypertrehalosemic neuropeptide).  
 OS Tenebrio molitor (Yellow mealworm), and  
 OS Zophobas rugipes.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
 OC Tenebrionidae; Tenebrio.  
 OX NCBI\_TaxID=7067, 7075;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=T.molitor, and Z.rugipes;  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=90341081; PubMed=2381871;  
 RA Gaede G., Rosinski G.;  
 RT "The primary structure of the hypertrehalosemic neuropeptide from  
 RT tenebrionid beetles: a novel member of the AKH/RPCH family.";  
 RL Peptides 11:455-459(1990).  
 CC -!- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT  
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A43976; A43976.  
 DR PIR; B43976; B43976.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PN 5  
 DB 6 PN 7  
 RESULT 34  
 PPK2\_PERAM  
 ID PPK2\_PERAM STANDARD; PRT; 8 AA.  
 AC P82692;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinnin-2 (Pea-PK-2) (FXPKL-amide).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=97353923; PubMed=9210163;  
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of two pyrokinins from the  
 RT retrocerebral complex of the American cockroach.";  
 RL Peptides 18:473-478(1997).  
 RN [2]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPKLamides in the nervous system of  
 RT the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=WALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKINNIN FAMILY.  
 DR InterPro; IPR001484; Pyrokinnin.  
 DR PROSITE; PS00539; PYROKINNIN; FALSE\_NEG.

KW Neuropeptide; Amidation; Pyrokinnin.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PP 4  
 DB 2 PP 3  
 RESULT 35  
 UPAL\_HUMAN  
 ID UPAL\_HUMAN STANDARD; PRT; 8 AA.  
 AC P30087;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing.";  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.  
 DR SWISS-2DPAGE; P30087; HUMAN.  
 FT NON\_TER 1 1  
 FT UNSURE 8 8  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 NV 6  
 DB 5 NV 6  
 RESULT 36  
 BS43\_SERPL  
 ID BS43\_SERPL STANDARD; PRT; 9 AA.  
 AC P83375;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bacteriocin serracin P 43 kDa subunit (Fragment).  
 OS Serratia plymuthica.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Serratia.  
 OX NCBI\_TaxID=82996;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC STRAIN=J7;  
 RX MEDLINE=22293561; PubMed=12406768;  
 RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,  
 RA Van Beumen J., Thonart P.;  
 RT "Characterization of serracin P, a phage-tail-like bacteriocin, and  
 RT its activity against *Erwinia amylovora*, the fire blight pathogen.";  
 RL Appl. Environ. Microbiol. 68:5704-5710(2002).  
 CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).

CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium  
CC InterPro; IP0006498; Tail\_tube.  
DR Pfam; PF04985; Phage tube; 1.  
KW Antibiotic; Bacteriocin.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1095 MW; 1E66D412C871E1FB CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VL 2  
DB 8 VL 9  
RESULT 37  
FAR2\_PANRE STANDARD; PRT; 9 AA.  
AC P41873;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide PF2 (SADPNFLRP-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93027659; PubMed=1408999;  
RA Geary T.G., Price D.A., Bowman J.W., Wintertord C.A., Mackenzie C.D.,  
RA Garlison R.D., Williams J.F., Friedman A.R.;  
RT "Two FMRFamide-like peptides from the free-living nematode  
RT Panagrellus redivivus.";  
RL Peptides 13:209-214(1992).  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
CC CAUDALLY TO THE BASE OF THE PHARYNX.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PN 5  
DB 4 PN 5  
RESULT 38  
FAR4\_CALVO STANDARD; PRT; 9 AA.  
AC P41659;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CalliFMRFamide 4.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated calliFMRFamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; D41978; D41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PN 5  
DB 2 PN 3  
RESULT 39  
FARA\_CALVO STANDARD; PRT; 9 AA.  
ID FARA\_CALVO STANDARD; PRT; 9 AA.  
AC P41865;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CalliFMRFamide 10.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated calliFMRFamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; A44787; A44787.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9  
FT UNSURE 1 1  
SQ SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PN 5  
DB 2 PN 3  
RESULT 40  
FIBB\_ERVPA STANDARD; PRT; 9 AA.  
ID FIBB\_ERVPA STANDARD; PRT; 9 AA.  
AC F19346;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Erythrocybus patas (Red guenon) (Hussar).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

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OC Cercopithecinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]_
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=328610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D24180; D24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
DB 4 VL 5

RESULT 41
ID KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]_
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjorson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -1- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
DB 2 PP 3

US-09-641-801-17.oligo.rsp

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RESULT 42
LITO LITAU STANDARD; PRT; 9 AA.
ID LITO LITAU
AC P08945;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Litorin.
OS Litoria aurea (Green and golden bell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=8371;
RN [1]_
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=75187011; PubMed=1140241;
RA Anastasi A., Ersamer V., Endean R.;
RT "Aminoacid composition and sequence of litorin, a bombesin-like
RT nonapeptide from the skin of the Australian leptodactylid frog
RT Litoria aurea.";
RT Litoria aurea.;
RL Experientia 31:510-511(1975).
RN [2]_
RP SEQUENCE (METHYLATED VARIANT).
RC TISSUE=Skin secretion;
RX MEDLINE=78003546; PubMed=908397;
RA Anastasi A., Montecucchi P.C., Angelucci F., Ersamer V., Endean R.;
RT "Glu(Ome)-litorin, the second bombesin-like peptide occurring in
RT methanol extracts of the skin of the Australian frog Litoria aurea.";
RL Experientia 33:1289-1289(1977).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR; S07204; S07204.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation; Methylation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 2 2 METHYLATION (PARTIAL).
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1103 MW; D7CCC1E862CDC366 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7
DB 5 VG 6

RESULT 43
ID OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]_
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophyseal hormones in cartilaginous

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RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides  
 RT isolated from the spotted dogfish (Scyliorhinus caniculus).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).  
 CC -!- FUNCTION: DISPLAYS OXYTOCIN ACTIVITY ON RAT UTERUS.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR InterPro; IPR000981; Neurohyp\_horm.  
 DR Pfam; PF00220; hormone4; 1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9  
 FT SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7

DB 8 VG 9

#### RESULT 44

OXFY\_SCYCA STANDARD; PRT; 9 AA.  
 AC P42997;

DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Phasvatocin.

OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyliorhinidae; Scyliorhinus.

OX NCBI\_TaxID=7830;

RN [1]

RP SEQUENCE.

RT TISSUE=Epithelial;

RC MEDLINE=95062247; PubMed=7972045;

RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;  
 "Special evolution of neurohypophyseal hormones in cartilaginous  
 fishes: asvatocin and phasvatocin, two oxytocin-like peptides  
 isolated from the spotted dogfish (Scyliorhinus caniculus).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).

CC -!- FUNCTION: DISPLAYS OXYTOCIN ACTIVITY ON RAT UTERUS.

CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR InterPro; IPR000981; Neurohyp\_horm.

DR Pfam; PF00220; hormone4; 1.

DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.

KW Hormone; Amidation.

FT DISULFID 1 6

FT MOD\_RES 9 9

FT SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

#### Query Match

Best Local Similarity 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7

DB 8 VG 9

#### RESULT 45

OXIV\_SQUAC

ID OXYV\_SQUAC STANDARD; PRT; 9 AA.

AC P43000;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Valitocin.

OS Squalus acanthias (Spiny dogfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.  
 OX NCBI\_TaxID=7797;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=73031727; PubMed=5083097;  
 RA Acher R., Chauvet J., Chauvet M.-T.;  
 "Phylogeny of the neurohypophyseal hormones. Two new active peptides  
 isolated from a cartilaginous fish, Squalus acanthias.";  
 RL Eur. J. Biochem. 29:12-19(1972).

RN [2]

RP SEQUENCE

RX MEDLINE=72128038; PubMed=4622083;

RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;

"Identification of 2 new neurohypophyseal hormones, valitocin (Val8-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias).";  
 RL C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).

CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR InterPro; IPR000981; Neurohyp\_horm.

DR Pfam; PF00220; hormone4; 1.

DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.

KW Hormone; Amidation.

FT DISULFID 1 6

FT MOD\_RES 9 9

FT SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7

DB 8 VG 9

#### RESULT 46

YBFR\_AZOVI

ID YBFR\_AZOVI STANDARD; PRT; 9 AA.

AC P25925;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein in bfr 3' region (Fragment).

OS Azotobacter vinelandii.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Azotobacter.

OX NCBI\_TaxID=354;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92196129; PubMed=1549605;

RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,

Stiefel E.I.;

"Unification of the ferritin family of proteins.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL; M83692; AAA22122.1; -

DR PIR; B41983; B41983.

KW Hypothetical protein.

FT NON\_TER 9

SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

#### Query Match

Best Local Similarity 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
||  
Db 3 PP 4

RESULT 47  
AH3\_PRUSE STANDARD; PRT; 10 AA.  
ID AH3\_PRUSE  
AC P29761;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase isozyme II) (AH II) (Fragment).  
OS Prunus serotina (Black cherry).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
RN NCBI\_TaxID=23207;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Seed;  
RA Li C.P., Swain E., Poulton J.E.;  
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
RL Plant Physiol. 100:282-290(1992).  
CC -|- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-glucose.  
CC -|- SUBUNIT: Monomer.  
CC -|- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR EMBRYONAL TISSUES.  
CC -|- PTM: GLYCOSYLATED.  
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
||  
Db 3 PP 4

RESULT 48  
BPP2\_BOTIN STANDARD; PRT; 10 AA.  
ID BPP2\_BOTIN  
AC P30422;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
RN NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -|- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.  
DR PIR; B37196; B37196.

KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1  
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
||  
Db 9 PP 10

RESULT 49  
BPP2\_BOTJA STANDARD; PRT; 10 AA.  
ID BPP2\_BOTJA  
AC P01022;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme inhibitor V-6-II).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
RN NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=72118526; PubMed=4334402;  
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R., Kocy O.;  
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis.";  
RL Biochemistry 10:4033-4039(1971).  
CC -|- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.  
DR PIR; A01255; XAVI6B.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1  
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
||  
Db 9 PP 10

RESULT 50  
BPP8\_BOTIN STANDARD; PRT; 10 AA.  
ID BPP8\_BOTIN  
AC P30426;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
RN NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom.";

CC J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.

DR PIR; H37196; H37196.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PP 4

DB 9 PP 10

RESULT 51

BPP\_VIPAS

ID\_BPP\_VIPAS STANDARD; PRT; 10 AA.

AC P31351;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide (Angiotensin-converting

DE enzyme inhibitor).

OS Vipera aspis (Aspic viper).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Viperinae; Vipera.

OX NCBI\_TaxID=8706;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=90382616; PubMed=2169439;

RA Komori Y., Sugihara H.;

RT "Characterization of a new inhibitor for angiotensin converting

RT enzyme from the venom of Vipera aspis aspis.";

RL Int. J. Biochem. 22:767-771(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of

CC bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.

DR PIR; A60377; XASNPC.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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OX NCBI\_TaxID=8022;

RN [1]

RP SEQUENCE.

RA MEDLINE=94039817; PubMed=8224232;

CC Conlon J.M., Olson K.R.;

RT "Purification of a vasoactive peptide related to lysyl-bradykinin from

RT trout plasma.";

RL FEBS Lett. 334:75-78(1993).

CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR

CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Plasma.

CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.

CC PIR; S39030; S39030.

KW Bradykinin; Vasodilator.

SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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QY 2 LP 3  
DB 1 LP 2

## RESULT 54

ESL\_LACCA STANDARD; PRT; 10 AA.  
AC P81758;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Putative esterase/lipase (EC 3.1.1.-) (Fragment).  
OS Lactobacillus casei.  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=1582;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=IFPL731;  
RA Lopez de Felipe F.;  
RL Submitted (MAR-1999) to the SWISS-PROT data bank.  
KW Hydrolase; Serine esterase.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
DB 6 VL 7

## RESULT 55

GON3 ONCKE STANDARD; PRT; 10 AA.  
AC P20367; P81751;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III) (LH-RH III) (Luliberin III).  
GN GNRH3.  
OS Oncorhynchus keta (Chum salmon), and  
OC Clupea pallasii (Pacific herring).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8018, 30724;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=O.keta;  
RX MEDLINE=83195140; PubMed=6341999;  
RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;  
RT "Characterization of a teleost gonadotropin-releasing hormone.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).  
RN [2]

SEQUENCE, AND FUNCTION.  
RP SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;  
RX MEDLINE=20114351; PubMed=10650929;  
RA Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,  
RA Chang J.P., Rivier J.E., Sherwood N.M.;  
RT "Primary structure and function of three gonadotropin-releasing hormones, including a novel form, from an ancient teleost, herring.";  
RL Endocrinology 141:505-512(2000).  
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the GNRH family.  
DR PIR; A21114; A21114.

DR InterPro; IPR002012; GNRH.  
DR Pfam; PF00446; GNRH; 1.  
DR PROSITE; PS00473; GNRH; 1.  
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1  
FT MOD\_RES 10  
FT MOD\_RES 10  
SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
DB 8 LP 9

## RESULT 56

GONL\_SQUAC STANDARD; PRT; 10 AA.  
AC P27429;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin (Gonadotropin-releasing hormone) (GNRH) (LH-RH) (Luliberin).  
DE Squalus acanthias (Spiny dogfish).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.  
OX NCBI\_TaxID=7797;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=92335300; PubMed=1631133;  
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,  
RA Nahornak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;  
RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in dogfish brain provides insight into GNRH evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).  
CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the GNRH family.  
DR PIR; A46030; A46030.  
DR InterPro; IPR002012; GNRH.  
DR Pfam; PF00446; GNRH; 1.  
DR PROSITE; PS00473; GNRH; 1.  
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1  
FT MOD\_RES 10  
FT MOD\_RES 10  
SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
DB 8 LP 9

## RESULT 57

GRP\_RANRI STANDARD; PRT; 10 AA.  
ID GRP\_RANRI  
AC P23260;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuromedin C.  
OS Rana ridibunda (Laughing frog) (Marsh frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
OX NCBI\_TaxID=8406;  
RN [1]

```

RP SEQUENCE.
RX TISSUE=Brain;
RC MEDLINE=91315477; PubMed=1859413;
RA Conlon J.M., O'Harte F., Vaudry H.;
RT "Primary structures of the bombesin-like neuropeptides in frog brain
RL show that bombesin is not the amphibian gastrin-releasing peptide.";
RL Biochem. Biophys. Res. Commun. 178:526-530(1991).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR: P00177; P00177.
DR InterPro: IPR000874; Bombesin.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7
Db 6 VG 7

RESULT 58
HTF1_ROMMI STANDARD; PRT; 10 AA.
AC P18110;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RO I (Hypertrehalosaemic factor).
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
RC MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 8 8
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5
Db 6 PN 7

RESULT 59
HTF2_CARMO STANDARD; PRT; 10 AA.
AC P11385;
DT 01-JUL-1989 (Rel. 11, Created)

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DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic factor II (HTF-II) (HPTH-II) (Hypertrehalosaemic
DE neuropeptide II).
OS Carausius morosus (Indian stick insect), and
OS Extatosoma tiaratum (Stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatodea;
OC Heteronemidae; Carausius.
OX NCBI_TaxID=7022, 7024;
RN [1]
RP SEQUENCE.
RX SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RC MEDLINE=87157103; PubMed=3828078;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structure of the hypertrehalosaemic factor II from the
RT corpus cardiaca of the Indian stick insect, Carausius morosus,
RT determined by fast atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN [2]
RP SEQUENCE.
RX SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
RC MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RP CARBOHYDRATE-LINKAGE SITE.
RX SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RC MEDLINE=93129188; PubMed=1482345;
RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT a stick insect corpus cardiaca.";
RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR: JCI1416; JCI1416.
DR PIR: S09138; S09138.
DR InterPro: IPR002047; AKH.
DR Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1
KW MOD_RES 8 8
KW MOD_RES 10 10
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5
Db 6 PN 7

RESULT 60
ODP2_BOVIN STANDARD; PRT; 10 AA.
AC P11180;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2) (Fragment).
GN DLAT.
OS Bos taurus (Bovine).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=8024154; PubMed=3117054;  
 RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;  
 RT "Primary structure around the lipate-attachment site on the E2  
 RT component of bovine heart pyruvate dehydrogenase complex.";  
 RL Biochem. J. 245:919-922(1987).  
 CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall  
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains  
 CC multiple copies of three enzymatic components: pyruvate  
 CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and  
 CC lipoamide dehydrogenase (E3).  
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-  
 CC acetyldihydrolipoamide.  
 CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL  
 CC COFACTOR.  
 CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL  
 CC SYMMETRY.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.  
 CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.  
 DR InterPro: IPR003016; Lipoyl.  
 DR PROSITE: PS00189; LIPOYL, PARTIAL.  
 KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;  
 KW Lipoyl.  
 FT NON TER 1 1  
 FT BINDING 5 5 LIPOYL.  
 FT NON TER 10 10  
 FT SEQUENCE 10 AA; 1066 MW; 899BECDDIADD33AB1 CRC64;  
 SQ  
 Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 VG 7  
 DB 8 VG 9  
 RESULT 61  
 TEMK\_RANTE  
 ID TEMK\_RANTE STANDARD; PRT; 10 AA.  
 AC P56923;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Temporin K.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed=9022710;  
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
 RA Barza D.;  
 RT "Temporins, antimicrobial peptides from the European red frog Rana  
 RT temporaria.";  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
 CC bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the brevinin family.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD RES 10 10  
 FT SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;  
 SQ

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 LP 3  
 DB 2 LP 3  
 RESULT 62  
 TKNB\_CHICK  
 ID TKNB\_CHICK STANDARD; PRT; 10 AA.  
 AC P19851;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Neurokinin A (Substance K) (Neuromedin L).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=88204263; PubMed=2452461;  
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;  
 RT "[Arg3] substance P and neurokinin A from chicken small intestine.";  
 RL Regul. Pept. 20:171-180(1988).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; JN0024; JN0024.  
 DR InterPro: IPR002040; Tachykinin.  
 DR Pfam: PF02202; Tachykinin; 1.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10 10  
 FT SEQUENCE 10 AA; 1134 MW; 8A6B4062C9D5B81 CRC64;  
 SQ  
 Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 VG 7  
 DB 7 VG 8  
 RESULT 63  
 TKNB\_ONCMY  
 ID TKNB\_ONCMY STANDARD; PRT; 10 AA.  
 AC P28500;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Neurokinin A (Substance K) (Neuromedin L).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), and  
 OS Gadus morhua (Atlantic cod).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022, 8049;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=O.mykiss, and G.morhua;  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain

RT of the cod and trout.";  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; S23186; S23186.  
 DR PIR; S23307; S23307.  
 DR InterPro: IPR002040; Tachykinin.  
 DR Pfam: PF02202; Tachykinin; 1.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 DR Tachykinin; Neuropeptide; Amidation.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10 10 AMIDATION (BY SIMILARITY).  
 SQ SEQUENCE 10 AA; 1145 MW; 136B4062C9D5B440 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VG 7  
 ||  
 Db 7 VG 8

## RESULT 64

TKNK\_PIG  
 ID TKNK\_PIG STANDARD; PRT; 10 AA.  
 AC P01292;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Neurokinin B (NKB) (Neuromedin K).  
 GN TAC3 OR NKNB.  
 OS Sus scrofa (Pig), and  
 OS Rana ridibunda (laughing frog) (Marsh frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823, 8406;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Pig; TISSUE=Spinal cord;  
 RX MEDLINE=83282812; PubMed=6576785;  
 RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;  
 RT "Neuromedin K: a novel mammalian tachykinin identified in porcine  
 RT spinal cord.";  
 RL Biochem. Biophys. Res. Commun. 114:533-540(1983).  
 RN [2]

RP SEQUENCE.  
 RC SPECIES=R. ridibunda; TISSUE=Brain;  
 RX MEDLINE=9204543; PubMed=1658233;  
 RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;  
 RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with  
 RT neurokinin B from the brain of the frog Rana ridibunda.";  
 RL J. Neurochem. 57:2086-2091(1991).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; A01560; SPPGNK.  
 DR InterPro: IPR002040; Tachykinin.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1211 MW; E1FA7C62C9C9CAA1 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VG 7  
 ||  
 Db 7 VG 8

## RESULT 65

TKN\_PHYBI  
 ID TKN\_PHYBI STANDARD; PRT; 10 AA.  
 AC P08610;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Phyllomedusa.  
 OS Phyllomedusa bicolor (Two-colored leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Phyllomedusinae; Phyllomedusa.  
 OX NCBI\_TaxID=8393;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=70267748; PubMed=5452018;  
 RA Anastasi A., Erspamer G.F.;  
 RT "Occurrence of phyllomedusin, a physalaemin-like decapeptide, in the  
 RT skin of Phyllomedusa bicolor.";  
 RL Experientia 26:866-867(1970).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; S07202; S07202.  
 DR InterPro: IPR002040; Tachykinin.  
 DR PROSITE: PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1189 MW; 3A257D7059D40457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PN 5  
 ||  
 Db 3 PN 4

## RESULT 66

TKOI\_UREUN  
 ID TKOI\_UREUN STANDARD; PRT; 10 AA.  
 AC P40751;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Urechis tachykinin I.  
 OS Urechis unicinctus.  
 OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.  
 OX NCBI\_TaxID=6432;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=ventral nerve cord;  
 RX MEDLINE=93236558; PubMed=8476410;  
 RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;  
 RT "Two novel tachykinin-related neuropeptides in the echiuroid worm,  
 RT Urechis unicinctus";  
 RL Biochem. Biophys. Res. Commun. 192:1-6(1993).  
 CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL  
 CC MUSCLE OF THE ANIMAL.  
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10 10 AMIDATION  
 SQ SEQUENCE 10 AA; 1177 MW; C6D1C462C9DC6C5A6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7  
 DB 7 VG 8

## RESULT 67

TMOP AEDAE  
 ID TMOP AEDAE STANDARD; PRT; 10 AA.

AC P19425;  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Trypsin-modulating oostatic factor (TMOP) (OOSH).  
 OS Aedes aegypti (Yellowfever mosquito).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
 OX NCBI\_TaxID=71159;  
 RN [1]

## SEQUENCE.

RP STRAIN=Vero beach; TISSUE=Ovary;  
 RC MEDLINE=90367888; PubMed=2394318;  
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
 RT "Mosquito oostatic factor: a novel decapeptide modulating  
 RT trypsin-like enzyme biosynthesis in the midgut.";  
 RL FASEB J. 4:3015-3020 (1990).  
 RN [2]

## SEQUENCE.

RP STRAIN=Vero beach; TISSUE=Ovary;  
 RC MEDLINE=93357794; PubMed=8353526;  
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
 RT "Mass spectrometry and characterization of Aedes aegypti trypsin  
 RT modulating oostatic factor (TMOP) and its analogs.";  
 RL Insect Biochem. Mol. Biol. 23:703-712 (1993).  
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS  
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN  
 CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE  
 CC DEVELOPMENT.  
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR  
 CC EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT  
 CC 36 HRS AND STOPS AT 56 HRS.  
 DR PIR: A36454; A36454.  
 KW Hormone.  
 FT DOMAIN 3 10 POLY-PRO.  
 FT VARIANT 1 2 YD -> DY (IN TMFO(B)).

QY SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;  
 DB 3 PP 4  
 5 PP 6

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 68

TPIS NICPL  
 ID TPIS NICPL STANDARD; PRT; 10 AA.

AC P19178;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).  
 OS Nicotiana glauca (Leadwort-leaved tobacco).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4092;  
 RN [1]

RP SEQUENCE.  
 RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;  
 RT "Alterations in the phenotype of plant cells studied by NH2-terminal  
 RT amino acid-sequence analysis of proteins electroblooded from two-  
 RT dimensional gel-separated total extracts.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810 (1987).

CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glyceralone  
 CC phosphate.  
 CC -!- PATHWAY: Plays an important role in several metabolic pathways.  
 CC -!- SUBUNIT: Homodimer.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
 CC -!- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC  
 CC AND PLASTID.  
 CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.

DR PIR: A27617; A27617.  
 DR InterPro; IPR000652; Triophos ismrse.  
 DR PROSITE; PS00171; TIM; PARTIAL.  
 KW isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;  
 KW Pentose shunt.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1140 MW; 80B9D37862C9C9D1 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7  
 DB 6 VG 7

## RESULT 69

UHA3 HUMAN

ID UHA3 HUMAN STANDARD; PRT; 10 AA.  
 AC P40930;

DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).  
 OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

## SEQUENCE.

RP TISSUE=Heart;  
 RC MEDLINE=95203287; PubMed=7895732;  
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;  
 RT "The human myocardial two-dimensional gel protein database: update  
 RT 1994.";  
 RL Electrophoresis 15:1459-1465 (1994).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.8, ITS MW IS: 47.3 kDa.  
 FT NON TER 10 10

QY SEQUENCE 10 AA; 1049 MW; 6BDCDE41A041B76B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7  
 DB 9 VG 10

## RESULT 70

UPA2 HUMAN

ID UPA2 HUMAN STANDARD; PRT; 10 AA.



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AC P30088;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.4, ITS MW IS: 49 kDa.
DR SWISS-2DPAGE; P30088; HUMAN.
FT NON_TER 1
FT UNSURE 6
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB7775B7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4
DB 5 PP 6

RESULT 71
UPA4_HUMAN
ID UPA4_HUMAN STANDARD; PRT; 10 AA.
AC P30090;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8, ITS MW IS: 40.5 kDa.
DR SWISS-2DPAGE; P30090; HUMAN.
FT NON_TER 1
FT UNSURE 4
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5
DB 11

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Db 3 PN 4

RESULT 72
UPA5_HUMAN
ID UPA5_HUMAN STANDARD; PRT; 10 AA.
AC P30091;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON_TER 1
FT VARIANT 9
FT NON_TER 9
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NV 6
DB 1 NV 2

RESULT 73
UPA8_HUMAN
ID UPA8_HUMAN STANDARD; PRT; 10 AA.
AC P30094;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 34) (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.2, ITS MW IS: 16 kDa.
DR SWISS-2DPAGE; P30094; HUMAN.
FT NON_TER 1
FT VARIANT 4
FT NON_TER 4
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1010 MW; 269492EB05A1A457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PN 5
DB 11

```

SQ SEQUENCE 10 AA; 977 MW; 2EA6E0C77AE325B8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7  
||  
DB 2 VG 3

## RESULT 74

URE3 MORMO STANDARD; PRT; 10 AA.

AC P17339;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea  
DE amidohydrolase) (Fragment).  
GN UREA.

OS Morganella morganii (Proteus morganii).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Morganella.  
OX NCBI\_TaxID=582;  
RN [1]

## SEQUENCE.

RX MEDLINE=90264298; PubMed=2345135;  
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
RT "Morganella morganii urease: purification, characterization, and  
RT isolation of gene sequences."  
RL J. Bacteriol. 172:3073-3080(1990).  
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.  
DR PIR; C35389; C35389.  
KW Hydrolase.  
FT NON\_TER 10 10.  
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
||  
DB 5 PP 6

## RESULT 75

UXA2\_CHLTR STANDARD; PRT; 10 AA.

AC P38003;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Unknown protein from 2D-page from elementary body (Fragment).  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]

## SEQUENCE.

RC STRAIN=L2/434/Bu;  
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,  
RA Comanducci M., Christensen G., Birkelund S., Vretou E., Ratti G.,  
RA Pallini V.;  
RL Submitted (SEP-1994) to the SWISS-PROT data bank.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.65, ITS MW IS: 26.5 kDa.  
DR Siena-2DPAGE; P38003; -  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1019 MW; 49C2B5C6CAE862C7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7  
||  
DB 4 VG 5

Search completed: November 25, 2003, 18:17:35  
Job time : 4.3883 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 16.867 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-17

Perfect score: 7

Sequence: 1 VLPPNVG 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_prodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	42.9	9	5	Q9TWV0
2	3	42.9	10	2	Q9R5T2
3	3	42.9	10	2	Q9R5N2
4	3	42.9	10	2	Q9R5N1
5	3	42.9	10	2	Q9R5N3
6	3	42.9	10	4	Q14096
7	3	42.9	10	11	Q9VHM9
8	3	42.9	10	11	Q9ESU5
9	3	42.9	10	12	Q8JV78
10	3	42.9	10	13	Q8JFE7
11	3	42.9	10	13	Q8J3J3
12	3	42.9	11	4	O60761
13	3	42.9	12	2	Q8K286
14	3	42.9	12	4	Q9BZ49
15	3	42.9	12	10	P82329
16	3	42.9	13	2	Q9L8K1

Q8WYB7 homo sapien  
Q14890 homo sapien  
Q9UC84 homo sapien  
Q9WMS5 sigma virus  
P82830 rana tatei  
Q26075 psammecolus  
Q9TW0 trypanosoma  
Q9TR83 sus scrofa  
P82326 pleum sativ  
O70599 rattus norv  
P83071 bacillus ce  
Q9TR03 bos taurus  
Q78794 pytaella l  
Q9UCG5 homo sapien  
Q9WMS6 sigma virus  
Q9TR90 gallus gall  
P9135 mycobacteri  
O15276 homo sapien  
Q95794 homo sapien  
Q95795 homo sapien  
P83061 spinacia ol  
Q65373 orgyia pseu  
Q9F5U2 pseudomonas  
Q9R5F9 alcaligenes  
Q9UC58 homo sapien  
Q8NFB4 homo sapien  
Q84129 influenzavi  
Q44608 buchnera ap  
Q9RBV1 pseudomonas  
Q9R4J9 mycobacteri  
Q9UR83 saccharomyc  
Q14737 homo sapien  
Q9UC80 homo sapien  
Q8NFI2 homo sapien  
Q9UC82 homo sapien  
P82600 aedes aegypt  
Q8HYW9 bos taurus  
O11338 molluscum c  
Q8KUI9 neisseria m  
Q9R4F4 aeromonas h  
Q9UC84 homo sapien  
Q9UC81 homo sapien  
Q9BME5 bacterocera  
Q8MCC9 drosophila  
Q9S903 vigna sinen  
Q9S8K2 solanum tub  
Q84860 unidentified  
Q9PT8 gadus morhu  
Q9PU0 gallus gall  
Q9P838 rana catesb  
P82232 rana tempor  
Q8433 rattus sp.  
P83308 gallus gall  
O50556 actinobacil  
Q47029 enterobacte  
P92214 amblyopyrum  
P92393 hordeum vul  
P92403 lophopyrum  
P92427 peridictyon  
P92430 aegilops ta  
P92221 bromus iner  
P92425 pseudoroegn  
P92381 hordeum bra  
P92387 henradia p  
P92210 agropyron c  
P92440 thinopyrum  
P92218 australopyr  
P92390 heteranthe  
P92472 haynaldia v  
P92442 taeniatheru  
P92226 crithopsis  
P92385 hordeum mar

90 P92421 psathyrosta  
 91 Q9C5B3 arabidopsis  
 92 P82445 nicotiana t  
 93 Q63668 rattus norv  
 94 Q66113 cherry leaf  
 95 Q9RG49 buchnera ap  
 96 Q9AGP4 arthrobacte  
 97 Q49534 mycoplasma  
 98 Q56429 thermus the  
 99 Q93SP2 pseudomonas  
 100 Q9r4m3 enterococcu

## ALIGNMENTS

RESULT 1  
 Q9TWV0  
 ID Q9TWV0 PRELIMINARY; PRT; 9 AA.  
 AC Q9TWV0;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
 DE Antho-RPAMIDE-NEUROPTIDE.  
 OS Anthopleura elegantissima (Sea anemone).  
 OC Eukaryota; Metazoa; Chidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nynanthaeae; Actiniidae; Anthopleura.  
 OC NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93126143; PubMed=1480510;  
 RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;  
 RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-Arg (Antho-RPamide),  
 an N-terminally protected, biologically active neuropeptide from sea  
 anemones.";  
 RL Peptides 13:851-857(1992).  
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
 DB 1 LPP 3

RESULT 2  
 Q9R5T2  
 ID Q9R5T2 PRELIMINARY; PRT; 10 AA.  
 AC Q9R5T2;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE NADP-linked glucose-6-phosphate dehydrogenase (fragment).  
 OC Acetobacter hansenii.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
 OC Acetobacteraceae; Gluconacetobacter.  
 OC NCBI\_TaxID=436;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92027789; PubMed=1929428;  
 RA Levy H.R., Cook C.;  
 RT "Purification and properties of NADP-linked glucose-6-phosphate  
 RT dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";  
 RL Arch. Biochem. Biophys. 291:161-167(1991).  
 FT NON\_TER 1  
 FT NON\_TER 1  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D77767 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
 DB 3 LPP 5

RESULT 3  
 Q9RSN2  
 ID Q9RSN2 PRELIMINARY; PRT; 10 AA.  
 AC Q9RSN2;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Neurotoxin type A HN+ 57 kDa SUBUNIT-SAMPLE 2 (Fragment).  
 OS Clostridium botulinum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OC NCBI\_TaxID=1491;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92143938; PubMed=1781887;  
 RA Somers E., DasGupta B.R.;  
 RT "Clostridium botulinum types A, B, C1, and E produce proteins with or  
 RT without hemagglutinating activity: do they share common amino acid  
 RT sequences and genes?";  
 RL J. Protein Chem. 10:415-425(1991).  
 FT NON\_TER 1  
 FT NON\_TER 10  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1225 MW; EC3DE932D366C1BA CRC64;

Query Match 42.9%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
 DB 7 VLP 9

RESULT 4  
 Q9RSN1  
 ID Q9RSN1 PRELIMINARY; PRT; 10 AA.  
 AC Q9RSN1;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Neurotoxin type A HN+ 57 kDa subunit (fragment).  
 OS Clostridium botulinum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OC NCBI\_TaxID=1491;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92143938; PubMed=1781887;  
 RA Somers E., DasGupta B.R.;  
 RT "Clostridium botulinum types A, B, C1, and E produce proteins with or  
 RT without hemagglutinating activity: do they share common amino acid  
 RT sequences and genes?";  
 RL J. Protein Chem. 10:415-425(1991).  
 FT NON\_TER 1  
 FT NON\_TER 10  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1172 MW; E5DAE932D416C1BA CRC64;

Query Match 42.9%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
 DB 7 VLP 9

RESULT 5

```
Q9RSN3          PRELIMINARY;      PRT;      10 AA.
ID Q9RSN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neurotoxin type B HN+ 57 kDa subunit (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143938; PubMed=1781887;
RA Somers E., DasGupta B.R.;
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
RT without hemagglutinating activity: do they share common amino acid
RT sequences and genes?";
RL J. Protein Chem. 10:415-425(1991).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1221 MW; C3DBE932D416C1B2 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
DB 7 VLP 9

RESULT 6
Q14096          PRELIMINARY;      PRT;      10 AA.
ID Q14096;
AC Q14096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYP2B6 gene cryptic exon 3A of cytochrome P45011B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174922; PubMed=2308828;
RA Miles J.S., McLaren A.W., Gonzalez F.J., Wolf C.R.;
RT "Alternative splicing in the human cytochrome P45011B6 gene: use of a
RT cryptic exon within intron 3 and splice acceptor site within exon 4.";
RL Nucleic Acids Res. 18:189-189(1990).
DR EMBL; X16864; CAA34754.1; -.
SQ SEQUENCE 10 AA; 885 MW; 4181B9087BC77767 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
DB 3 LPP 5

RESULT 7
Q8VHM9          PRELIMINARY;      PRT;      10 AA.
ID Q8VHM9;
AC Q8VHM9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Interferon receptor 2a' (Fragment).
GN IFNAR2.
OS Mus musculus (Mouse).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The genomic structure and expression patterns of the gene encoding
RT the second chain of the murine interleukin 10 receptor, IL-10R2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The organization, transcriptional regulation and chromosomal
RT localization of the locus encoding the gene for the murine type I
RT interferon receptor, Ifnar2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440786; AAL40944.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA; 1139 MW; 322A36A72449C737 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
DB 1 LPP 3

RESULT 8
Q9ESU5          PRELIMINARY;      PRT;      10 AA.
ID Q9ESU5;
AC Q9ESU5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Fas death receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He;
RX MEDLINE=20127858; PubMed=10660538;
RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,
RA Yonish-Rouach E., Reisdorf P.;
RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a
RT p53-responsive element that is activated by p53 mutants unable to
RT induce apoptosis.";
RL J. Biol. Chem. 275:3867-3872(2000).
DR EMBL; AF282865; AAG02410.1; -.
KW Receptor.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
DB 7 VLP 9

RESULT 9
Q8JV78          PRELIMINARY;      PRT;      10 AA.
ID Q8JV78;
AC Q8JV78;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
```

DT -01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Large 1 antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN (1)  
RN SEQUENCE FROM N.A.  
RP STRAIN=USA1;  
RC MEDLINE=21465052; PubMed=11581397;  
RX Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA.";  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL; AF303946; AAM97796.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1183 MW; 4CD6A96731A32763 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 2 LPP 4  
DB 7 LPP 9

## RESULT 10

08JFE7 PRELIMINARY; PRT; 10 AA.  
AC 08JFE7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Myelin proteolipid protein (Fragment).  
OS Picedula albicollis.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.  
OX NCBI\_TaxID=59894;  
RN (1)  
RN SEQUENCE FROM N.A.  
RP MEDLINE=Bc5, and Bc8;  
RX MEDLINE=21918460; PubMed=11918793;  
RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;  
RT "Single-nucleotide polymorphism characterization in species with  
RT limited available sequence information: high nucleotide diversity  
RT revealed in the avian genome.";  
RL Mol. Ecol. 11:603-612(2002).  
DR EMBL; AF454217; AAM22903.1; -.  
DR EMBL; AF454218; AAM22904.1; -.  
FT NON\_TER 1  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 42.9%; Score 3; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 1 VLP 3  
DB 5 VLP 7

## RESULT 11

08J33 PRELIMINARY; PRT; 10 AA.  
AC 08J33;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Myelin proteolipid protein (Fragment).  
OS Picedula hypoleuca.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.  
OX NCBI\_TaxID=46689;  
RN (1)  
RN SEQUENCE FROM N.A.  
RP STRAIN=Op86;  
RX MEDLINE=21918460; PubMed=11918793;  
RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;  
RT "Single-nucleotide polymorphism characterization in species with  
RT limited available sequence information: high nucleotide diversity  
RT revealed in the avian genome.";  
RL Mol. Ecol. 11:603-612(2002).  
DR EMBL; AF454216; AAM22902.1; -.  
FT NON\_TER 1  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 42.9%; Score 3; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 1 VLP 3  
DB 5 VLP 7

## RESULT 12

060761 PRELIMINARY; PRT; 11 AA.  
AC 060761;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NPT-1 protein (Fragment).  
GN NPT-1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RN SEQUENCE FROM N.A.  
RP MEDLINE=98207718; PubMed=9545579;  
RX Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,  
RA Tatsuami S., Morita K., Takeda E.;  
RT "Characterization of the 5' flanking region of the human NPT-1  
RT Na<sup>+</sup>/phosphate cotransporter gene.";  
RL Biochim. Biophys. Acta 1396:267-272(1998).  
DR EMBL; D83236; BAA25645.1; -.  
FT NON\_TER 11  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 42.9%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 2 LPP 4  
DB 7 LPP 9

## RESULT 13

08K286 PRELIMINARY; PRT; 12 AA.  
AC 08K286;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Class I integron DNA integrase (Fragment).  
GN INT1.  
OS Acinetobacter baumannii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=470;

RN SEQUENCE FROM N.A.  
 RP STRAIN=2044;  
 RC Dolzani L., Gombac F., Lagatolla C., Riccio M.L., Rossolini G.M.,  
 RA Tonin E., Monti-Bradin C.,  
 RT "Carriage of class I and II integrins in Italian clinical isolates of  
 RT Acinetobacter baumannii";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ313334; CAC85941.1; -  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1296 MW; 904268585E376DC1 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
 Db 8 LPP 10

RESULT 14  
 Q9BZ49 PRELIMINARY; PRT; 12 AA.  
 AC Q9BZ49;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Glycophorin C (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,  
 RA Zimmerman P.A.;  
 RT "The association of the glycoporphin C exon 3 deletion with  
 RT ovalocytosis and malaria susceptibility in the Wosera, Papua New  
 RT Guinea";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF342984; AAK01459.1; -  
 FT NON TER 1 1  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
 Db 8 LPP 10

RESULT 15  
 P82329 PRELIMINARY; PRT; 12 AA.  
 AC P82329;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Unknown protein from 2D-page of thylakoid lumen (SPOT11) (Fragment).  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eusoids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 OX NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
 RX MEDLINE=20181728; PubMed=10715320;  
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,

RA Adamska I., van Wijk K.J.;  
 RT "Proteomics of the chloroplast: systematic identification and  
 RT targeting analysis of luminal and peripheral thylakoid proteins.";  
 RL Plant Cell 12:319-341(2000).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.  
 CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.5, ITS MW IS: 24.1 KDA.  
 KW Chloroplast; Thylakoid membrane.  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1244 MW; CBE0AD74B3D5B862 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
 Db 9 LPP 11

RESULT 16  
 Q9L8K1 PRELIMINARY; PRT; 13 AA.  
 AC Q9L8K1;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Vans (Fragment).  
 GN VANSB.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BM4281;  
 RX MEDLINE=20307504; PubMed=10846225;  
 RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundeffjord A.;  
 RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin  
 RT resistant enterococci and characterization of two novel insertion  
 RT sequences";  
 RL Microbiology 146:1469-1479(2000).  
 DR EMBL: AF201896; AAF73374.1; -  
 FT NON TER 1 1  
 FT NON TER 1 1  
 SQ SEQUENCE 13 AA; 1502 MW; 8D0E282189F9672A CRC64;

Query Match 42.9%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
 Db 7 LPP 9

RESULT 17  
 Q8WYB7 PRELIMINARY; PRT; 13 AA.  
 AC Q8WYB7;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Dystrophin (Fragment).  
 GN DMD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chamberlain J.S.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
RA den Dunnen J.T.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF213444; AAL61589.1; -  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1456 MW; 4DA2737F7BF9E9C7 CRC64;  
Query Match 42.9%; Score 3; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 5 NVG 7  
DB 2 NVG 4  
RESULT 18  
Q14890 PRELIMINARY; PRT; 13 AA.  
ID Q14890  
AC Q14890;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Mucin (Fragment).  
GN MUC5AC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tracheobronchial mucosa;  
RA Guyonnet-Duperat V., Audie J., Debailleul V., Laine A., Buisine M.,  
Zoutina-Gallegue S., Pigny P., Degand P., Aubert J., Porchet N.;  
RT "Characterization of the human mucin gene MUC5AC: a consensus  
RT cysteine-rich domain for 11p15 mucin genes.";  
RL Biochem. J. 0:0-0(1994).  
DR EMBL; Z34280; CAA84034.1; -  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1580 MW; 535DF5A5183B7767 CRC64;  
Query Match 42.9%; Score 3; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 LPP 4  
DB 6 LPP 8  
RESULT 19  
Q9UCS4 PRELIMINARY; PRT; 13 AA.  
ID Q9UCS4  
AC Q9UCS4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE TROPOMYOSIN-33 kDa calcium binding protein fragment E (Fragment).  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92090441; PubMed=1836432;  
RA Crabos M., Yamakado T., Heizmann C.W., Cerletti N., Buhler F.R.,  
Erne P.;  
RT "The calcium binding protein tropomyosin in human platelets and  
RT cardiac tissue: elevation in hypertensive cardiac hypertrophy.";  
RL Eur. J. Clin. Invest. 21:472-478(1991).  
FT NON\_TER 1 1

FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1453 MW; CA711A6F085131B6 CRC64;  
Query Match 42.9%; Score 3; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 5 NVG 7  
DB 1 NVG 3  
RESULT 20  
Q9WNG5 PRELIMINARY; PRT; 13 AA.  
ID Q9WNG5  
AC Q9WNG5;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
DE 3 protein (Fragment).  
GN GENE 3.  
OS Sigma virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Rhabdoviridae; unclassified Rhabdoviridae.  
OX NCBI\_TaxID=11301;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212481; PubMed=8384742;  
RA Teninges D., Bras F., Dezelee S.;  
RT "Genome organization of the sigma rhabdovirus: six genes and a gene  
RT overlap.";  
RL Virology 193:1018-1023(1993).  
DR EMBL; S57850; AAD40700.1; -  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1456 MW; 9AF4F3FDB75E32D5 CRC64;  
Query Match 42.9%; Score 3; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VLP 3  
DB 7 VLP 9  
RESULT 21  
P82830 PRELIMINARY; PRT; 13 AA.  
ID P82830  
AC P82830;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Temporin-11A.  
OS Rana luteiventris.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
OX NCBI\_TaxID=58176;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RX TISSUE=SKIN;  
RX MEDLINE=20117700; PubMed=10651828;  
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,  
Conlon J.M.;  
RT "Peptides with antimicrobial activity from four different families  
RT isolated from the skins of the North American frogs Rana luteiventris,  
RT Rana berlandieri and Rana pipiens.";  
RL Eur. J. Biochem. 267:894-900(2000).  
CC -1- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM  
CC S.AUREUS.  
CC -1- MASS SPECTROMETRY: MW=1366.8; METHOD=ELECTROSPRAY.  
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN  
CC FAMILY.  
KW Antibiotic; Amidation.



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FT  MOD_RES      13      13      AMIDATION.
SQ  SEQUENCE      13 AA; 1368 MW; 92541A7649A3D685 CRC64;

Query Match
Best Local Similarity 42.9%; Score 3; DB 13; Length 13;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 VLP 3
    |||
Db  1 VLP 3

RESULT 22
ID  Q26075      PRELIMINARY;      PRT;      14 AA.
AC  Q26075;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Histone H2A (Fragment).
OS  Psammecchinus miliaris (Sand sea urchin).
OC  Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC  Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
OC  Psammecchinus.
OX  NCBI_TaxID=7660;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=85140235; PubMed=2858095;
RA  Nordstrom J.L., Hall S.L., Kessler M.M.;
RT  "Polyadenylation of sea urchin histone RNA sequences in transfected
RT  COS cells.";
DR  EMBL; M12542; AAA30028.1; -.
FT  NON_TER      1
FT  CHAIN         1
SQ  SEQUENCE      14 AA; 1620 MW; .298A3F878A462268 CRC64;

Query Match
Best Local Similarity 42.9%; Score 3; DB 5; Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PPN 5
    |||
Db  8 PPN 10

RESULT 23
ID  Q9TWM0      PRELIMINARY;      PRT;      14 AA.
AC  Q9TWM0;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE  Histone C (fragment).
OS  Trypanosoma brucei.
OC  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX  NCBI_TaxID=5691;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=93064852; PubMed=1437281;
RA  Bender K., Beteschart B., Schaller J., Kampfer U., Hecker H.;
RT  "Sequence differences between histones of procyclic Trypanosoma brucei
RT  brucei and higher eukaryotes.";
RL  Parasitology 105:97-104(1992).
SQ  SEQUENCE      14 AA; 1480 MW; 460FF4E8876C4EC7 CRC64;

Query Match
Best Local Similarity 42.9%; Score 3; DB 5; Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 VLP 3
    |||
Db  8 VLP 10

FT  MOD_RES      13      13      AMIDATION.
SQ  SEQUENCE      13 AA; 1368 MW; 92541A7649A3D685 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 VLP 3
    |||
Db  1 VLP 3

RESULT 24
ID  Q9TR83      PRELIMINARY;      PRT;      14 AA.
AC  Q9TR83;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE  TRIKINASE (EC 2.7.1.28) (Fragment).
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=95132498; PubMed=7831203;
RA  Miwa I., Kito Y., Okuda J.;
RL  Prep. Biochem. 24:203-223(1994).
SQ  SEQUENCE      14 AA; 1441 MW; C1F10C81590001DD CRC64;

Query Match
Best Local Similarity 42.9%; Score 3; DB 6; Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 PNV 6
    |||
Db  10 PNV 12

RESULT 25
ID  P82326      PRELIMINARY;      PRT;      14 AA.
AC  P82326;
DT  01-JUN-2000 (TrEMBLrel. 14, Created)
DT  01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT  01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE  Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).
OS  Pisum sativum (Garden pea)
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX  NCBI_TaxID=3888;
RN  [1]
RP  SEQUENCE, SUBCELLULAR LOCATION AND DEVELOPMENTAL STAGE.
RC  STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX  MEDLINE=20181728; PubMed=10715320;
RA  Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA  Adamska I., van Wijk K.J.;
RT  "Proteomics of the chloroplast: systematic identification and
RT  targeting analysis of luminal and peripheral thylakoid proteins.";
RL  Plant Cell 12:319-341(2000).
CC  -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC  -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC  -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC  PROTEIN IS: 6.0. ITS MW IS: 18.3 KDA.
KW  Chloroplast; Thylakoid membrane.
RN  NON_TER      14
SQ  SEQUENCE      14 AA; 1580 MW; 314ACB514E1B237 CRC64;

Query Match
Best Local Similarity 42.9%; Score 3; DB 10; Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 LPP 4
    |||
Db  5 LPP 7

RESULT 26
ID  O70599      PRELIMINARY;      PRT;      14 AA.
AC  O70599;

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DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Thymidine kinase [EC 2.7.1.21] (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RA Sauer M.;  
 RL Thesis (1999), University of Vienna, Inst. of Molecular Biology.  
 DR EMBL; AJ006455; CAA07030.1; -;  
 KW Kinase; Transferrase.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E8B7 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
 |||  
 DB 9 VLP 11

## RESULT 27

P83071 ID P83071 PRELIMINARY; PRT; 15 AA.  
 AC P83071;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE 62 kDa protein (Fragment).  
 OS Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1396;  
 RN [1]  
 RP SEQUENCE, AND INDUCTION.  
 RC STRAIN=NCIMB 11796;  
 RA Browne N., Dowds B.C.A.;  
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
 CC -I- INDUCTION: BY PH REGULATION.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1603 MW; 6E9E778D6E231342 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NVG 7  
 |||  
 DB 10 NVG 12

## RESULT 28

Q9TR03 ID Q9TR03 PRELIMINARY; PRT; 15 AA.  
 AC Q9TR03;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Neuron-specific ASH/GRB-2 SH3 domain-binding protein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=96257761; PubMed=8687411;  
 RA Miura K., Miki H., Shimazaki K., Kawai N., Takenawa T.;

RT "Interaction of Ash/Grb-2 via its SH3 domains with neuron-specific  
 RT p150 and p65.";  
 RL Biochem. J. 316:639-645(1996).  
 SQ SEQUENCE 15 AA; 1635 MW; 25161E83C374F9CD CRC64;

Query Match 42.9%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEN 5  
 |||  
 DB 4 PEN 6

## RESULT 29

O78794 ID O78794 PRELIMINARY; PRT; 15 AA.  
 AC O78794;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Mitochondrial ribosomal protein S14 (Fragment).  
 GN RPS14.  
 OS Pythia littoralis.  
 OC Mitochondrion.  
 OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;  
 OC Acinetosporaceae; Pythiella.  
 OX NCBI\_TaxID=2885;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ROSCOFF;  
 RX MEDLINE=98239704; PubMed=9571021;  
 RA Rousvoal S., Oudot M.-P., Fontaine J.-M., Kloareg B.,  
 RA Loiseau-de Goer S.L.;  
 RT "Witnessing the evolution of transcription in mitochondria: the  
 RT mitochondrial genome of the primitive brown alga Pythiella littoralis  
 RT (L.) Kjellm. encodes a T7-like RNA polymerase.";  
 RL J. Mol. Biol. 277:1047-1057(1998).  
 CC -I- SUBCELLULAR LOCATION: MITOCHONDRIAL.  
 CC -I- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.  
 DR EMBL; AF034976; AAC23952.1; -;  
 DR InterPro; IPR001209; Ribosomal S14.  
 DR PROSITE; PS00527; RIBOSOMAL S14; PARTIAL.  
 KW Ribosomal protein; Mitochondrion; Hypothetical protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 15 AA; 1599 MW; 2D406410C588731B CRC64;

Query Match 42.9%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
 |||  
 DB 6 VLP 8

## RESULT 30

Q9UCG5 ID Q9UCG5 PRELIMINARY; PRT; 16 AA.  
 AC Q9UCG5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE T-suppressor LYMPHOKINE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93231626; PubMed=7682534;  
 RA Quan C.P., Watanabe S., Vuillier F., Pires R., Matsuo T.,  
 Stanislawski M., Pillot J., Bouvet J.P.;

RT "Purification and partial amino acid sequence of suppressive  
 RT lymphokine from a CD8+ CD57+ human T hybridoma."  
 RL Immunology 78:205-209(1993).  
 SQ SEQUENCE 16 AA; 1587 MW; 4565578B6F6F9C29 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NVG 7  
 ||||  
 Db 4 NVG 6

RESULT 31  
 Q9WMG6 PRELIMINARY; PRT; 16 AA.  
 AC Q9WMG6;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE 2 protein (Fragment).  
 GN 2.  
 OS Sigma virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Rhabdoviridae; unclassified Rhabdoviridae.  
 OX NCBI\_TaxID=11301;  
 RN [1]\_TaxID=11301;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=93212481; PubMed=8384742;  
 RA Teninges D., Bras F., Dezelee S.;  
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene  
 RT overlap."  
 RL Virology 193:1018-1023(1993).  
 DR EMBL; S57847; AAD40699.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 16 AA; 1904 MW; F96DBC468601967E CRC64;

Query Match 42.9%; Score 3; DB 12; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
 ||||  
 Db 12 VLP 14

RESULT 32  
 Q9PT90 PRELIMINARY; PRT; 16 AA.  
 AC Q9PT90;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Osteonectin (Fragment).  
 GN SPARC.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.

OX NCBI\_TaxID=9031;  
 RN [1]\_TaxID=9031;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20499267; PubMed=11042589;  
 RA Vial E., Perez S., Castellazzi M.;  
 RT "Transcriptional control of SPARC by v-Jun and other members of the  
 RT AP1 family of transcription factors."  
 RL Oncogene 19:5020-5029(2000).

DR EMBL; AJ243178; CAB63946.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1778 MW; 91B2C62F4E5D3B89 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
 ||||  
 Db 1 VLP 3

RESULT 33  
 P97135 PRELIMINARY; PRT; 17 AA.  
 AC P97135;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE GyrA protein (Fragment).  
 GN GYRA.

OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]\_TaxID=1773;

RP SEQUENCE FROM N.A.  
 RC STRAIN=H37Ra;  
 RX MEDLINE=95072534; PubMed=7981652;  
 RA Madhusudan K., Ramesh V., Nagaraja V.;  
 RT "Molecular cloning of gyrA and gyrB genes of Mycobacterium  
 RT tuberculosis: analysis of nucleotide sequence."  
 RL Biochem. Mol. Biol. Int. 33:651-660(1994).  
 DR EMBL; X78888; CAA55487.1; -.  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1916 MW; EF0B750A36E365AE CRC64;

Query Match 42.9%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
 ||||  
 Db 6 LPP 8

RESULT 34  
 O15276 PRELIMINARY; PRT; 17 AA.  
 AC O15276;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Mitochondrial translation elongation factor EF-Tu (Fragment).  
 GN TUFM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;

RP SEQUENCE FROM N.A.  
 RA Jacobs H.T., Smurthwaite L., Koshiy R.;  
 RT "Human genomic sequences encoding mitochondrial elongation factor EF-  
 RT Tu: Evidence for post-endosymbiotic intron insertion."  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y11797; CAA72493.1; -.  
 KW Elongation factor.  
 FT NON\_TER 1  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 2019 MW; BF737D12D2AB0A7E CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4

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Db      13 LPP 15
|||||
RESULT 35
O95794 PRELIMINARY; PRT; 17 AA.
AC O95794;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Advanced glycosylation end product-specific receptor (Fragment).
GN RAGE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Blazkova M., Kankova K.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF065210; AAD15887.1; -
DR Receptor.
KW NON TER 1 1
FT VARIANT 10 10 C -> R.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1629 MW; 27FE20FF40E97502 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
Db 11 VLP 13

RESULT 36
O95795 PRELIMINARY; PRT; 17 AA.
AC O95795;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Advanced glycosylation end product-specific receptor (Fragment).
GN RAGE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Blazkova M., Kankova K.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF065211; AAD15888.1; -
DR Receptor.
KW NON TER 1 1
FT VARIANT 9 9 S -> G.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1727 MW; 38C7EB8959E00D72 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
Db 5 VLP 7

RESULT 37
P83061 PRELIMINARY; PRT; 17 AA.
ID P83061

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AC P83061;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE Putative FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans
isomerase) (PPIase) (EC 5.2.1.8) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RA Schubert M., Peterson U., Funk C., Haas B., Schroeder W.P.,
RL Kieselbach T.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR InterPro; IPR001179; FKBP_PPIase.
KW Isomerase; Rotamase; Chloroplast.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1771 MW; E2013F998EBFB908 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
Db 3 LPP 5

RESULT 38
O65373 PRELIMINARY; PRT; 17 AA.
ID O65373
AC O65373;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE ORF 2 minicene.
OS Orgyia pseudotsugata single capsid nuclear polyhedrosis virus
(opsNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10450;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93286576; PubMed=83899803;
RA Russell R.L., Rohrmann G.F.;
RT "Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia
pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
RL J. Gen. Virol. 74:1191-1195(1993).
DR EMBL; D13375; BAA02640.1; -
SQ SEQUENCE 17 AA; 1882 MW; BFEC2A959495FE6A CRC64;

Query Match 42.9%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
Db 2 VLP 4

RESULT 39
Q9RSU2 PRELIMINARY; PRT; 18 AA.
ID Q9RSU2
AC Q9RSU2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE 2-amino-benzoate-CoA LIGASE=E3 (Fragment).  
OS Pseudomonas.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae.  
OX NCBI\_TaxID=286;  
RN [1]  
RN SEQUENCE.  
RP MEDLINE=91358327; PubMed=1885526;  
RA Altenschmidt U., Oswald B., Fuchs G.;  
RT "Purification and characterization of benzoate-coenzyme A ligase and  
RT 2-amino-benzoate-coenzyme A ligases from a denitrifying Pseudomonas  
sp.";  
RL J. Bacteriol. 173:5494-5501(1991).  
FT NON\_TER 1  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2061 MW; C43F8799692771EF CRC64;  
  
Query Match 42.9%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 LPP 4  
Db 12 LPP 14  
  
RESULT 40  
Q9RSF9 PRELIMINARY; PRT; 18 AA.  
ID Q9RSF9  
AC Q9RSF9  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Arsenite oxidase, AOI (Fragment).  
OS Alcaligenes faecalis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Alcaligenaceae; Alcaligenes.  
OX NCBI\_TaxID=511;  
RN [1]  
RN SEQUENCE.  
RP MEDLINE=93054722; PubMed=1331037;  
RA Anderson G.L., Williams J., Hille R.;  
RT "The purification and characterization of arsenite oxidase from  
RT Alcaligenes faecalis, a molybdenum-containing hydroxylase.";  
RL J. Biol. Chem. 267:23674-23682(1992).  
FT NON\_TER 1  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 1938 MW; 4EDDC418B71A4574 CRC64;  
  
Query Match 42.9%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 LPP 4  
Db 9 LPP 11  
  
RESULT 41  
Q9UC58 PRELIMINARY; PRT; 18 AA.  
ID Q9UC58  
AC Q9UC58  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
DE Uronic-acid-rich protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE

RP SEQUENCE.  
RX MEDLINE=95406991; PubMed=7676539;  
RA Atmani F., Khan S.R.;  
RT "Characterization of uronic-acid-rich inhibitor of calcium oxalate  
RT crystallization isolated from rat urine.";  
RL Urol. Res. 23:95-101(1995).  
SQ SEQUENCE 18 AA; 1867 MW; 15DE1BF37294B836 CRC64;  
  
Query Match 42.9%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 VLP 3  
Db 2 VLP 4  
  
RESULT 42  
Q8NFB4 PRELIMINARY; PRT; 18 AA.  
ID Q8NFB4  
AC Q8NFB4  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Mutant enamelin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RA Kida M., Ariga T.;  
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused  
RT by an enamelin gene mutation at exon-intron boundary.";  
RL J. Dent. Res. 0:0-0(2002).  
DR EMBL; AF530444; AAM97323.1; -.  
FT NON\_TER 1  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 1893 MW; 492D2B2E3E8BE512 CRC64;  
  
Query Match 42.9%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 LPP 4  
Db 2 LPP 4  
  
RESULT 43  
Q84129 PRELIMINARY; PRT; 18 AA.  
ID Q84129  
AC Q84129  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg  
DE 8). COOH terminus of NSI (Fragment).  
OS Influenzavirus A.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses.  
OX NCBI\_TaxID=197911;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=83303830; PubMed=6612993;  
RA Parvin J.D., Young J.F., Palese P.;  
RT "nonsense mutations affecting the lengths of the ns1 nonstructural  
RT proteins of influenza A virus isolates.";  
RL Virology 128:512-517(1983).  
DR EMBL; X00959; AAA43541.1; -.  
DR InterPro; IPR000256; Flu\_NS1.  
DR Pfam; PF00600; Flu\_NS1; 1.  
FT NON\_TER 1

SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FFEBEF CRC64;  
Query Match 42.9%; Score 3; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;  
QY 2 LPP 4  
DB 13 LPP 15  
RESULT 44  
Q44608 PRELIMINARY; PRT; 19 AA.  
AC Q44608;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE SHikimate dehydrogenase (Fragment).  
GN AROE  
OS Buchnera aphidicola.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Buchnera.  
OX NCBI\_TaxID=9;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95212914; PubMed=7535281;  
RA Roubaksh D., Baumann P.;  
RT "Characterization of a putative 23S-5S rRNA operon of Buchnera  
RT aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding  
RT gene."  
RL Gene 155:107-112(1995).  
DR EMBL; U10497; AAA79126.1; --  
FT NON\_TER 1  
SQ SEQUENCE 19 AA; 2214 MW; 2C1A573F6A4D01D5 CRC64;  
Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;  
QY 1 VLP 3  
DB 8 VLP 10  
RESULT 45  
Q9RBV1 PRELIMINARY; PRT; 19 AA.  
AC Q9RBV1;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Integrase (Fragment).  
OS Pseudomonas sp. R9.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=101164;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R9; TRANSPOS=Trn1404;  
RX MEDLINE=20011227; PubMed=10543801;  
RA Schnabel E.L., Jones A.L.;  
RT "Distribution of tetracycline resistance genes and transposons among  
RT phylloplane bacteria in Michigan apple orchards."  
RL Appl. Environ. Microbiol. 65:4898-4907(1999).  
DR EMBL; AF157798; AAD47998.1; --  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2065 MW; 19BF26DDCA6290F0 CRC64;  
Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;  
QY 2 LPP 4  
DB 13 LPP 15  
RESULT 46  
Q9R4J9 PRELIMINARY; PRT; 19 AA.  
AC Q9R4J9;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE Catalase-peroxidase (Fragment).  
OS Mycobacterium smegmatis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1772;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95403422; PubMed=7673210;  
RA Marcinkiewicz J.A., Magliozzo R.S., Blanchard J.S.;  
RT "Purification and characterization of the Mycobacterium smegmatis  
RT catalase-peroxidase involved in isoniazid activation."  
RL J. Biol. Chem. 270:22290-22295(1995).  
SQ SEQUENCE 19 AA; 1964 MW; 5A1E4700EFAAB828 CRC64;  
Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;  
QY 3 PPN 5  
DB 9 PPN 11  
RESULT 47  
Q9UR83 PRELIMINARY; PRT; 19 AA.  
AC Q9UR83;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Alcohol acetyltransferase (Fragment).  
OS Saccharomyces cerevisiae (Baker's Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94122444; PubMed=7764365;  
RA Minetoki T., Bogaki T., Iwamatsu A., Fujii T., Hamachi M.;  
RL Biosci. Biotechnol. Biochem. 57:2094-2098(1993).  
SQ SEQUENCE 19 AA; 2155 MW; F3562C9A57F6720A CRC64;  
Query Match 42.9%; Score 3; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;  
QY 5 NVG 7  
DB 9 NVG 11  
RESULT 48  
Q14737 PRELIMINARY; PRT; 19 AA.  
AC Q14737;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Fc receptor (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9618852; PubMed=8614621;
RA Jackson D.A., Bartlett J.M., Cook P.R.;
RT "Sequence attaching loops of nuclear and mitochondrial DNA to
underlying structures in human cells: the role of transcription
units.";
RL Nucleic Acids Res. 24:1212-1219 (1996).
DR EMBL; X91574; CAA62816.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2287 MW; 2381052883584A2F CRC64;

Query Match 42.9%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NVG 7
Db 17 NVG 19

RESULT 49
Q9UC80
ID Q9UC80 PRELIMINARY; PRT; 19 AA.
AC Q9UC80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 21.5 kDa stone matrix protein (EC 1.15.1.1) (Superoxide dismutase
[Mn/Fel]) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95215817; PubMed=7701298;
RA Binette J.P., Binette M.B.;
RT "Sequencing of proteins extracted from stones.";
RL Scanning Microsc. 8:233-239 (1994).
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
KW Oxidoreductase.
SQ SEQUENCE 19 AA; 2116 MW; A0D0DAE848EE7894 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
Db 4 LPP 6

RESULT 50
Q8NFL2
ID Q8NFL2 PRELIMINARY; PRT; 19 AA.
AC Q8NFL2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Prolyl isomerase (Fragment).
GN PINI.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22095969; PubMed=12101225;
RA Ryo A., Liou Y.C., Wulf G., Nakamura M., Lee S.W., Lu K.P.;
RT "PIN1 is an E2F Target Gene Essential for Neu/Ras-Induced
Transformation of Mammary Epithelial Cells.";
RL Mol. Cell. Biol. 22:5281-5295 (2002).
DR EMBL; AF501321; AAM81970.1; -.
KW Isomerase.
FT NON_TER 19 19
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2235 MW; 1C4FC381C8A0F17F CRC64;

Query Match 42.9%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
Db 7 LPP 9

RESULT 51
Q9UC82
ID Q9UC82 PRELIMINARY; PRT; 19 AA.
AC Q9UC82;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 22 kDa stone matrix protein (EC 1.15.1.1) (Superoxide dismutase
[Mn/Fel]) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95215817; PubMed=7701298;
RA Binette J.P., Binette M.B.;
RT "Sequencing of proteins extracted from stones.";
RL Scanning Microsc. 8:233-239 (1994).
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
FAMILY.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
KW Oxidoreductase.
SQ SEQUENCE 19 AA; 2162 MW; AD703A074F3C9655 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
Db 4 VLP 6

RESULT 52
Q9TWQ6
ID Q9TWQ6 PRELIMINARY; PRT; 19 AA.
AC Q9TWQ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Small granule S2 (Fragment).
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
```

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OX NCBI_TaxID=6853;
RN [1]_TaxID=6853;
RP SEQUENCE.
RX MEDLINE=94110249; PubMed=8282718;
RA Shigenaga T., Takayanoki Y., Kawasaki S., Seki N., Muta T., Toh Y.,
RA Ito A., Iwanaga S.;
RL J. Biochem. 114:307-316(1993).
SQ SEQUENCE 19 AA; 2155 MW; 3FCAB879573ED8F6 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6
DB 17 PNV 19

RESULT 53
P82600 PRELIMINARY; PRT; 19 AA.
ID P82600;
AC P82600;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Chorion peroxidase (EC 1.11.1.7).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]_TaxID=7159;
RP SEQUENCE.
RC STRAIN=Liverpool / Blackeye; TISSUE=Ovary;
RX MEDLINE=20326865; PubMed=10871050;
RA Han Q., Li G., Li J.;
RT "Purification and characterization of chorion peroxidase from Aedes
RT aegypti eggs".
RL Arch. Biochem. Biophys. 378:107-115(2000).
RN [2]
RP FUNCTION.
RC STRAIN=Liverpool / Blackeye; TISSUE=Ovary;
RX MEDLINE=97056259; PubMed=8900599;
RA Li J., Hodgeman B.A., Christensen B.M.;
RT "Involvement of peroxidase in chorion hardening in Aedes aegypti.";
RL Insect Biochem. Mol. Biol. 26:309-317(1996).
CC -!- FUNCTION: INVOLVED IN THE FORMATION OF A RIGID AND INSOLUBLE EGG
CC CHORION BY CATALYZING CHORION PROTEIN CROSSLINKING THROUGH
CC DITYROSINE FORMATION.
CC -!- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
CC -!- COFACTOR: BINDS HEME.
CC -!- ENZYME REGULATION: EXTREMELY RESISTANT TO DENATURATING AGENTS,
CC SUCH AS SDS AND ORGANIC SOLVENTS.
CC -!- SUBCELLULAR LOCATION: IN THE CHORION LAYER OF THE MATURE EGGS.
CC -!- MISCELLANEOUS: HAS HIGHEST ACTIVITY AT PH 8.0 WITH GUAIACOL AS A
CC REDUCING AGENT.
KW Oxidoreductase; Glycoprotein; Peroxidase; Heme; Chorion.
FT CARBOHYD 9 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 19 AA; 2172 MW; 022F95BA72E14998 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6
DB 3 PNV 5

RESULT 54
Q8HYW9 PRELIMINARY; PRT; 19 AA.
ID Q8HYW9;
AC Q8HYW9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
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DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium channel alpha-2/delta subunit 1 (Fragment).
GN CACNA2D1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hofstein-Friesian; TISSUE=Leukocyte;
RA Buitkamp J.;
RT "The bovine alpha(2)/delta calcium channel subunit gene (CACNA2D1)
RT maps to chromosome 4 but can be excluded as a candidate for
RT progressive degenerative myeloencephalopathy.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439531; CAD28621.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2143 MW; 4B078FAL355E79E1 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6
DB 16 PNV 18

RESULT 55
O11338 PRELIMINARY; PRT; 19 AA.
ID O11338;
AC O11338;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE H1-7-1 protein (Fragment).
GN H1-7-1.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]_TaxID=10280;
RP SEQUENCE FROM N.A.
RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.;
RT "A Random DNA Sequencing, Computer-Based Approach for the Generation
RT of a Gene Map of Molluscum Contagiosum Virus.";
RL Virus Genes 0:0-0(1997).
DR EMBL; U86916; AAB57971.1; -.
DR InterPro; IPR004900; Pox_P35.
DR Pfam; PF03213; Pox_P35; 1.
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2018 MW; 1BCAF8E98F95ED65 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
DB 12 VLP 14

RESULT 56
Q8KUI9 PRELIMINARY; PRT; 20 AA.
ID Q8KUI9;
AC Q8KUI9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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DE Nitrogen regulatory protein P-II (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]_TaxID=487;
RP SEQUENCE FROM N.A.
RC STRAIN=C11;
RX MEDLINE=22040572; PubMed=12045242;
RA Comanducci M., Bambini S., Brunelli B., Adu-Bobie J., Arico B.,
RA Capocchi B., Giuliani M.M., Maignani V., Santini L., Savino S.,
RA Granoff D.M., Cautant D.A., Pizzo M., Rappuoli R., Mora M.;
RT "Nada, a novel vaccine candidate of Neisseria meningitidis.";
RL J. Exp. Med. 195;1445-1454(2002).
RL EMBL; AF452480; AAM53107.1; -.
DR InterPro; IPR002187; PII_glnB.
DR Pfam; PF00543; P-II; 1.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2165 MW; 5CE529B59D995B5C CRC64;

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
DB 1 VLP 3

RESULT 57
Q9R4F4 PRELIMINARY; PRT; 20 AA.
AC Q9R4F4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CHO cell-ELONGATING TOXIN (Fragment).
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP SEQUENCE.
RX MEDLINE=96123351; PubMed=8559035;
RA McCardell B.A., Madden J.M., Kothary M.H., Sathymoorthy V.;
RT "Purification and characterization of a CHO cell-elongating toxin
RT produced by Aeromonas hydrophila.";
RL Microb. Pathog. 19;1-9(1995).
SQ SEQUENCE 20 AA; 2000 MW; FCB9377F4F27AD02 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NVG 7
DB 8 NVG 10

RESULT 58
Q9UCAB PRELIMINARY; PRT; 20 AA.
AC Q9UCAB;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Tumor-derived adhesion factor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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RX MEDLINE=94161713; PubMed=8117260;
RA Akaogi K., Okabe Y., Funahashi K., Yoshitake Y., Nishikawa K.,
RA Yasumitsu H., Umeda M., Miyazaki K.;
RT "Cell adhesion activity of a 30-kDa major secreted protein from human
RT bladder carcinoma cells.";
RL Biochem. Biophys. Res. Commun. 198;1046-1053(1994).
SQ SEQUENCE 20 AA; 1979 MW; EF6F9DC6DCA0AEBD CRC64;

Query Match 42.9%; Score 3; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
DB 17 LPP 19

RESULT 59
Q9UCE1 PRELIMINARY; PRT; 20 AA.
AC Q9UCE1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Chemotaxin/interleukin 8 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93346069; PubMed=8344717;
RA Suzuki K., Yamakawa Y., Matsuo Y., Kamiya T., Minowada J., Mizuno S.;
RT "Isolation and amino acid sequence of a chemotactic protein, ML-1.";
RT LECT/interleukin 8, from a human myeloid leukemia cell line, ML-1.";
RL Immunol. Lett. 36;71-81(1993).
SQ SEQUENCE 20 AA; 2309 MW; 7FAEGAECFDB7096E CRC64;

Query Match 42.9%; Score 3; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
DB 2 VLP 4

RESULT 60
Q9BME5 PRELIMINARY; PRT; 20 AA.
AC Q9BME5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Actin (Fragment).
OS Bactrocera pyrifoliae.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritoidea; Tephritidae; Bactrocera.
OX NCBI_TaxID=152327;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RA Douglas L.J., Haymer D.S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332589; AAK11635.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2155 MW; 8CD58094D7F89515 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLP 3  
 Db 11 VLP 13  
 RESULT 61  
 Q8MWC9 PRELIMINARY; PRT; 20 AA.  
 AC Q8MWC9; (TREMELrel. 22, Created)  
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
 DT 01-WAR-2003 (TREMELrel. 23, Last annotation update)  
 DE CG30423-PA.  
 GN CG30423.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,  
 RA Foster K.J., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svrtkas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Amanatides P.G., Brandon R.C., Rogers Y., An H., Baldwin D.,  
 RA Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A.,  
 RA Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V.,  
 RA Doup L.E., Doyle C., Drensek D., Farfan D., Ferriera S., Frise E.,  
 RA Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J.,  
 RA Haskins R.A., Hoston D., Howland T.J., Ibegwam C., Jalali M.,  
 RA Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M.,  
 RA Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Paragas V.,  
 RA Park S., Patel S., Pfeiffer B., Phouanavong S., Pittman G.S.,

RA Puri V., Richards S., Scheeler F., Stapleton M., Strong R.,  
 RA Svrtkas R., Tector C., Tyler D., Williams S.M., Zaveri J.S.,  
 RA Smith H.O., Venter J.C.; Rubin G.M.;  
 RT "Sequencing of Drosophila melanogaster genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,  
 RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,  
 RA Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J.,  
 RA Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F.,  
 RA Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Mungall C.J., Lewis S.E.;  
 RT "Annotation of Drosophila melanogaster genome.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003465; AAM70796.1; -;  
 DR FlyBase; FBgn0050423; CG30423.  
 SQ SEQUENCE 20 AA; 2041 MW; DA2A16C89F845EBA CRC64;  
 Query Match 42.9%; Score 3; DB 5; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLP 3  
 Db 17 VLP 19  
 RESULT 62  
 Q3S903 PRELIMINARY; PRT; 20 AA.  
 AC Q3S903;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)  
 DE C2 peptide (Fragment).  
 OS Vigna sinensis (Cowpea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
 OX NCBI\_TaxID=3920;  
 RN (1)  
 RP SEQUENCE.  
 RX MEDLINE=92232221; PubMed=1368037;  
 RA Hirano H., Kagawa H., Okubo K.;  
 RL Phytochemistry 31:731-735(1992).  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2169 MW; C53AD069B17B81FB CRC64;  
 Query Match 42.9%; Score 3; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLP 3  
 Db 11 VLP 13  
 RESULT 63  
 Q9S8K2 PRELIMINARY; PRT; 20 AA.  
 AC Q9S8K2;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-OCT-2001 (TREMELrel. 18, Last annotation update)  
 DE 20 kDa kunitz-type proteinase inhibitor (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.

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OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RX MEDLINE=95093035; PubMed=8000008;
RA Mitumori C., Yanagishi K., Fujino K., Kikuta Y.;
RT "Detection of immunologically related Kunitz and Bowman-Birk.
RT proteinase inhibitors expressed during potato tuber development.";
RL Plant Mol. Biol. 26:961-969(1994).
DR InterPro; IPR002160; Kunitz_legume.
DR Pfam; PF00197; Kunitz_legume; 1.
SQ SEQUENCE 20 AA; 2346 MW; 5641DC473C6E38EC CRC64;

Query Match 42.9%; Score 3; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
DB 2 VLP 4

RESULT 64
Q84860 PRELIMINARY; PRT; 20 AA.
AC Q84860;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 2.0 kDa protein (Fragment).
OS unidentified human poliovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=40278;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87169734; PubMed=3031313;
RA Kuge S., Saito I., Nomoto A.;
RT "Primary structure of poliovirus defective-interfering particle
RT genomes and possible generation mechanisms of the particles.";
RL J. Mol. Biol. 192:473-487(1986).
DR EMBL; M30217; AA86826.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 1997 MW; 07546E99F075818F CRC64;

Query Match 42.9%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3
DB 8 VLP 10

RESULT 65
Q9PRT8 PRELIMINARY; PRT; 20 AA.
AC Q9PRT8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Collagenolytic serine proteinase (Fragment).
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE.
RX MEDLINE=95268699; PubMed=7749622;
RA Kristjansson M.M., Guthmundsdottir S., Fox J.W., Bjarnason J.B.;
RT "Characterization of a collagenolytic serine proteinase from the

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RT Atlantic cod (Gadus morhua).";
RL Comp. Biochem. Physiol. 110B:707-717(1995).
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2364 MW; 6FFC0365A5269269 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPN 5
DB 8 PPN 10

RESULT 66
Q9PRU0 PRELIMINARY; PRT; 20 AA.
AC Q9PRU0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Osteocalcin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=95209705; PubMed=7695644;
RA Gotch Y., Salih E., Glimcher M.J., Gerstenfeld L.C.;
RT "Characterization of the major non-collagenous proteins of chicken
RT bone: identification of a novel 60 kDa non-collagenous
RT phosphoprotein.";
RL Biochem. Biophys. Res. Commun. 208:863-870(1995).
SQ SEQUENCE 20 AA; 2078 MW; 2A519C73A76EB9DC CRC64;

Query Match 42.9%; Score 3; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPN 5
DB 12 PPN 14

RESULT 67
Q9PS38 PRELIMINARY; PRT; 20 AA.
AC Q9PS38;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PO GLYCOPROTEIN-MYELIN major structural protein (Fragment).
OS Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RX MEDLINE=93002191; PubMed=1382532;
RA Karthigasan J., Bauer T.K., Teplow D.B., Saavedra R.A.,
RA Kirschner D.A.;
RT "Phylogenetically conserved amino acids of MBP and P0 from amphibian
RT myelin.";
RL J. Mol. Neurosci. 3:185-188(1992).
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2351 MW; AB238ACED7837676 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NVG 7  
 Db 12 NVG 14

RESULT 68  
 P82232 ID P82232 PRELIMINARY; PRT; 20 AA.  
 AC P82232;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
 DE Brevinin-17.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=SKIN SECRETION;  
 RX MEDLINE=99266278; PubMed=10333736;  
 RA Simmaco M., Mignogna G., Barra D.;  
 RT "Antimicrobial peptides from amphibian skin: what do they tell us?";  
 RL Biopolymers 47:435-450(1998).  
 CC -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST REPRESENTATIVE  
 CC GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIAL SPECIES, AND A VERY  
 CC HIGH HEMOLYTIC ACTIVITY.  
 CC -!- SUBCELLULAR LOCATION: SECRETED.  
 CC -!- TISSUE SPECIFICITY: SKIN.  
 CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GABGURIN/RUGOSIN  
 CC FAMILY.  
 KW Amphibian skin; Antibiotic; Hemolysis.  
 FT DISULFID 14 20 BY SIMILARITY.  
 SQ SEQUENCE 20 AA; 2199 MW; 937236DC8EAE8B84 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
 Db 8 VLP 10

RESULT 69  
 Q08433 ID Q08433 PRELIMINARY; PRT; 4 AA.  
 AC Q08433;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gunn;  
 RX MEDLINE=91282758; PubMed=1840486;  
 RA Sato H., Aono S., Kashiwata S., Koiwai O.;  
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
 RT hyperbilirubinemic Gunn rat.";  
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).  
 DR EMBL; S38636; AAB19259.1; -;  
 KW Transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 28.6%; Score 2; DB 11; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
 Db 2 VL 3

RESULT 70  
 P83308 ID P83308 PRELIMINARY; PRT; 5 AA.  
 AC P83308;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE FMRPamide-like neuropeptide (LPLRF-amide).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RX PubMed=6137771;  
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
 RT "A novel active pentapeptide from chicken brain identified by  
 RT antibodies to FMRPamide.";  
 RL Nature 305:328-330(1983).  
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 28.6%; Score 2; DB 13; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
 Db 1 LP 2

RESULT 71  
 O50556 ID O50556 PRELIMINARY; PRT; 7 AA.  
 AC O50556;  
 DT 01-JUN-1998 (TReMBLrel. 06, Created)  
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE GLYA (Fragment).  
 GN GLYA.  
 OS Actinobacillus actinomycetemcomitans (Haemophilus  
 OS actinomycetemcomitans).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Actinobacillus.  
 OX NCBI\_TaxID=714;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33384;  
 RX MEDLINE=96355846; PubMed=8751884;  
 RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,  
 RA Kraig E.;  
 RT "cis Elements and trans factors are both important in strain-specific  
 RT regulation of the leukotoxin gene in Actinobacillus  
 RT actinomycetemcomitans.";  
 RL Infect. Immun. 64:3451-3460(1996).  
 DR EMBL; U51862; AAB88721.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
||  
Db 3 LP 4

## RESULT 72

Q47029 PRELIMINARY; PRT; 7 AA.  
AC Q47029  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Aad A1 protein (Fragment).  
GN AAD A1.  
OS Enterobacter cloacae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxID=550;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94079349; PubMed=8257126;  
RA Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;  
RT "Analysis of the aac(3)-Via gene encoding a novel 3-N-  
RT acetyltransferase."  
RL Antimicrob. Agents Chemother. 37:2074-2079(1993).  
DR EMBL; M88012; AAA16193.1; --  
FT NON\_TER  
SQ SEQUENCE 7 AA; 744 MW; 633862D2C321A030 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VG 7  
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Db 5 VG 6

## RESULT 73

P92214 PRELIMINARY; PRT; 7 AA.  
ID P92214  
AC P92214  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Amblyopyrum muticum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Amblyopyrum.  
OX NCBI\_TaxID=4595;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=H5572; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77756; CAB01346.1; --  
FT Chloroplast.  
KW NON\_TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4

Db 1 PP 2  
||

## RESULT 74

P92393 PRELIMINARY; PRT; 7 AA.  
ID P92393  
AC P92393  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Hordeum vulgare (Barley).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=H3139; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77764; CAB01370.1; --  
FT Chloroplast.  
KW NON\_TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PP 4  
||  
Db 1 PP 2

## RESULT 75

P92403 PRELIMINARY; PRT; 7 AA.  
ID P92403  
AC P92403  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Lophopyrum.  
OX NCBI\_TaxID=4588;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=H6692; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77743; CAB01307.1; --  
FT Chloroplast.  
KW NON\_TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 pp 4  
||  
Db 1 pp 2

Search completed: November 25, 2003, 18:25:40  
Job time : 17.917 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 22.6755 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-17

Perfect score: 7  
Sequence: 1 VLPPNVG 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 15872573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
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- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	22	Colostrin derive
2	7	100.0	7	22	Colostrin peptid
3	7	100.0	7	22	Colostrin peptid
4	7	100.0	7	22	Ewe colostrin pe
5	7	100.0	7	23	Colostrin consti
6	7	100.0	7	23	Colostrin consti
7	7	100.0	7	23	Neural cell regula
8	7	100.0	9	22	Ewe colostrin pe
9	5	71.4	11	22	Vascular dementia-

10	5	71.4	11	22	ABBS2007	Human API-4 trypti
11	5	71.4	11	22	ABBS2121	Human API-201 trypt
12	5	71.4	11	22	AAU28427	DPI tryptic digest
13	5	71.4	11	22	AAU28430	DPI tryptic digest
14	5	71.4	11	22	AAU28620	DPI tryptic digest
15	5	71.4	11	22	AAU28625	DPI tryptic digest
16	5	71.4	11	22	AAU28832	DPI tryptic digest
17	5	71.4	11	22	AAU28870	DPI tryptic digest
18	5	71.4	11	22	AAU24911	Schizophrenia-Asso
19	5	71.4	11	22	AAU26073	Schizophrenia-Asso
20	5	71.4	11	22	AAU26076	Depression-Asso
21	5	71.4	11	22	AAU26268	Depression-Asso
22	5	71.4	11	22	AAU26273	Depression-Asso
23	5	71.4	11	22	AAU26480	Depression-Asso
24	5	71.4	11	22	AAU26518	Depression-Asso
25	5	71.4	11	22	AAU15255	Schizophrenia-Asso
26	5	71.4	11	22	ABG78535	Multiple sclerosis
27	5	71.4	11	22	ABP57182	Breast cancer asso
28	5	71.4	14	22	AAU96974	Human peptide #249
29	4	57.1	4	22	AAU79766	Chicken bone deriv
30	4	57.1	6	17	AAU90467	Antibody 561 diapl
31	4	57.1	6	20	AAU55202	Anti CD34 antibody
32	4	57.1	6	21	AAU86948	Human haematopoiet
33	4	57.1	7	19	AAW66740	Dolastatin-15 deri
34	4	57.1	7	20	AAW08842	Dolastatin-15 deri
35	4	57.1	7	20	AAW08835	Peptide which bind
36	4	57.1	7	22	AAU79265	Bacteriophage Type
37	4	57.1	7	22	AAE09112	Consensus sequence
38	4	57.1	8	22	AAU35601	Sequence of trypsi
39	4	57.1	9	15	AAU50242	Rabbit 50 kDa dyst
40	4	57.1	9	16	AAU80233	Immunogenic epitop
41	4	57.1	9	18	AAU31595	158P1D7 related HL
42	4	57.1	9	23	ABJ01310	158P1D7 related HL
43	4	57.1	9	23	ABJ01313	158P1D7 related HL
44	4	57.1	9	23	ABJ01333	158P1D7 related HL
45	4	57.1	9	23	ABJ01433	158P1D7 related HL
46	4	57.1	9	23	ABJ01511	158P1D7 related HL
47	4	57.1	9	23	ABJ01798	158P1D7 related HL
48	4	57.1	9	23	ABJ01886	158P1D7 related HL
49	4	57.1	9	24	ABU11109	House dust mite De
50	4	57.1	10	18	AAU14897	Phakellistatin 8.
51	4	57.1	10	18	AAU14898	Phakellistatin 9.
52	4	57.1	10	22	AAE05732	Complementarity-de
53	4	57.1	10	23	ABJ01356	158P1D7 related HL
54	4	57.1	10	23	ABJ01361	158P1D7 related HL
55	4	57.1	10	23	ABJ01456	158P1D7 related HL
56	4	57.1	10	23	ABJ01461	158P1D7 related HL
57	4	57.1	10	23	ABJ01479	158P1D7 related HL
58	4	57.1	10	23	ABJ01586	158P1D7 related HL
59	4	57.1	10	23	ABJ01936	158P1D7 related HL
60	4	57.1	10	24	ABG75571	CDR3 peptide seque
61	4	57.1	11	15	AAU7937	Peptide fragment o
62	4	57.1	11	18	AAU45201	Vasoactive intesti
63	4	57.1	11	21	AAU21131	Src homology 3 dom
64	4	57.1	11	21	AAU17502	VIP-mimetic peptid
65	4	57.1	11	21	AAU17522	VIP-mimetic peptid
66	4	57.1	11	22	AAU69073	Bacterial conserve
67	4	57.1	11	23	AAU97808	Synthetic thrombop
68	4	57.1	11	23	ABU73104	VIP mimetic peptid
69	4	57.1	11	23	ABU73124	VIP mimetic peptid
70	4	57.1	12	21	AAU51854	Human secreted pro
71	4	57.1	12	23	ABU05302	Polyurethane and n
72	4	57.1	12	23	ABU04979	Bovine adenovirus
73	4	57.1	13	19	AAU20712	Human neurofilamen
74	4	57.1	13	22	AAU68459	Mutated peptide de
75	4	57.1	13	24	ABP81154	Human TPO peptide
76	4	57.1	13	24	ABP81155	Human TPO peptide
77	4	57.1	14	21	AAU51609	Human soluble guan
78	4	57.1	14	22	ABU56650	Human SNP related
79	4	57.1	14	22	AAU98337	Human peptide #161
80	4	57.1	15	12	AAU10926	Serine-threonine r
81	4	57.1	15	18	AAU27074	Proline rich pepti
82	4	57.1	15	21	AAU65571	Oestrogen receptor

83 4 57.1 15 23 AAM49479 Human zinc finger  
 84 4 57.1 15 23 ABP46214 Human BLYS binding  
 85 4 57.1 15 23 AAU79923 Blue tongue virus-  
 86 4 57.1 15 23 AAU86308 Oestrogen receptor  
 87 4 57.1 15 23 AAG68277 Human phospholipase  
 88 4 57.1 16 12 AAR15234 CD46 exon 7 (STP A  
 89 4 57.1 16 18 AAW25416 Crk N-terminal SH3  
 90 4 57.1 16 18 AAW39007 Peptide resembling  
 91 4 57.1 16 18 AAW25377 Src SH3 domain bin  
 92 4 57.1 16 20 AAY40685 A3 derivative #6,  
 93 4 57.1 16 21 AAB30024 Scaffold protein S  
 94 4 57.1 16 22 AAB35608 Peptide associated  
 95 4 57.1 16 23 ABG62278 Eubacterial DNA po  
 96 4 57.1 17 21 AAB38498 Fragment of human  
 97 4 57.1 17 24 AAE32986 Human sperm activa  
 98 4 57.1 18 14 AAR37012 18-35 peptide A.  
 99 4 57.1 18 18 AAW43656 Bactericidal/perme  
 100 4 57.1 18 19 AAW66650 HSV-2 glycoprotein

## ALIGNMENTS

## RESULT 1

ID AAB72262 standard; peptide; 7 AA.  
 XX

AC AAB72262;  
 XX

DT 14-MAY-2001 (first entry)  
 XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 17.  
 XX

KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.

XX WO200111937-A2.  
 PN

XX 22-FEB-2001.  
 PD

XX 17-AUG-2000; 2000WO-US22818.  
 PF

XX 17-AUG-1999; 99US-0149311.  
 PR

XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA

PA (REG- ) REGEN THERAPEUTICS PLC.  
 XX

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 PI

XX WPI; 2001-202804/20.  
 DR

XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator .  
 XX

PS Claim 1; Page 34; 50pp; English.  
 XX

CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX  
 SQ

Sequence 7 AA;

Query Match 100.0%; Score 7; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPPNVG 7  
 |||||

Db 1 VLPPNVG 7  
 |||||

## RESULT 2

AAB72515

ID AAB72515 standard; Peptide; 7 AA.

XX AAB72515;  
 AC

XX 09-MAY-2001 (first entry)  
 DT

XX Colostrinin peptide #16.  
 DE

XX Dermatological; oxidative stress regulator; colostrinin.  
 KW

XX Unidentified.  
 OS

XX WO200112650-A2.  
 PN

XX 22-FEB-2001.  
 PD

XX 17-AUG-2000; 2000WO-US22665.  
 PF

XX 17-AUG-1999; 99US-0149310.  
 PR

XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA

XX Stanton GJ, Hughes TK, Boldogh I;  
 PI

XX WPI; 2001-218342/22.  
 DR

XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations .  
 PT  
 PS Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.

XX  
 SQ

Sequence 7 AA;

Query Match 100.0%; Score 7; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPPNVG 7  
 |||||

Db 1 VLPPNVG 7  
 |||||

## RESULT 3

AAB72547

ID AAB72547 standard; Peptide; 7 AA.

XX AAB72547;  
 AC

XX 09-MAY-2001 (first entry)  
 DT

XX



DE Colostrinin peptide #16.  
XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.  
XX Unidentified.  
OS  
XX  
XX WO200112651-A2.  
XX  
XX PD 22-FEB-2001.  
XX  
XX PF 17-AUG-2000; 2000WO-US22774.  
XX  
XX PR 17-AUG-1999; 99US-0149633.  
XX  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX PI Boldogh I;  
XX  
XX DR WPI; 2001-226545/23.  
XX  
XX PT Use of colostrinin, its constituent peptide or analog as a neural cell  
PT regulator, for promoting neural cell differentiation and treating  
PT damaged neural cells in a patient -  
XX  
XX PS Claim 6; Page 21; 35pp; English.  
XX  
XX CC The present invention relates to a method for promoting neural cell  
CC differentiation and treating damaged neural cells, using colostrinin and  
CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
XX  
XX SQ Sequence 7 AA;  
  
Query Match 100.0%; Score 7; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VLPPNVG 7  
DB 1 VLPPNVG 7  
|||||  
|||||  
1 VLPPNVG 7  
  
RESULT 5  
AAE20244  
ID AAE20244 standard; peptide; 7 AA.  
XX  
XX AC AAE20244;  
XX  
XX DT 18-JUN-2002 (first entry)  
XX  
XX DE Colostrinin constituent peptide #16.  
XX  
XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnary.  
XX  
XX OS Unidentified.  
XX  
XX FH Key Location/Qualifiers  
ET Modified-site 7 /note= "Optionally C-terminal amide"  
FT  
XX  
XX FN WO200213850-A1.  
XX  
XX PD 21-FEB-2002.  
XX  
XX PF 17-AUG-2000; 2000WO-US22776.  
XX  
XX PR 17-AUG-2000; 2000WO-US22776.  
XX  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX PI Stanton GJ, Hughes TK, Boldogh I;  
XX  
XX DR WPI; 2002-269151/31.  
XX  
XX PT Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog -  
XX  
XX PS Claim 6; Page 25; 51pp; English.  
XX  
XX CC The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress  
CC level in a cell e.g. mammalian or human cell present in a cell culture,  
CC tissue, organ, or organism; or for treating oxidative damage to the skin  
CC of a patient e.g. animal or human; to modulate oxidative stress during/  
  
DE Colostrinin peptide #16.  
XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.  
XX Unidentified.  
OS  
XX  
XX PN WO200112651-A2.  
XX  
XX PD 22-FEB-2001.  
XX  
XX PF 17-AUG-2000; 2000WO-US22774.  
XX  
XX PR 17-AUG-1999; 99US-0149633.  
XX  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX PI Boldogh I;  
XX  
XX DR WPI; 2001-226545/23.  
XX  
XX PT Use of colostrinin, its constituent peptide or analog as a neural cell  
PT regulator, for promoting neural cell differentiation and treating  
PT damaged neural cells in a patient -  
XX  
XX PS Claim 6; Page 21; 35pp; English.  
XX  
XX CC The present invention relates to a method for promoting neural cell  
CC differentiation and treating damaged neural cells, using colostrinin and  
CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
XX  
XX SQ Sequence 7 AA;  
  
Query Match 100.0%; Score 7; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VLPPNVG 7  
DB 1 VLPPNVG 7  
|||||  
|||||  
1 VLPPNVG 7  
  
RESULT 4  
AAB59316  
ID AAB59316 standard; Peptide; 7 AA.  
XX  
XX AC AAB59316;  
XX  
XX DT 21-MAR-2001 (first entry)  
XX  
XX DE Ewe colostrinin peptide fragment B-1.  
XX  
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX  
XX OS Ovis sp.  
XX  
XX PN WO200075173-A2.  
XX  
XX PD 14-DEC-2000.  
XX  
XX PF 02-JUN-2000; 2000WO-GB02128.  
XX  
XX PR 02-JUN-1999; 99GB-0012852.  
XX  
XX PA (REGE-) REGEN THERAPEUTICS PLC.  
XX  
XX PI Georgiades JA;  
XX  
XX DR WPI; 2001-071058/08.  
XX  
XX PT Peptides having an N-terminal amino acid sequence isolated from

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPPNVG 7  
 |||||  
 Db 1 VLPPNVG 7

RESULT 6

AA051051  
 ID AAM51051 standard; Peptide; 7 AA.

XX AC AAM51051;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide.

CC Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; beta-casein; human.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Modified-site 7  
 FT /note= "Optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. It is  
 CC classified as having a beta-casein homologue precursor. Methods  
 CC are claimed for: inducing a cytokine in a cell by contact with an  
 CC immunological regulator, where the cell is present in a cell  
 CC culture, a tissue, an organ or an organism, and the cell is  
 CC mammalian, including human; modulating an immune response in a cell  
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator  
 CC is administered topically or as part of a dietary supplement, and  
 CC where the immune response is specific or non specific; an interferon  
 CC response or an antibody response; modulating blood cell proliferation  
 CC by contacting blood cells with a blood cell regulator, where the  
 CC blood cells are present in a cell culture or an organism, are  
 CC mammalian or human, and where the blood cells are increased in  
 CC number or differentiated; and a method for modulating blood cell  
 CC proliferation in a patent. A claimed cytokine-inducing composition  
 CC comprises a pharmaceutical carrier and an active agent such as the  
 CC present peptide. Cytokines induced by this peptide in human  
 CC leucocyte cultures include interferon-gamma, tumour necrosis  
 CC factor-alpha, interleukin-6 and interleukin-10. It was one of the  
 CC best overall inducers in almost all cytokine and blood cell  
 CC proliferation experiments conducted.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPPNVG 7  
 |||||  
 Db 1 VLPPNVG 7

RESULT 7

AA014593  
 ID AAO14593 standard; peptide; 7 AA.

XX AC AAO14593;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 16.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 XX neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers  
 FH Modified-site 7  
 FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich

CC polypeptide aggregate that is present in colostrum. The method of the  
CC invention is useful for promoting the differentiation of cells and for  
CC treating damaged neural cells in a patient. The present amino acid  
CC sequence represents a specifically claimed colostrinin peptide used in  
CC the method of the invention.

SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPPNVG 7  
Db 1 VLPPNVG 7  
|||||

RESULT 8  
AAB59346  
ID AAB59346 standard; Peptide; 9 AA.  
XX AC AAB59346;  
XX DT 21-MAR-2001 (first entry)  
XX DE Ewe colostrinin peptide fragment derived sequence #6.  
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX OS Ovis sp.  
XX WO200075173-A2.  
XX PD 14-DEC-2000.  
XX PF 02-JUN-2000; 2000WO-GB02128.  
XX PR 02-JUN-1999; 99GB-0012852.  
XX PA (REG- ) REGEN THERAPEUTICS PLC.  
XX PI Georgiades JA;  
XX WPI; 2001-071058/08.  
XX PT Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system  
PT and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -  
XX Claim 8; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrum. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.

SQ Sequence 9 AA;  
Query Match 100.0%; Score 7; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPPNVG 7  
Db 3 VLPPNVG 9  
|||||

RESULT 9  
AAB56038  
ID AAB56038 standard; Peptide; 11 AA.  
XX AC AAB56038;  
XX DT 15-FEB-2002 (first entry)  
XX DE Vascular dementia-associated protein isoform (VPI) 238.  
XX KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;  
KW diagnosis; prognosis; gene therapy.  
XX OS Homo sapiens.  
XX PN WO200169261-A2.  
XX PD 20-SEP-2001.  
XX PF 14-MAR-2001; 2001WO-GB01106.  
XX PR 15-MAR-2000; 2000GB-0006285.  
XX PR 24-NOV-2000; 2000GB-0028734.  
XX PR 28-NOV-2000; 2000US-0724391.  
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX PI Herath HMAc, Parekh RB, Rohlf C;  
XX WPI; 2001-557937/62.  
XX PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for  
PT determining stage of VD and monitoring the effect of VD therapy,  
PT comprises analysing body fluid by 2-dimensional electrophoresis for  
PT features correlated with VD -  
XX Claim 6; Page 34; 151pp; English.

CC The invention relates to screening, diagnosis or prognosis of Vascular  
CC Dementia (VD) in a subject comprising analysing body fluid from the  
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of  
CC features containing at least one chosen feature whose relative abundance  
CC correlates with the presence, absence, stage or severity of VD or  
CC predicts the onset or course of VD, especially detecting in a sample of  
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated  
CC protein isoforms (VPIs) (AAB55801-AAB56295) as fully defined in the  
CC specification. Detecting VD-associated features and VPI is useful for the  
CC screening, diagnosis or prognosis of VD, for determining the stage or  
CC severity of VD, for identifying a subject at risk of VD or for  
CC monitoring the effect of therapy administered to a subject having VD.  
CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are  
CC useful for the treatment of VD and for gene therapy.

SQ Sequence 11 AA;  
Query Match 71.4%; Score 5; DB 22; Length 11;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6  
Db 1 LPPNV 5  
|||||

RESULT 10  
AAB52007  
ID AAB52007 standard; Peptide; 11 AA.  
XX AC AAB52007;  
XX DT 08-FEB-2002 (first entry)  
XX DE Human API-4 tryptic digest peptide #3.

```
XX Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX Homo sapiens.
OS
XX WO200175454-A2.
PN
XX
XX
PD 11-OCT-2001.
XX
XX
PF 03-APR-2001; 2001WO-US10908.
XX
XX
PR 03-APR-2000; 2000US-194504P.
XX
PR 28-NOV-2000; 2000US-253647P.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ ) PFIZER INC.
XX
XX Durham KL, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
XX WPI; 2001-639384/73.
XX
XX Screening for Alzheimer's disease in a mammal, by making
PT two-dimensional array of a feature whose relative abundance correlates
PT with disease, and comparing with abundance of the feature in samples of
PT healthy persons -
XX
XX Example; Page 25; 162pp; English.
XX
XX The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection
CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
CC serum or plasma. The abundance of the AFs and APIs is then
CC normalised to an Expression Reference Protein Isoform (ERPI) in
CC order to determine whether a patient is suffering from, or has
CC a predisposition to, Alzheimer's Disease. The relative abundance of
CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
CC The present sequence is a peptide produced from an API by proteolysis.
XX
SQ Sequence 11 AA;
Query Match 71.4%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6
Db |||||
1 LPPNV 5

RESULT 11
ABB52121
ID ABB52121 standard; Peptide; 11 AA.
XX
XX ABB52121;
AC
XX
DT 08-FEB-2002 (first entry)
DE
XX Human API-201 tryptic digest peptide.
XX
XX Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
XX Homo.sapiens.
OS
XX WO200175454-A2.
PN
```

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XX 11-OCT-2001.
PD
XX
PF 03-APR-2001; 2001WO-US10908.
XX
XX
PR 03-APR-2000; 2000US-194504P.
XX
PR 28-NOV-2000; 2000US-253647P.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ ) PFIZER INC.
XX
XX Durham KL, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
XX WPI; 2001-639384/73.
XX
XX Screening for Alzheimer's disease in a mammal, by making
PT two-dimensional array of a feature whose relative abundance correlates
PT with disease, and comparing with abundance of the feature in samples of
PT healthy persons -
XX
XX Example; Page 28; 162pp; English.
XX
XX The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection
CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
CC serum or plasma. The abundance of the AFs and APIs is then
CC normalised to an Expression Reference Protein Isoform (ERPI) in
CC order to determine whether a patient is suffering from, or has
CC a predisposition to, Alzheimer's Disease. The relative abundance of
CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
CC The present sequence is a peptide produced from an API by proteolysis.
XX
SQ Sequence 11 AA;
Query Match 71.4%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6
Db |||||
1 LPPNV 5

RESULT 12
AAU28427
ID AAU28427 standard; Peptide; 11 AA.
XX
XX AAU28427;
AC
XX
DT 03-JAN-2002 (first entry)
DE
XX DPI tryptic digest peptide #24.
XX
XX Human; depression associated protein isoform; tryptic digest peptide;
KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
KW maniac-depressive illness; schizoaffective disorder.
XX
XX Homo sapiens.
OS
XX WO200162787-A1.
PN
XX
XX 30-AUG-2001.
PD
XX
XX 23-FEB-2001; 2001WO-GB00786.
PF
XX
XX 24-FEB-2000; 2000GB-0004412.
PR
XX 08-DEC-2000; 2000GB-0030050.
PR
XX 12-DEC-2000; 2000US-0254830.
XX
```

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX Herath HMCAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
 XX WPI; 2001-570626/64.  
 DR Novel nucleic acid encoding a protein associated with bipolar affective  
 XX disorder, which is used for diagnosis, prophylaxis and therapy of  
 PT neuropsychiatric disorders, such as bipolar affective disorder -  
 PT neuropsychiatric disorders, such as bipolar affective disorder -  
 XX  
 XX Disclosure; Page 31; 153pp; English.  
 XX The present invention relates to the identification of depression  
 CC associated protein isoforms (DPIs), particularly the tryptic digest  
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD  
 CC (bipolar affective disorder) subjects, whilst other DPIs  
 CC (AAU28626-AAU28887) are increased in BAD subjects. Also described  
 CC are peptide sequences identified from DPI-45 and DPI-213 and the  
 CC nucleic acid sequences they are encoded by. The sequences of the  
 CC invention are useful for clinical screening, diagnosis, prognosis,  
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also  
 CC known as bipolar mood disorder, BP), maniac-depressive illnesses,  
 CC attention deficit disorders, schizoaffective disorders, and unipolar  
 CC affective disorders. The present sequence represents one of the DPI  
 CC tryptic digest peptides of the present invention.  
 XX  
 XX Sequence 11 AA;  
 SQ

Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LPPNV 6  
 DB 1 LPPNV 5  
 |||||

RESULT 13  
 AAU28430  
 ID AAU28430 standard; Peptide; 11 AA.  
 XX AC AAU28430;  
 XX 03-JAN-2002 (first entry)  
 XX DPI tryptic digest peptide #27.  
 XX Human; depression associated protein isoform; tryptic digest peptide;  
 KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;  
 KW maniac-depressive illness; schizoaffective disorder.  
 XX Homo sapiens.  
 XX WO200162787-A1.  
 XX 30-AUG-2001.  
 XX 23-FEB-2001; 2001WO-GB00786.  
 XX 24-FEB-2000; 2000GB-0004412.  
 XX 08-DEC-2000; 2000GB-0030050.  
 XX 12-DEC-2000; 2000US-0254830.  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX Herath HMCAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
 XX WPI; 2001-570626/64.  
 XX Novel nucleic acid encoding a protein associated with bipolar affective  
 PT disorder, which is used for diagnosis, prophylaxis and therapy of

PT neuropsychiatric disorders, such as bipolar affective disorder -  
 XX Disclosure; Page 31; 153pp; English.  
 XX The present invention relates to the identification of depression  
 CC associated protein isoforms (DPIs), particularly the tryptic digest  
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD  
 CC (bipolar affective disorder) subjects, whilst other DPIs  
 CC (AAU28626-AAU28887) are increased in BAD subjects. Also described  
 CC are peptide sequences identified from DPI-45 and DPI-213 and the  
 CC nucleic acid sequences they are encoded by. The sequences of the  
 CC invention are useful for clinical screening, diagnosis, prognosis,  
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also  
 CC known as bipolar mood disorder, BP), maniac-depressive illnesses,  
 CC attention deficit disorders, schizoaffective disorders, and unipolar  
 CC affective disorders. The present sequence represents one of the DPI  
 CC tryptic digest peptides of the present invention.  
 XX  
 XX Sequence 11 AA;  
 SQ

Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LPPNV 6  
 DB 1 LPPNV 5  
 |||||

RESULT 14  
 AAU28620  
 ID AAU28620 standard; Peptide; 11 AA.  
 XX AC AAU28620;  
 XX 03-JAN-2002 (first entry)  
 XX DPI tryptic digest peptide #217.  
 XX Human; depression associated protein isoform; tryptic digest peptide;  
 KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;  
 KW maniac-depressive illness; schizoaffective disorder.  
 XX Homo sapiens.  
 XX WO200162787-A1.  
 XX 30-AUG-2001.  
 XX 23-FEB-2001; 2001WO-GB00786.  
 XX 24-FEB-2000; 2000GB-0004412.  
 XX 08-DEC-2000; 2000GB-0030050.  
 XX 12-DEC-2000; 2000US-0254830.  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX Herath HMCAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
 XX WPI; 2001-570626/64.  
 XX Novel nucleic acid encoding a protein associated with bipolar affective  
 PT disorder, which is used for diagnosis, prophylaxis and therapy of  
 PT neuropsychiatric disorders, such as bipolar affective disorder -  
 XX Disclosure; Page 35; 153pp; English.  
 XX The present invention relates to the identification of depression  
 CC associated protein isoforms (DPIs), particularly the tryptic digest  
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD

CC (bipolar affective disorder) subjects, whilst other DPIs  
 CC (AAU28626-AAU2887) are increased in BAD subjects. Also described  
 CC are peptide sequences identified from DPI-45 and DPI-213 and the  
 CC nucleic acid sequence they are encoded by. The sequences of the  
 CC invention are useful for clinical screening, diagnosis, prognosis,  
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also  
 CC known as bipolar mood disorder, BP), maniac-depressive illnesses,  
 CC attention deficit disorders, schizoaffective disorders, and unipolar  
 CC affective disorders. The present sequence represents one of the DPI  
 CC tryptic digest peptides of the present invention.

XX  
 SQ Sequence 11 AA;

Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6  
 Db 1 LPPNV 5  
 |||||

RESULT 15  
 AAU28625  
 ID AAU28625 standard; Peptide; 11 AA.  
 XX  
 AC AAU28625;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE DPI tryptic digest peptide #222.  
 XX  
 KW Human; depression associated protein isoform; tryptic digest peptide;  
 KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;  
 KW maniac-depressive illness; schizoaffective disorder.

XX Homo sapiens.  
 XX WO200162787-A1.  
 XX 30-AUG-2001.  
 XX 23-FEB-2001; 2001WO-GB00786.  
 XX 24-FEB-2000; 2000GB-0004412.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herath HMCAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
 XX  
 WPI; 2001-570626/64.  
 XX  
 PT Novel nucleic acid encoding a protein associated with bipolar affective  
 PT disorder, which is used for diagnosis, prophylaxis and therapy of  
 PT neuropsychiatric disorders, such as bipolar affective disorder -  
 XX  
 PS Disclosure; Page 35; 153pp; English.

CC The present invention relates to the identification of depression  
 CC associated protein isoforms (DPIs), particularly the tryptic digest  
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD  
 CC (bipolar affective disorder) subjects, whilst other DPIs  
 CC (AAU28626-AAU2887) are increased in BAD subjects. Also described  
 CC are peptide sequences identified from DPI-45 and DPI-213 and the  
 CC nucleic acid sequence they are encoded by. The sequences of the  
 CC invention are useful for clinical screening, diagnosis, prognosis,  
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also  
 CC known as bipolar mood disorder, BP), maniac-depressive illnesses,  
 CC attention deficit disorders, schizoaffective disorders, and unipolar  
 CC affective disorders. The present sequence represents one of the DPI  
 CC tryptic digest peptides of the present invention.

XX  
 SQ Sequence 11 AA;

Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC affective disorders. The present sequence represents one of the DPI  
 CC tryptic digest peptides of the present invention.

XX  
 SQ Sequence 11 AA;

Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6  
 Db 1 LPPNV 5  
 |||||

RESULT 16  
 AAU28832  
 ID AAU28832 standard; Peptide; 11 AA.  
 XX  
 AC AAU28832;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE DPI tryptic digest peptide #429.  
 XX  
 KW Human; depression associated protein isoform; tryptic digest peptide;  
 KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;  
 KW maniac-depressive illness; schizoaffective disorder.

XX Homo sapiens.  
 XX WO200162787-A1.  
 XX 30-AUG-2001.  
 XX 23-FEB-2001; 2001WO-GB00786.  
 PR 24-FEB-2000; 2000GB-0004412.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herath HMCAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
 XX  
 WPI; 2001-570626/64.  
 XX  
 PT Novel nucleic acid encoding a protein associated with bipolar affective  
 PT disorder, which is used for diagnosis, prophylaxis and therapy of  
 PT neuropsychiatric disorders, such as bipolar affective disorder -  
 XX  
 PS Disclosure; Page 39; 153pp; English.

CC The present invention relates to the identification of depression  
 CC associated protein isoforms (DPIs), particularly the tryptic digest  
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD  
 CC (bipolar affective disorder) subjects, whilst other DPIs  
 CC (AAU28626-AAU2887) are increased in BAD subjects. Also described  
 CC are peptide sequences identified from DPI-45 and DPI-213 and the  
 CC nucleic acid sequence they are encoded by. The sequences of the  
 CC invention are useful for clinical screening, diagnosis, prognosis,  
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also  
 CC known as bipolar mood disorder, BP), maniac-depressive illnesses,  
 CC attention deficit disorders, schizoaffective disorders, and unipolar  
 CC affective disorders. The present sequence represents one of the DPI  
 CC tryptic digest peptides of the present invention.

XX  
 SQ Sequence 11 AA;

Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPPNV 6  
 |||||  
 Db 1 LPPNV 5

RESULT 17  
 AAU28870  
 ID AAU28870 standard; Peptide; 11 AA.  
 AC  
 XX  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE DPI tryptic digest peptide #467.  
 XX  
 KW Human; depression associated protein isoform; tryptic digest peptide;  
 KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;  
 KW maniac-depressive illness; schizoaffective disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200162787-A1.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-GB00786.  
 XX  
 PR 24-FEB-2000; 2000GB-0004412.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herath HMC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
 XX  
 DR WPI; 2001-570626/64.  
 XX  
 PT Novel nucleic acid encoding a protein associated with bipolar affective  
 disorder, which is used for diagnosis, prophylaxis and therapy of  
 PT neuropsychiatric disorders, such as bipolar affective disorder -  
 XX  
 PS Disclosure; Page 40; 153pp; English.  
 XX  
 CC The present invention relates to the identification of depression  
 CC associated protein isoforms (DPIs), particularly the tryptic digest  
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD  
 CC (bipolar affective disorder) subjects, whilst other DPIs  
 CC (AAU28626-AAU28887) are increased in BAD subjects. Also described  
 CC are peptide sequences identified from DPI-45 and DPI-213 and the  
 CC nucleic acid sequences they are encoded by. The sequences of the  
 CC invention are useful for clinical screening, diagnosis, prognosis,  
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also  
 CC known as bipolar mood disorder, BP), maniac-depressive illnesses,  
 CC attention deficit disorders, schizoaffective disorders, and bipolar  
 CC affective disorders. The present sequence represents one of the DPI  
 CC tryptic digest peptides of the present invention.  
 XX  
 SQ Sequence 11 AA;

Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPPNV 6  
 |||||  
 Db 1 LPPNV 5

RESULT 19  
 AAU26073  
 ID AAU26073 standard; Peptide; 11 AA.  
 XX  
 AC AAU26073;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Depression-Associated Protein isoform DPI-105 #2.  
 XX  
 KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
 KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;  
 KW attention deficient disorder; schizoaffective disorder;  
 KW unipolar affective disorder.  
 XX  
 OS Homo sapiens.  
 XX

AAU24911 standard; Peptide; 11 AA.  
 AAU24911;  
 18-DEC-2001 (first entry)  
 Schizophrenia-Associated Protein Isoform (SPI) peptide #140.  
 Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;  
 neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.  
 Homo sapiens.  
 WO200162785-A2.  
 30-AUG-2001.  
 23-FEB-2001; 2001WO-GB00792.  
 24-FEB-2000; 2000GB-0004415.  
 28-NOV-2000; 2000US-0750395.  
 (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 Herath HMC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
 WPI; 2001-570624/64.  
 New schizophrenia associated protein isoforms and encoding nucleic acid  
 molecules, useful for treatment, diagnosis and prognosis of  
 schizophrenia and screening for potential drugs for treatment and new  
 drug targets -  
 Disclosure; Page 31; 148pp; English.  
 The sequence represents a schizophrenia-associated protein isoform (SPI).  
 These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable  
 in cerebrospinal fluid, serum or plasma and are useful markers of  
 schizophrenia. The sequences can be used for treatment and diagnosis of  
 schizophrenia, screening, prognosis, monitoring the results of therapy,  
 identifying patients most likely to respond to a particular therapy and  
 identification of new targets for drug treatment. SPI DNA is useful as a  
 nucleic acid probe to detect the presence of nucleic acids or SPIs.

PN WO200163294-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-GB00791.  
 XX  
 XX 24-FEB-2000; 2000GB-0004412.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 XX  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PA Herath HMAC, Parekh RB, Rohlf C;  
 XX WPI; 2001-582081/65.  
 XX Preparation for diagnosing or treating bipolar affected disorder (BAD)  
 PT or unipolar depression, or for screening for modulators, comprises a  
 PT BAD-associated protein isoform -  
 XX Claim 8; Page 31; 163pp; English.  
 XX The invention relates to a preparation comprising an isolated Bipolar  
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are  
 CC used to screen, diagnose or prognosis of BAD or unipolar depression.  
 CC determine the stage or severity of BAD or unipolar depression, identify a  
 CC subject at risk of developing BAD or unipolar depression, or monitor the  
 CC effect of therapy in a subject. They are also used to screen for or  
 CC identify agents that interact with a DPI. These agents, antibodies  
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
 CC or prevent BAD or unipolar depression. Diseases that can be treated are  
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
 CC unipolar affective disorder. The DPIs are used in proteomics. The  
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
 CC BAD or unipolar depression overcomes the problems of using gene  
 CC expression analysis, such as not being able to obtain central nervous  
 CC system (CNS) tissue from a living patient under normal circumstances.  
 CC The present sequence is a DIP decreased in the CSF (cerebro-spinal  
 CC fluid) of subjects having BAD.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPPNV 6  
 Db |||||  
 1 LPPNV 5  
 RESULT 20  
 AAU26076  
 ID AAU26076 standard; Peptide; 11 AA.  
 XX  
 AC AAU26076;  
 XX  
 XX 18-DEC-2001 (first entry)  
 DT Depression-Associated Protein isoform DPI-106.  
 DE Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
 KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;  
 KW attention deficient disorder; schizoaffective disorder;  
 KW unipolar affective disorder.  
 XX Homo sapiens.  
 OS  
 XX WO200163294-A2.  
 PN 30-AUG-2001.  
 XX

PF 23-FEB-2001; 2001WO-GB00791.  
 XX  
 PR 24-FEB-2000; 2000GB-0004412.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 XX  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PA Herath HMAC, Parekh RB, Rohlf C;  
 XX WPI; 2001-582081/65.  
 XX Preparation for diagnosing or treating bipolar affected disorder (BAD)  
 PT or unipolar depression, or for screening for modulators, comprises a  
 PT BAD-associated protein isoform -  
 XX Claim 8; Page 31; 163pp; English.  
 XX The invention relates to a preparation comprising an isolated Bipolar  
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are  
 CC used to screen, diagnose or prognosis of BAD or unipolar depression.  
 CC determine the stage or severity of BAD or unipolar depression, identify a  
 CC subject at risk of developing BAD or unipolar depression, or monitor the  
 CC effect of therapy in a subject. They are also used to screen for or  
 CC identify agents that interact with a DPI. These agents, antibodies  
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
 CC or prevent BAD or unipolar depression. Diseases that can be treated are  
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
 CC unipolar affective disorder. The DPIs are used in proteomics. The  
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
 CC BAD or unipolar depression overcomes the problems of using gene  
 CC expression analysis, such as not being able to obtain central nervous  
 CC system (CNS) tissue from a living patient under normal circumstances.  
 CC The present sequence is a DIP decreased in the CSF (cerebro-spinal  
 CC fluid) of subjects having BAD.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPPNV 6  
 Db |||||  
 1 LPPNV 5  
 RESULT 21  
 AAU26268  
 ID AAU26268 standard; Peptide; 11 AA.  
 XX  
 AC AAU26268;  
 XX  
 XX 18-DEC-2001 (first entry)  
 DT Depression-Associated Protein isoform DPI-219 #2.  
 DE Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
 KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;  
 KW attention deficient disorder; schizoaffective disorder;  
 KW unipolar affective disorder.  
 XX Homo sapiens.  
 OS  
 XX WO200163294-A2.  
 PN 30-AUG-2001.  
 PD  
 XX 23-FEB-2001; 2001WO-GB00791.  
 PF 24-FEB-2000; 2000GB-0004412.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR



PR 12-DEC-2000; 2000US-0254830.  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herath HMAC, Parekh RB, Rohlf C;  
 XX WPI; 2001-582081/65.  
 XX  
 PT Preparation for diagnosing or treating bipolar affected disorder (BAD)  
 PT or unipolar depression, or for screening for modulators, comprises a  
 PT BAD-associated protein isoform -  
 XX  
 PS Claim 8; Page 35; 163pp; English.  
 XX  
 CC The invention relates to a preparation comprising an isolated Bipolar  
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are  
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,  
 CC determine the stage or severity of BAD or unipolar depression, identify a  
 CC subject at risk of developing BAD or unipolar depression, or monitor the  
 CC effect of therapy in a subject. They are also used to screen for or  
 CC identify agents that interact with a DPI. These agents, antibodies  
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
 CC or prevent BAD or unipolar depression. Diseases that can be treated are  
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
 CC unipolar affective disorder. The DPIs are used in proteomics. The  
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
 CC BAD or unipolar depression overcomes the problems of using gene  
 CC expression analysis, such as not being able to obtain central nervous  
 CC system (CNS) tissue from a living patient under normal circumstances.  
 CC The present sequence is a DIP decreased in the CSF (cerebro-spinal  
 CC fluid) of subjects having BAD.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPPNV 6  
 Db 1 LPPNV 5  
 |||||  
 RESULT 22  
 AAU26273  
 ID AAU26273 standard; Peptide; 11 AA.  
 XX  
 AC AAU26273;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Depression-Associated Protein isoform DPI-222 #2.  
 XX  
 KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
 KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;  
 KW attention deficient disorder; schizoaffective disorder;  
 KW unipolar affective disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200163294-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-GB00791.  
 XX  
 PR 24-FEB-2000; 2000GB-0004412.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herath HMAC, Parekh RB, Rohlf C;  
 XX WPI; 2001-582081/65.  
 XX

PI Herath HMAC, Parekh RB, Rohlf C;  
 XX WPI; 2001-582081/65.  
 XX  
 PT Preparation for diagnosing or treating bipolar affected disorder (BAD)  
 PT or unipolar depression, or for screening for modulators, comprises a  
 PT BAD-associated protein isoform -  
 XX  
 PS Claim 8; Page 35; 163pp; English.  
 XX  
 CC The invention relates to a preparation comprising an isolated Bipolar  
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are  
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,  
 CC determine the stage or severity of BAD or unipolar depression, identify a  
 CC subject at risk of developing BAD or unipolar depression, or monitor the  
 CC effect of therapy in a subject. They are also used to screen for or  
 CC identify agents that interact with a DPI. These agents, antibodies  
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
 CC or prevent BAD or unipolar depression. Diseases that can be treated are  
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
 CC unipolar affective disorder. The DPIs are used in proteomics. The  
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
 CC BAD or unipolar depression overcomes the problems of using gene  
 CC expression analysis, such as not being able to obtain central nervous  
 CC system (CNS) tissue from a living patient under normal circumstances.  
 CC The present sequence is a DIP decreased in the CSF (cerebro-spinal  
 CC fluid) of subjects having BAD.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPPNV 6  
 Db 1 LPPNV 5  
 |||||  
 RESULT 23  
 AAU26480  
 ID AAU26480 standard; Peptide; 11 AA.  
 XX  
 AC AAU26480;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Depression-Associated Protein isoform DPI-256.  
 XX  
 KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
 KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;  
 KW attention deficient disorder; schizoaffective disorder;  
 KW unipolar affective disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200163294-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-GB00791.  
 XX  
 PR 24-FEB-2000; 2000GB-0004412.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herath HMAC, Parekh RB, Rohlf C;  
 XX WPI; 2001-582081/65.  
 XX

PT Preparation for diagnosing or treating bipolar affected disorder (BAD)  
 PT or unipolar depression, or for screening for modulators, comprises a  
 PT BAD-associated protein isoform -  
 XX  
 PS Claim 8; Page 39; 163pp; English.  
 XX  
 CC The invention relates to a preparation comprising an isolated Bipolar  
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are  
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,  
 CC determine the stage or severity of BAD or unipolar depression, identify a  
 CC subject at risk of developing BAD or unipolar depression, or monitor the  
 CC effect of therapy in a subject. They are also used to screen for or  
 CC identify agents that interact with a DPI. These agents, antibodies  
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
 CC or prevent BAD or unipolar depression. Diseases that can be treated are  
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
 CC unipolar affective disorder. The DPIs are used in proteomics. The  
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
 CC BAD or unipolar depression overcomes the problems of using gene  
 CC expression analysis, such as not being able to obtain central nervous  
 CC system (CNS) tissue from a living patient under normal circumstances.  
 CC The present sequence is a DIP increased in the CSF (cerebro-spinal  
 CC fluid) of subjects having BAD.  
 XX  
 SQ Sequence 11 AA;

Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6  
 Db 1 LPPNV 5

## RESULT 24

AAU26518  
 ID AAU26518 standard; Peptide; 11 AA.

AC AAU26518;

XX 18-DEC-2001 (first entry)

DE Depression-Associated Protein isoform DPI-277.

XX Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
 KW CSF; antidepressant; antianemic; nootropic; tranquiliser; neuroleptic;  
 KW attention deficient disorder; schizoaffective disorder;  
 KW unipolar affective disorder.

XX Homo sapiens.

XX WO200163294-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB00791.

XX 24-FEB-2000; 2000GB-0004412.

XX 08-DEC-2000; 2000GB-0030050.

XX 12-DEC-2000; 2000US-0254830.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAC, Parekh RB, Rohlf C;

XX WPI; 2001-582081/65.

XX Preparation for diagnosing or treating bipolar affected disorder (BAD)  
 PT or unipolar depression, or for screening for modulators, comprises a  
 PT BAD-associated protein isoform -  
 XX

PS Claim 8; Page 40; 163pp; English.  
 XX  
 CC The invention relates to a preparation comprising an isolated Bipolar  
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are  
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,  
 CC determine the stage or severity of BAD or unipolar depression, identify a  
 CC subject at risk of developing BAD or unipolar depression, or monitor the  
 CC effect of therapy in a subject. They are also used to screen for or  
 CC identify agents that interact with a DPI. These agents, antibodies  
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
 CC or prevent BAD or unipolar depression. Diseases that can be treated are  
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
 CC unipolar affective disorder. The DPIs are used in proteomics. The  
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
 CC BAD or unipolar depression overcomes the problems of using gene  
 CC expression analysis, such as not being able to obtain central nervous  
 CC system (CNS) tissue from a living patient under normal circumstances.  
 CC The present sequence is a DIP increased in the CSF (cerebro-spinal  
 CC fluid) of subjects having BAD.  
 XX  
 SQ Sequence 11 AA;

Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6  
 Db 1 LPPNV 5

## RESULT 25

AAU15255  
 ID AAU15255 standard; Peptide; 11 AA.

XX AAU15255;

XX 24-OCT-2001 (first entry)

XX Schizophrenia-associated isoform peptide #140.

XX Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;  
 KW neurological disorder; neuropathy.

XX Homo sapiens.

XX WO200163293-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB00783.

XX 24-FEB-2000; 2000GB-0004415.

XX 28-NOV-2000; 2000US-0750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAC, Parekh RB, Rohlf C;

XX WPI; 2001-502868/55.

XX Diagnosing and monitoring Schizophrenia by detecting the presence of  
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
 PT Isoforms in samples of cerebrospinal fluid -  
 XX

PS Claim 6; Page 31; 160pp; English.

XX The invention relates to methods and compositions for screening,  
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting  
 CC the presence of Schizophrenia (SCH) Associated Features (SfEs) and SCH  
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,  
 CC immunoassay or hybridisation assay, for diagnosing and monitoring SCH,  
 CC studying the effectiveness of treatments and for identifying potential

CC therapeutic agents. The method is used for (1) screening or diagnosis of  
 CC SCH and the relative abundance of at least 1 chosen feature correlates  
 CC with the presence or absence of SCH; and (2) monitoring the effect of  
 CC therapy administered to a subject with SCH and the relative abundance of  
 CC at least 1 chosen feature which correlates with the severity of SCH.  
 CC The expression and activity of the SPS, SPIS and related molecules  
 CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the  
 CC progress of the disorder and the effectiveness of treatment and as  
 CC targets to identify and produce potential therapeutic agents for the  
 CC treatment of SCH. The paucity of detectable neurologic defects  
 CC distinguishes neuropsychiatric disorders such as SCH from neurological  
 CC disorders, where manifestations of anatomical and biochemical changes  
 CC have been identified in many cases. Consequently the identification and  
 CC characterisation of cellular and/or molecular causative defects and  
 CC neuropathies are necessary for improved treatment of neuropsychiatric  
 CC disorders. AAU15114-AAU15762 represent the amino acid sequences of  
 CC schizophrenia-associated isoforms used in the method of the invention.  
 CC

XX Sequence 11 AA;

Query Match 71.4%; Score 5; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6  
 |||||  
 Db 1 LPPNV 5

#### RESULT 26

ABG78535  
 ID ABG78535 standard; Peptide; 11 AA.

AC ABG78535;

XX 29-NOV-2002 (first entry)

DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #23.  
 XX  
 KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF;  
 KW human; multiple sclerosis-associated protein isoform; MSPI;  
 KW antiinflammatory; neuroprotective.

XX Homo sapiens.

XX WO200259604-A2.

XX 01-AUG-2002.

XX 25-JAN-2002; 2002WO-GB00330.

XX 26-JAN-2001; 2001US-264404P.

XX 20-NOV-2001; 2001US-331647P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAC, Perekh RB, Rohlf C;

XX WPI; 2002-599812/64.

XX Screening or diagnosing multiple sclerosis (MS), useful for e.g.  
 PT determining the stage or severity of MS, comprises detecting the  
 PT presence of MS-associated features or protein isoforms by 2-dimensional  
 PT electrophoresis -

XX Disclosure; Page 20; 128pp; English.

XX This invention relates to a novel method for screening or diagnosing  
 CC multiple sclerosis (MS) in a subject to determine the stage or severity  
 CC of MS, to identify a subject at risk of developing MS or to monitor the  
 CC effect of a therapy administered. The method comprises analysing a  
 CC sample body fluid from the subject by two-dimensional electrophoresis  
 CC and detecting the presence of multiple sclerosis-associated features

CC (MSFs), or multiple sclerosis-associated protein isoforms (MSPIs).  
 CC The MSFs of the invention correspond to spots identified on a 2D gel  
 CC these proteins may have antiinflammatory or neuroprotective activity.  
 CC The methods of the invention and the compositions are useful for  
 CC clinical screening, diagnosis and treatment of MS, for monitoring the  
 CC effectiveness of MS treatment, for selecting participants in clinical  
 CC trials, for identifying patients most likely to respond to a particular  
 CC therapeutic treatment and for screening and developing drugs for  
 CC treatment of MS. Agents that modulate the expression or activity of an  
 CC MSPI are useful for treating MS, for preventing or delaying the onset or  
 CC development of MS, to prevent or delay the progression of MS, or to  
 CC ameliorate the symptoms MS. Nucleic acids comprising a sequence encoding  
 CC an MSPI, MSPI-related polypeptide, or their fragments are useful for  
 CC promoting MSPI function by gene therapy. The present sequence represents  
 CC a human multiple sclerosis associated feature tryptic digest  
 CC peptide of the invention.  
 CC

XX Sequence 11 AA;

Query Match 71.4%; Score 5; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6  
 |||||  
 Db 1 LPPNV 5

#### RESULT 27

ABP57182  
 ID ABP57182 standard; Peptide; 11 AA.

AC ABP57182;

XX 16-APR-2003 (first entry)

DE Breast cancer associated tryptic digest peptide SEQ ID NO:83.

XX Breast cancer associated feature; BF; BPI; breast cancer; diagnosis;  
 KW breast cancer associated protein isoform; cytostatic; gene therapy.

XX Homo sapiens.

XX Synthetic.

XX WO200288750-A2.

XX 07-NOV-2002.

XX 02-MAY-2002; 2002WO-GB02022.

XX 02-MAY-2001; 2001GB-0010790.

XX 27-JUL-2001; 2001GB-0018385.

XX 14-AUG-2001; 2001GB-0019791.

XX 16-AUG-2001; 2001GB-0020045.

XX 22-NOV-2001; 2001GB-0028062.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAC;

XX WPI; 2003-175048/17.

XX Screening, diagnosing or determining the stage or severity of breast  
 PT cancer, comprises analyzing and quantitatively detecting Breast  
 PT Cancer-Associated Features or Breast Cancer-Associated Protein Isoforms  
 PT in a biological sample -

XX Disclosure; Page 18; 88pp; English.

XX The present invention describes a method for screening, diagnosing or  
 CC determining the stage or severity of breast cancer, identifying a subject  
 CC at risk of developing breast cancer, or monitoring the effect of therapy  
 CC administered to a subject with breast cancer, by generating a

two-dimensional array of features comprising breast cancer-associated features (BPs), or quantitatively detecting breast cancer-associated protein isoforms (BPs). Also described: (1) an antibody capable of immunospecifically binding to one of the BPs; (2) a pharmaceutical compositions comprising: (a) a BPI, or a nucleic acid encoding a BPI, and a carrier; or (b) the antibody of (1), or a fragment or derivative of the antibody, and a carrier; (3) screening for agents that interact with one or more BPIs, BPI fragments, polypeptides related to BPIs, or BPI-fusion proteins; (4) screening for or identifying agents that modulate the expression or activity of one or more BPIs, a BPI fragment, a BPI-related polypeptide, or BPI-fusion proteins; and (5) treating or preventing breast cancer. BPIs have cytostatic activity and can be used in gene therapy. Methods and kits comprising antibodies or the BPIs from the present invention can be used for screening, diagnosing or determining the stage or severity of breast cancer, identifying a subject at risk of developing breast cancer, or monitoring the effect of therapy administered to a subject with breast cancer. The antibodies, BPIs, nucleic acids encoding the BPIs, or an agent that modulates the activity of one or more BPIs are useful for treating or preventing breast cancer. ABP57104 to ABP57250 represent breast cancer associated tryptic digest peptides, which are used in the exemplification of the present invention.

XX Sequence 11 AA;  
 Query Match 71.4%; Score 5; DB 24; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LPPNV 6  
 |||||  
 Db 1 LPPNV 5

RESULT 28  
 AAM96974  
 ID AAM96974 standard; Peptide; 14 AA.

AC AAM96974;

DT 24-JAN-2002 (first entry)

DE Human peptide #249 encoded by a SNP oligonucleotide.

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiotensin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease.

OS Homo sapiens.

XX WO200147944-A2.

PD 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

PA Shimketa RA, Leach M;

PI WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, PT oncogenes and histones, useful for diagnosing and treating, e.g. PT cancer, autoimmune diseases and infections -

XX

PS Disclosure; Page 3722; 4143pp; English.  
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogene, histone, kinase, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

XX Sequence 14 AA;

Query Match 71.4%; Score 5; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LPPNV 6  
 |||||

Db 3 LPPNV 7

RESULT 29  
 AAU79766  
 ID AAU79766 standard; peptide; 4 AA.

XX AAU79766;

DT 30-JUL-2002 (first entry)

XX Chicken bone derived peptide #1, useful as ACE inhibitor.

XX Angiotensin converting enzyme inhibitor; ACEI; health food;  
 KW food additive; pharmaceutical product; lowering blood pressure;  
 KW hypertension; chicken essence by-product; chicken bone.

XX Gallus sp.

XX JP2001163896-A.

PN 19-JUN-2001.

XX 03-APR-2000; 2000JP-0105410.

XX 01-DEC-1999; 99TW-0120997.

XX (FOOD-) FOOD IND RES & DEV INST.

XX WPI; 2001-574451/65.

XX New peptides capable of inhibiting angiotensin converting enzyme for use in pharmaceutical compositions, in health foods and as food additives -

XX Claim 1; Page 2; 39pp; Japanese.

XX The present invention relates to novel peptides having angiotensin converting enzyme (ACE) inhibitory activity. Also described are methods for preparing products having ACE inhibitory activity, a pharmaceutical composition for use in the inhibition of ACE, and a health food or a food additive for use in the inhibition of ACE. The peptides of the invention are useful as ACE inhibitors (ACEI). They are useful in pharmaceutical products and health foods, and as food additives. Such compositions may be used for lowering blood pressure and treating hypertension. The manufacturing cost of the peptides of the

CC invention is considerably less than prior art as the peptide can be  
 CC produced from waste materials. Also the values of chicken essence  
 CC by-products can be improved. The present peptide derived from chicken  
 CC bone is useful as an ACE inhibitor.

XX Sequence 4 AA;

Query Match 57.1%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
 DB 1 VLPP 4

## RESULT 30

AAR90467  
 ID AAR90467 standard; peptide; 6 AA.

XX AC AAR90467;

DT 03-SEP-1996 (first entry)

DE Antibody 561 displacing peptide #35.

XX Antibody; displacement; cell separation system; cell surface antigen; Ag;  
 KW random peptide display library; complementarity determining region; CDR;  
 KW antibody; Ab; peptide; CD34 cell; haematopoietic cell; tumour cell;  
 KW lymphocyte; high dose therapy; immune system; chemotherapy;  
 KW patient-specific vaccine.

XX Synthetic.

XX WO9534817-A1.

PN 21-DEC-1995.

PD 13-JUN-1995; 95WO-US07491.

PF 14-JUN-1994; 94US-0259427.

PR (BAXT ) BAXTER INT INC.

PA Al-Abdaly FA, Deans RJ, Guillermo R, Helgerson SL;

PI Kobori JA, Tseng-law J;

XX WPI; 1996-049806/05.

DR Selecting target cells by reacting specific antibody to surface  
 PT antigen - then disrupting the complex formed with peptide displacer,  
 PT partic. for selecting CD34 cells for reconstitution of immune system  
 PT after anticancer treatment

XX Claim 25; Page 156; 170pp; English.

XX AAR90413-R30468 represent antibody displacing peptides. These sequences  
 CC displace the monoclonal antibody designated 561. These sequences can be  
 CC used in a method to select target cells from a heterogeneous cell  
 CC suspension. In the suspension, there is at least one complex of a cell  
 CC separation system, linked to a primary antibody (Ab) which is bound to  
 CC the cell surface antigen (Ag). The complex is separated from the rest  
 CC of the suspension, and contacted with a peptide (such as this sequence)  
 CC that binds to the Ab, displacing it from the Ag and releasing the cell.  
 CC These sequences can be identified by bioassaying random peptide display  
 CC libraries with the Ab, by analysis of potential antigenic peaks of the  
 CC cell surface antigen, or by analysis of the complementarity determining  
 CC regions of the Ab. These sequences can also be used in a method for  
 CC determining the number of specific cells in a composition. The methods  
 CC can be used for positive selection of CD34 haematopoietic cells, and  
 CC removal of undesired tumour cells or lymphocytes from the selected  
 CC cells. The pure CD34 cells are reinfused into a cancer patient after high  
 CC dose therapy to reconstitute the immune system. Cancer cells can also

CC be isolated to determine their chemotherapeutic susceptibility, or for  
 CC the production of patient-specific vaccines or antibodies. These  
 CC sequences allow for the recovery of cells from solid supports, in high  
 CC yield, without enzymatic cleavage. They are relatively inexpensive and  
 CC safe, and leave cell surface proteins intact.

XX Sequence 6 AA;

Query Match 57.1%; Score 4; DB 17; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPNV 6  
 DB 1 PPNV 4

## RESULT 31

AAV5202  
 ID AAV5202 standard; peptide; 6 AA.

XX AC AAV5202;

XX 07-JAN-2000 (first entry)

DE Anti CD34 antibody 561 releasing peptide SEQ ID NO:96.

XX Antibody releasing peptide; CD34; hybridoma; binding; antigen;  
 KW cell surface antigen; identification; haematopoietic stem cell;  
 KW tumour; cancer; immune system; therapy; displacement.

XX Synthetic.

OS Homo sapiens.

XX US5968753-A.

PN 19-OCT-1999.

PD 07-JUN-1995; 95US-0482228.

PF 14-JUN-1994; 94US-0259427.

PR (NEXE-) NEXELL THERAPEUTICS INC.

PA Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;

PI Al-Abdaly FA;

XX WPI; 1999-590399/50.

DR Short peptides useful for displacing antibodies from cell surface  
 PT antigens.

XX Claim 7; Column 145; 81pp; English.

XX The present invention describes peptides of 4-17 amino acids which  
 CC displace either the anti-CD34 monoclonal antibody designated 561, the  
 CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC  
 CC HB-11646 (designated 9069), the anti-CD34 antibody produced by  
 CC hybridoma ATCC HB-11885 (9079), or the anti-human breast cancer  
 CC antibody produced by hybridoma ATCC HB-11894 (9187), from a cell  
 CC surface antigen on a target cell. The peptides are useful for  
 CC displacing antibodies bound to cell surfaces to release cells that  
 CC have been positively selected by antibody-mediated binding to beads  
 CC or other solid support. AAV5107 to AAV5319 represent peptides used in  
 CC the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 57.1%; Score 4; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPNV 6

```

Db      1 PPNV 4
|||||
RESULT 32
AAY86948
ID AAY86948 standard; Peptide; 6 AA.
XX
AC AAY86948;
XX
XX 09-MAY-2000 (first entry)
XX
XX Human haematopoietic CD34+ cell binding peptide SEQ ID #96.
XX
XX Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody;
KW non-enzymatic cell selection method; haematopoietic stem cell;
KW haematopoietic progenitor cell; antibody 561; breast cancer cell;
KW antibody 9187; cell surface determinant; diagnostic cell based assay.
XX
XX Homo sapiens.
OS
XX US6017719-A.
PN
XX 25-JAN-2000.
PD
XX 07-JUN-1995; 95US-0482528.
PF
XX 14-JUN-1994; 94US-0259427.
PR
XX (NEXE-) NEXELL THERAPEUTICS INC.
PA
XX Guillermo R. Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
PI Al-Abdaly FA;
PI
XX WPI; 2000-136676/12.
DR
XX Non-enzymatic method for the positive selection of target cells from a
PT heterogeneous cell suspension, useful for selecting human breast cancer
PT cells from a patient's blood or bone marrow -
PT
XX Example 13; Column 19; 82pp; English.
PS
XX This sequence represents a human haematopoietic CD34+ cell binding
CC peptide, and was used to test the method of the invention. The method is
CC a non-enzymatic method for the positive selection of one or more target
CC cells from a heterogeneous cell suspension, by using specific peptides
CC which effect the displacement and release of a specific target cell
CC from a specific monoclonal antibody. The method is useful for positive
CC selection and specific release of target human haematopoietic
CC stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and
CC the antibody 561. The method is also useful for positive selection and
CC specific release of target human breast cancer cells, bound by the
CC monoclonal anti-breast cancer antibody 9187, from a patient's blood or
CC bone marrow. Identification of peptide epitopes for antibodies which
CC recognise cell surface determinants also allows construction of
CC diagnostic cell based assays. The peptide mediated release is enzyme free
CC and thus leaves the cell surface proteins intact. Moreover, peptide
CC mediated release leaves the target cell free of bound antibody or
CC antibody fragments. The method also produces a high yield of functional
CC target cells and is relatively inexpensive to carry out.
XX
SQ Sequence 6 AA;
Query Match 57.1%; Score 4; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 PPNV 6
|||||
Db 1 PPNV 4
|||||
RESULT 33
AAW66740 standard; peptide; 7 AA.
XX
AC AAW66740;
XX
XX 02-DEC-1998 (first entry)
XX
XX Dolastatin-15 derivative in composition for treatment of cancer.
DE
XX dolastatin-15; cancer; paclitaxel; taxane; taxoid; taxotere.
KW
XX Synthetic.
OS
XX Dolabella auricularia.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N,N-dimethyl-Val"
FT Modified-site 3
FT Modified-site 7 /note= "N-methyl-leucine"
FT Modified-site 7 /note= "Phe-NH2"
FT
XX WO9840092-A1.
PN
XX 17-SEP-1998.
PD
XX 09-MAR-1998; 98WO-US04594.
PF
XX 13-MAR-1997; 97US-0819101.
PR
XX (BADI ) BASF AG.
PA (BADI ) BASF BIORESEARCH CORP.
PA
XX Barlozzari T, Haupt A;
PI
XX WPI; 1998-520790/44.
DR
XX Composition used for treating cancer - comprises paclitaxel,
PT taxotere or modified taxane or taxoid analogs and tetra- to hepta-
PT peptide(s)
PT
XX Example 154; Page 56; 114pp; English.
PS
XX The invention relates to a composition for the treatment of cancer. The
CC composition comprises: (a) paclitaxel, taxotere or modified taxane or
CC taxoid analogs; (b) tetra- to hepta- peptides of formula
CC R1R2N-CHX-CO-A-B-D-(E/Fs)-(F)-c-(Glu-K (1) or their salts and optionally (c)
CC a carrier. R1 = alkyl, cycloalkyl, alkylsulphonyl, fluoroalkyl or
CC aminosulphonyl; R2 = H, alkyl, fluoroalkyl, or cycloalkyl or NR1R2 =
CC pyrrolidino or piperidino; A = valyl, isoleucyl, leucyl, alloisoleucyl,
CC 2,2-dimethylglycyl, 2-cyclopropylglycyl, 2-cyclopentylglycyl,
CC 3-tert-butylalanyl, 2-tert-butylglycyl, 3-cyclohexylalanyl,
CC 2-ethylglycyl, 2-cyclohexylglycyl, norleucyl or norvalyl; B = an N-alkyl
CC derivative of A except alloisoleucyl or cyclohexylalanyl; D, E = prolyl,
CC homoprolyl, hydroxyprolyl, 3,4-dihydroxyprolyl, 4-fluoroprolyl, 3-, 4- or
CC 5- methylprolyl, azetidine-2-carbonyl, 3,3-dimethylprolyl,
CC 4,4-difluoroprolyl, oxazolidine-4-carbonyl, or thiazolidine-4-carbonyl;
CC F, G = prolyl, homoprolyl, hydroxyprolyl, thiazolidine-4-carbonyl,
CC 1-aminoprolyl-1-carbonyl, valyl, 2-tert-butylglycyl, isoleucyl, leucyl,
CC 3-cyclohexylalanyl, phenylalanyl, N-methyl-phenylalanyl, 3-pyridylalanyl,
CC tetrahydroisoquinolyl-2-histidyl, 1-aminoindyl-1-carbonyl,
CC 2-cyclohexylglycyl, norleucyl, norvalyl, neopentylglycyl, tryptophanyl,
CC H, alkyl, cycloalkyl, methylcyclohexyl or arylalkyl; s, t, u = 0 or 1 and
CC K = hydroxy, alkoxy, phenoxy, benzyloxy or amino (optionally
CC substituted). The composition is used for treating lung, breast, colon,
CC prostate, bladder, rectal, endometrial and haematological cancers e.g.
CC leukaemias and lymphomas. The present sequence represents a specific
CC example of a heptapeptide disclosed in the specification.
XX
SQ Sequence 7 AA;
Query Match 57.1%; Score 4; DB 19; Length 7;

```

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
Db 2 VLPP 5

## RESULT 34

AAW08842  
ID AAW08842 standard; peptide; 7 AA.

XX AC AAW08842;

XX 06-JUL-1999 (first entry)

XX Dolaetatin-15 derivative for treatment of rheumatoid arthritis.

XX Dolaetatin; antiarthritic; rheumatoid arthritis.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N,N-dimethyl-Val"

FT Modified-site 3

FT Modified-site 7 /note= "N-methyl-Leu"

FT Modified-site 7 /note= "Phe-NH2"

XX WO9917792-A1.

XX 15-APR-1999.

XX 24-SEP-1998; 98WO-US19841.

XX 06-OCT-1997; 97US-0944479.

XX (BADI ) BASF AG.

XX Banerjee S, Barlozzari T, Haupt A;

XX WPI; 1999-277207/23.

XX Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,  
alone or in combination with other antiarthritic drugs

XX Example 154; Page 51; 106pp; English.

XX The invention relates to a method for treating rheumatoid arthritis  
using dolastatin-15 derivatives. The present peptide is a specific  
example of a dolastatin compound which was prepared for use in the  
method.

XX SQ Sequence 7 AA;

Query Match 57.1%; Score 4; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4

Db 2 VLPP 5

## RESULT 35

AAW08835

ID AAW08835 standard; peptide; 7 AA.

XX AC AAW08835;

XX 06-JUL-1999 (first entry)

XX Dolaetatin-15 derivative for treatment of rheumatoid arthritis.

XX Dolaetatin; antiarthritic; rheumatoid arthritis.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N,N-dimethyl-Val"

FT Modified-site 3

FT Modified-site 7 /note= "N-methyl-Leu"

FT Modified-site 7 /note= "Phe-NH2"

XX WO9917709-A2.

XX 15-APR-1999.

XX 30-SEP-1998; 98WO-US20465.

XX 06-OCT-1997; 97US-0944479.

XX (BADI ) BASF AG.

XX Banerjee S, Barlozzari T, Haupt A;

XX WPI; 1999-277175/23.

XX Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,  
alone or in combination with other antiarthritic drugs

XX Example 154; Page 51; 103pp; English.

XX The invention relates to a method for treating rheumatoid arthritis  
using dolastatin-15 derivatives. The present peptide is a specific  
example of a dolastatin compound which was prepared for use in the  
method.

XX SQ Sequence 7 AA;

Query Match 57.1%; Score 4; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4

Db 2 VLPP 5

## RESULT 36

AAW08835

ID AAW08835 standard; peptide; 7 AA.

XX AC AAW08835;

XX 06-JUL-1999 (first entry)

XX Dolaetatin-15 derivative for treatment of rheumatoid arthritis.

XX Dolaetatin; antiarthritic; rheumatoid arthritis.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N,N-dimethyl-Val"

FT Modified-site 3

FT Modified-site 7 /note= "N-methyl-Leu"

FT Modified-site 7 /note= "Phe-NH2"

XX WO9917709-A2.

XX 15-APR-1999.

XX 30-SEP-1998; 98WO-US20465.

XX 06-OCT-1997; 97US-0944479.

XX (BADI ) BASF AG.

XX Banerjee S, Barlozzari T, Haupt A;

XX WPI; 1999-277175/23.

XX Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,  
alone or in combination with other antiarthritic drugs

XX Example 154; Page 51; 103pp; English.

XX The invention relates to a method for treating rheumatoid arthritis  
using dolastatin-15 derivatives. The present peptide is a specific  
example of a dolastatin compound which was prepared for use in the  
method.

XX SQ Sequence 7 AA;

Query Match 57.1%; Score 4; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4

Db 2 VLPP 5

## RESULT 37

AAW08835

ID AAW08835 standard; peptide; 7 AA.

XX AC AAW08835;

XX 06-JUL-1999 (first entry)

XX Dolaetatin-15 derivative for treatment of rheumatoid arthritis.

XX Dolaetatin; antiarthritic; rheumatoid arthritis.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N,N-dimethyl-Val"

FT Modified-site 3

FT Modified-site 7 /note= "N-methyl-Leu"

FT Modified-site 7 /note= "Phe-NH2"

XX WO9917709-A2.

XX 15-APR-1999.

XX 30-SEP-1998; 98WO-US20465.

XX 06-OCT-1997; 97US-0944479.

XX (BADI ) BASF AG.

XX Banerjee S, Barlozzari T, Haupt A;

XX WPI; 1999-277175/23.

XX Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,  
alone or in combination with other antiarthritic drugs

XX Example 154; Page 51; 103pp; English.

XX The invention relates to a method for treating rheumatoid arthritis  
using dolastatin-15 derivatives. The present peptide is a specific  
example of a dolastatin compound which was prepared for use in the  
method.

XX SQ Sequence 7 AA;

Query Match 57.1%; Score 4; DB 20; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4

Db 2 VLPP 5

```

PA (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
PA (UYPA-) UNIV PARIS 13 NORD.
XX
PI Tournaire R, Demangel C, Derbin C, Perret G, Mazie J, Plouet J;
PI Vassy R;
XX
DR WPI; 2001-616471/71.
XX
XX Novel peptides inhibiting binding of vascular endothelial growth factor
PT (VEGF) to kinase domain receptor, or inhibiting binding of anti-VEGF
PT antibody to VEGF, useful for treating diabetic retinopathy and
PT psoriasis
XX
XX Claim 15; Page 19; 55pp; English.
XX
CC AAG79260-73 represent peptides which affect vascular endothelial growth
CC factor (VEGF) binding to antibodies or the kinase domain receptor (KDR).
CC Peptides AAG79260-66 were selected by their ability to bind to an
CC anti-VEGF antibody, and peptides AAG79267-73 were selected for their
CC ability to bind to CHO cells expressing a KDR which binds VEGF. The
CC peptides inhibit the binding of VEGF to KDR, and inhibit binding of
CC anti-VEGF antibody to VEGF. The peptides are useful for inhibiting
CC angiogenesis and for treating diseases including cancer, diabetic
CC retinopathy, psoriasis, hemangioblastoma, and Kaposi's sarcoma.
XX
SQ Sequence 7 AA;
Query Match 57.1%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LPPN 5
Db 1 LPPN 4
RESULT 37
AAE09112
ID AAE09112 standard; peptide; 7 AA.
AC AAE09112;
DT
DT 15-NOV-2001 (first entry)
XX
DE Bacteriophage Type I peptide #3, used in the invention.
XX
KW Vaccine; therapy; autoimmune disorder; Epstein-Barr virus; EBV; anaemia;
KW polymyositis; systemic lupus erythematosus; SLE; rheumatoid arthritis;
KW Sjogren's syndrome; diabetes mellitus; adenitis; multiple sclerosis;
KW demyelinating disease; Hashimoto's thyroiditis; autoimmune infertility;
KW hypoparathyroidism; primary biliary cirrhosis; ankylosing spondylitis;
KW inflammatory bowel disease; Addison's disease; thyroiditis; filariasis;
KW Graves' disease; ulcerative colitis; dermatomyositis; myasthenia gravis;
KW Crohn's disease; CREST syndrome; autoimmune cystitis; glomerulonephritis;
KW polyarthritis nodosa; hepatitis; atopic rhinitis; Goodpasture's syndrome;
KW sarcoidosis; rheumatic fever; anti-phospholipid syndrome; farmer's lung;
KW Cushing's syndrome; bird-fancier's lung; alveolitis; erythema nodosum;
KW pyoderma gangrenosum; fibromyalgia; Kawasaki's disease; cardiomyopathy;
KW Sampter's syndrome; asthma; polymyalgia rheumatica; psoriasis; arteritis;
KW erythroblastosis foetalis; cyclitis; IgA nephropathy; Hodgkin's lymphoma;
KW renal cell carcinoma; eosinophilia; immunosuppressive; ophthalmological;
KW thrombemic; neuroprotective; cytostatic; nephrotropic; antiallergic;
KW dengue; antileuker; vasotropic; antipyretic; hepatotropic.
XX
OS Bacteriophage.
XX
XX WO200158481-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US04191.
XX

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PR 09-FEB-2000; 2000US-0500904.
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI Harley JB, James JA, Kaufman KM;
XX
XX WPI; 2001-522437/57.
XX
XX Novel vaccine for alleviating or preventing autoimmune disorders
PT induced Epstein-Barr virus (EBV) infection e.g. systemic lupus
PT erythematosus, juvenile onset diabetes mellitus, comprises EBV virus or
PT its component
XX
XX Example 10; Page 56; 114pp; English.
XX
CC The present invention relates to a vaccine for alleviating or preventing
CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV),
CC comprising EBV or its component in a carrier. The vaccine is useful for
CC preventing or alleviating autoimmune disorders induced by EBV, e.g.
CC systemic lupus erythematosus (SLE), Sjogren's syndrome, juvenile onset
CC diabetes mellitus, rheumatoid arthritis, Wegener's granulomatosis,
CC inflammatory bowel disease, polymyositis, dermatomyositis, multiple
CC endocrine failure, Schmidt's syndrome, autoimmune uveitis, Addison's
CC disease, adenitis, primary biliary cirrhosis, Graves' disease,
CC thyroiditis, Hashimoto's thyroiditis, autoimmune thyroid disease,
CC pernicious and haemolytic anaemia, lupoid hepatitis, demyelinating
CC disease, multiple sclerosis, subacute cutaneous lupus erythematosus,
CC hypoparathyroidism, Dressler's syndrome, myasthenia gravis, autoimmune
CC idiopathic thrombocytopenic purpura, autoimmune pemphigus vulgaris,
CC pemphigus, bullous pemphigoid, dermatitis herpetiformis, alopecia
CC areata, autoimmune cystitis, pemphigoid, scleroderma, progressive
CC systemic sclerosis, CREST syndrome (calcinosis, Raynaud's oesophageal
CC dysmotility, sclerodactyly and telangiectasia), adult onset diabetes
CC mellitus (type II diabetes), male or female autoimmune infertility,
CC ankylosing spondylitis, ulcerative colitis, Crohn's disease, mixed
CC connective tissue disease, polyarthritis nodosa, systemic necrotising
CC vasculitis, glomerulonephritis, atopic dermatitis, atopic rhinitis,
CC Goodpasture's syndrome, Chagas' disease, sarcoidosis, rheumatic fever,
CC asthma, recurrent abortion, anti-phospholipid syndrome, farmer's lung,
CC erythema multiforme, postcardotomy syndrome, Cushing's syndrome,
CC autoimmune chronic active hepatitis, bird-fancier's lung, allergic
CC encephalomyelitis, toxic necrodermal lysis, alopecia, Alport's syndrome,
CC allergic alveolitis, fibrosing alveolitis, interstitial lung disease,
CC erythema nodosum, pyoderma gangrenosum, transfusion reaction, chronic
CC fatigue syndrome, fibromyalgia, Takayasu's arteritis, Kawasaki's disease,
CC polymyalgia rheumatica, temporal arteritis, giant cell arteritis, dengue,
CC Sampter's syndrome (triaditis, nasal polyps, eosinophilia) and Behcet's
CC disease, Caplan's syndrome, encephalomyositis, erythema elevatum et
CC diutinum, psoriasis, erythroblastosis foetalis, Shulman's syndrome, IgA
CC nephropathy, Felty's syndrome, fascitis with eosinophilia, filariasis,
CC chronic cyclitis, heterochromic cyclitis, Fuch's cyclitis, Hodgkin's and
CC non-Hodgkin's lymphoma, cardiomyopathy, Henoch-Schonlein purpura, post
CC vaccination syndromes, renal cell carcinoma, Eaton-Lambert syndrome or
CC relapsing polychondritis. The present sequence is Bacteriophage Type I
CC peptide used in the invention.
XX
SQ Sequence 7 AA;
Query Match 57.1%; Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPP 4
Db 1 VLPP 4
RESULT 38
AAB35601
ID AAB35601 standard; Protein; 8 AA.
XX
XX AAB35601;
XX

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DT 13-FEB-2001 (first entry)  
 XX Consensus sequence for G-1.  
 DE Era; cell cycle; anti-cancer.  
 KW Escherichia coli.  
 XX US6132954-A.  
 PN 17-OCT-2000.  
 XX 20-AUG-1997; 97US-0915498.  
 XX 20-AUG-1996; 96US-0023353.  
 XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Court DL, Powell BS, Lupski JR, Britton RA;  
 XX WPI; 2001-006131/01.  
 XX Screening for an agent that delays the cell cycle by combining a  
 PT purified Bxa protein moiety and an test agent with guanosine  
 PT triphosphate, and measuring resulting guanosine diphosphate -  
 XX Examples; Column 28; 58pp; English.  
 XX The present invention relates to screening for an agent that delays  
 CC the cell cycle involving combining a purified Bxa protein moiety and  
 CC at least one test agent with GTP, measuring resulting GDP and  
 CC comparing this to a control. The method is useful for detecting agents  
 CC that delay the cell cycle and for screening for anti-cancer agents.  
 CC Agents identified by the method may be used for reducing or stopping  
 CC the growth of infectious organisms and thus decreasing or eliminating  
 CC infection. The present sequence is a protein of the invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 57.1%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PNVG 7  
 DB 3 PNVG 6  
 RESULT 39  
 AAR50242  
 ID AAR50242 standard; Peptide; 9 AA.  
 AC AAR50242;  
 XX 25-MAR-2003 (updated)  
 DT 12-OCT-1994 (first entry)  
 XX Sequence of trypsin digestion peptide of 50 kDa species of  
 DE dystrophin-associated protein (DAP).  
 XX Autosomal muscular dystrophy; dystrophy associated glycoprotein;  
 KW diagnosis; 50 kDa; trypsin peptide.  
 XX Homo sapiens.  
 OS WO9407143-A1.  
 PN 31-MAR-1994.  
 PD 13-SEP-1993; 93WO-US08585.  
 XX 14-SEP-1992; 92US-0946234.  
 PR

XX (IOWA ) UNIV IOWA STATE RES FOUND INC.  
 PA Campbell KP, Matsumura K;  
 XX WPI; 1994-118616/14.  
 XX Diagnosis of autosomal muscular dystrophy - by determining  
 PT binding of an antibody to a dystrophin-associated protein to  
 PT experimental muscle tissue  
 XX Claim 23; Page 70; 82pp; English.  
 XX Dystrophin is a large molecular wt. protein product of the  
 CC defective gene responsible for Duchenne's muscular dystrophy.  
 CC It exists as a component of a large oligomeric complex - the  
 CC dystrophin glycoprotein complex. Other components comprise  
 CC glycoproteins of 156 kDa, 50 kDa, 43 kDa, 35 kDa, and a triplet of  
 CC proteins of 59 kDa. When skeletal muscle biopsy samples of  
 CC patients with severe childhood autosomal recessive muscular  
 CC dystrophy (SCARMD) were compared with normal muscle, immunostaining  
 CC for the 50 kDa DAP was greatly reduced in the sarcolemma of all  
 CC the muscle fibres of the SCARMD patients. The 50 kDa species of  
 CC the dystrophin glycoprotein complex was separated from the other  
 CC components and subjected to trypsin digestion. The digestion  
 CC products were sequenced and are given in AAR50241-45. AAR50241  
 CC (claimed) was chemically synthesised and attached to a solid  
 CC support to generate an affinity matrix. Polyclonal antibodies  
 CC specifically reactive with this peptide were isolated using  
 CC the affinity purification method. Peptides identified in this  
 CC manner can be used to immunise animals to generate antibodies  
 CC specifically reactive with a single epitope of the 50 kDa  
 CC protein.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 9 AA;  
 Query Match 57.1%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLP 4  
 DB 6 VLP 9  
 RESULT 40  
 AAR80233  
 ID AAR80233 standard; Peptide; 9 AA.  
 AC AAR80233;  
 XX 25-MAR-2003 (updated)  
 DT 27-MAY-1996 (first entry)  
 XX Rabbit 50 kDa dystrophin-associated glycoprotein antigenic peptide.  
 DE Duchenne muscular dystrophy; neuromuscular disease; diagnosis;  
 KW gene therapy; gene transfer; non-dystrophin component;  
 KW severe childhood autosomal recessive muscular dystrophy;  
 KW sarcolemmal glycoprotein; antigenic peptide.  
 XX Oryctolagus cuniculus.  
 OS US5449616-A.  
 PN 12-SEP-1995.  
 PD 16-SEP-1993; 93US-0123161.  
 XX 16-SEP-1993; 93US-0123161.  
 PR 23-MAY-1990; 90US-0527583.  
 XX 20-FEB-1992; 92US-0841654.  
 PR

```
PR 14-SEP-1992; 92US-0946234.
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
PI Anderson RD, Campbell KP, Roberts SL;
XX WPI; 1995-327696/42.
DR
XX New nucleic acid encoding component of dystrophin glyco:protein
PT complex - and related vectors and transformed cells, useful in
PT diagnosis and treatment of various forms of muscular dystrophy
XX
XX Example 11; Column 47-48; 42pp; English.
XX
CC This antigenic peptide may be used to immunize animals to
CC generate antibodies specifically reactive with a single epitope
CC of the 50 kDa protein. Degenerate probes can be designed which
CC can then be used to isolate the gene which encodes the 50 kDa
CC dystrophin-associated protein.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX SQ Sequence 9 AA;
Query Match 57.1%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPP 4
Db 6 VLPP 9
|||||
RESULT 41
AAW31595
ID AAW31595 standard; Protein; 9 AA.
AC AAW31595;
XX
XX 10-MAR-1998 (first entry)
XX
XX Immunogenic epitope 2 of 50 kDa dystrophin-associated protein.
XX
XX dystrophin; dysroglycan; immunogen; antibody; diagnosis; human;
XX muscular dystrophy; epitope; rabbit; ss.
XX
OS Synthetic.
OS Homo sapiens.
OS Oryctolagus cuniculus.
XX
XX US5686073-A.
XX
XX 11-NOV-1997.
XX
XX 07-JUN-1995; 95US-0483278.
XX
XX 07-JUN-1995; 95US-0483278.
XX 23-MAY-1990; 90US-0527583.
XX 20-FEB-1991; 91WO-US03632.
XX 14-SEP-1992; 92US-0841654.
XX 16-SEP-1993; 92US-0946234.
XX 93US-0123161.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Campbell KP, Ervasti JM, Ibraghimov OB, Leveille CJ;
XX WPI; 1997-558087/51.
XX
XX Peptide fragment of dystrophin-associated protein - useful as
XX immunogen for antibody production
XX
XX Example 11; Columns 45-46; 41pp; English.
XX
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```
CC This is an immunogenic epitope of 50 kDa dystrophin-associated protein.
CC This immunogenic peptide can stimulate the production of antibodies which
CC bind specifically to the 50 kDa dystrophin-associated protein. The
CC molecular weight of the protein can be determined by electrophoretic
CC separation under denaturing conditions, and transferring to a solid
CC support and staining with wheat germ agglutinin. The peptide is useful
CC for producing polyclonal and monoclonal antibodies that bind specifically
CC to the 50 kDa dystrophin-associated protein and can be used in the
CC diagnosis of some forms of muscular dystrophy.
XX
XX SQ Sequence 9 AA;
Query Match 57.1%; Score 4; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPP 4
Db 6 VLPP 9
|||||
RESULT 42
ABJ01310
ID ABJ01310 standard; Peptide; 9 AA.
XX
XX AC ABJ01310;
XX
XX 19-SEP-2002 (first entry)
XX
XX 158P1D7 related HLA peptide SEQ ID No 10.
XX
XX Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX HLA.
XX
XX Homo sapiens.
XX
XX WO200216593-A2.
XX
XX 28-FEB-2002.
XX
XX 22-AUG-2001; 2001WO-US26276.
XX
XX 22-AUG-2000; 2000US-227098P.
XX 10-APR-2001; 2001US-282739P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX Challita-eid PM, Jakobovits A;
XX
XX WPI; 2002-425659/45.
XX
XX New compositions comprising a gene (designated 158P1D7), its encoded
XX protein or their modulators, useful for treating or diagnosing cancers,
XX particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX or humans)
XX
XX Disclosure; Page 126; 181pp; English.
XX
XX The invention relates to a novel nucleic acid, designated 158P1D7. The
XX compositions are useful for treating or diagnosing cancers, particularly
XX bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX horses or humans). The compositions are also useful for monitoring
XX genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX of the invention can be used in gene therapy to treat the said disorders.
XX This sequence represents a human leukocyte antigen (HLA) peptide relating
XX to the 158P1D7 protein of the invention.
XX
XX SQ Sequence 9 AA;
Query Match 57.1%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
```



XX 22-AUG-2000; 2000US-227098P.  
PR 10-APR-2001; 2001US-282739P.  
XX (AGEN-) AGENSYS INC.  
XX Paris M, Hubert RS, Raitano AB, Afar DEH, Levin E;  
PI Challita-eid PM, Jakobovits A;  
XX WPI; 2002-425659/45.  
XX New compositions comprising a gene (designated 158P1D7), its encoded  
PT protein or their modulators, useful for treating or diagnosing cancers,  
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses  
or humans)  
XX Disclosure; Page 130; 181pp; English.  
XX The invention relates to a novel nucleic acid, designated 158P1D7. The  
CC compositions are useful for treating or diagnosing cancers, particularly  
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,  
CC horses or humans). The compositions are also useful for monitoring  
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid  
CC of the invention can be used in gene therapy to treat the said disorders.  
CC This sequence represents a human leukocyte antigen (HLA) peptide relating  
CC to the 158P1D7 protein of the invention.  
XX Sequence 9 AA;  
PS Query Match 57.1%; Score 4; DB 23; Length 9;  
PS Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
PS Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLPP 4  
DB 4 VLPP 7  
RESULT 46  
ABJ01511  
ID ABJ01511 standard; Peptide; 9 AA.  
XX AC ABJ01511;  
XX 19-SEP-2002 (first entry)  
XX 158P1D7 related HLA peptide SEQ ID No 211.  
XX Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;  
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;  
KW HLA.  
XX Homo sapiens.  
XX WO200216593-A2.  
XX 28-FEB-2002.  
XX 22-AUG-2001; 2001WO-US26276.  
XX 22-AUG-2000; 2000US-227098P.  
PR 10-APR-2001; 2001US-282739P.  
XX (AGEN-) AGENSYS INC.  
XX Paris M, Hubert RS, Raitano AB, Afar DEH, Levin E;  
PI Challita-eid PM, Jakobovits A;  
XX WPI; 2002-425659/45.  
XX New compositions comprising a gene (designated 158P1D7), its encoded  
PT protein or their modulators, useful for treating or diagnosing cancers,  
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses  
or humans)

PT or humans)  
XX Disclosure; Page 133; 181pp; English.  
XX The invention relates to a novel nucleic acid, designated 158P1D7. The  
CC compositions are useful for treating or diagnosing cancers, particularly  
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,  
CC horses or humans). The compositions are also useful for monitoring  
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid  
CC of the invention can be used in gene therapy to treat the said disorders.  
CC This sequence represents a human leukocyte antigen (HLA) peptide relating  
CC to the 158P1D7 protein of the invention.  
XX Sequence 9 AA;  
PS Query Match 57.1%; Score 4; DB 23; Length 9;  
PS Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
PS Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LPPN 5  
DB 2 LPPN 5  
RESULT 47  
ABJ01798  
ID ABJ01798 standard; Peptide; 9 AA.  
XX AC ABJ01798;  
XX 19-SEP-2002 (first entry)  
XX 158P1D7 related HLA peptide SEQ ID No 498.  
XX Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;  
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;  
KW HLA.  
XX Homo sapiens.  
XX WO200216593-A2.  
XX 28-FEB-2002.  
XX 22-AUG-2001; 2001WO-US26276.  
XX 22-AUG-2000; 2000US-227098P.  
PR 10-APR-2001; 2001US-282739P.  
XX (AGEN-) AGENSYS INC.  
XX Paris M, Hubert RS, Raitano AB, Afar DEH, Levin E;  
PI Challita-eid PM, Jakobovits A;  
XX WPI; 2002-425659/45.  
XX New compositions comprising a gene (designated 158P1D7), its encoded  
PT protein or their modulators, useful for treating or diagnosing cancers,  
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses  
or humans)  
XX Disclosure; Page 144; 181pp; English.  
XX The invention relates to a novel nucleic acid, designated 158P1D7. The  
CC compositions are useful for treating or diagnosing cancers, particularly  
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,  
CC horses or humans). The compositions are also useful for monitoring  
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid  
CC of the invention can be used in gene therapy to treat the said disorders.  
CC This sequence represents a human leukocyte antigen (HLA) peptide relating  
CC to the 158P1D7 protein of the invention.  
XX Sequence 9 AA;  
PS

Query Match 57.1%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
DB 1 LPPN 4  
|||||

RESULT 48  
ABJ01886  
ID ABJ01886 standard; Peptide; 9 AA.  
XX AC ABJ01886;  
XX 19-SEP-2002 (first entry)  
XX DE 158P1D7 related HLA peptide SEQ ID No 586.  
XX KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;  
XX KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;  
XX KW HLA.  
XX OS Homo sapiens.  
XX XX  
XX PN WQ200216593-A2.  
XX XX  
XX PD 28-FEB-2002.  
XX XX  
XX PF 22-AUG-2001; 2001WO-US26276.  
XX XX  
XX PR 22-AUG-2000; 2000US-227098P.  
XX PR 10-APR-2001; 2001US-282739P.  
XX XX  
XX PA (AGEN-) AGENSYS INC.  
XX XX  
XX PI Paris M, Hubert RS, Raitano AB, Afar DEH, Levin E;  
XX PI Challita-eid PM, Jakobovits A;  
XX DR WPI; 2002-425659/45.  
XX XX  
XX PT New compositions comprising a gene (designated 158P1D7), its encoded  
XX PT protein or their modulators, useful for treating or diagnosing cancers,  
XX PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses  
XX PT or humans)  
XX PS Disclosure; Page 147; 181pp; English.  
XX XX  
XX CC The invention relates to a novel nucleic acid, designated 158P1D7. The  
XX CC compositions are useful for treating or diagnosing cancers, particularly  
XX CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,  
XX CC horses or humans). The compositions are also useful for monitoring  
XX CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid  
XX CC of the invention can be used in gene therapy to treat the said disorders.  
XX CC This sequence represents a human leukocyte antigen (HLA) peptide relating  
XX CC to the 158P1D7 protein of the invention.  
XX XX  
SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
DB 1 LPPN 4  
|||||

RESULT 49  
ABU11109  
ID ABU11109 standard; peptide; 9 AA.  
XX XX

AC ABU11109;  
XX 05-FEB-2003 (first entry)  
XX DE House dust mite Der p1 antigen peptide #32.  
XX XX  
XX KW House dust mite; Der p1 antigen; human CD8 cell epitope; allergy;  
XX KW immune response; atopic patient; CD8+ T-cell epitope; anti-allergic.  
XX OS Dermatophagoides pteronyssinus.  
XX XX  
XX PN WQ200281512-A1.  
XX PD 17-OCT-2002.  
XX XX  
XX PF 03-APR-2002; 2002WO-GB01534.  
XX PR 06-APR-2001; 2001GB-0008752.  
XX XX  
XX PA (ISIS-) ISIS INNOVATION LTD.  
XX PI Ogg G, Seneviratne S;  
XX XX  
XX DR WPI; 2003-058499/05.  
XX XX  
XX PT New peptide fragments of the Der p1 antigen of the house dust mite  
XX PT Dermatophagoides pteronyssinus contain a human CD8+ T cell epitope and  
XX PT are useful to treat and prevent allergy to the major house dust mite  
XX PT allergen  
XX PS Disclosure; Page 31; 47pp; English.  
XX XX  
XX CC The present invention relates to house dust mite (Dermatophagoides  
XX CC pteronyssinus) Der p1 antigen peptides containing human CD8 cell  
XX CC epitopes. The peptides of the invention are useful in the treatment  
XX CC of human or animal patients, particularly to raise an immune response  
XX CC to the Der p1 antigen. They are useful in the treatment and prevention  
XX CC of allergies to the major house dust mite antigen, and to monitor  
XX CC disease activity in atopic patients. ABU11078-ABU11146 represent  
XX CC house dust mite Der p1 antigen peptides containing CD8+ T-cell  
XX CC epitopes.  
SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPNV 6  
DB 4 PPNV 7  
|||||

RESULT 50  
AAW14897  
ID AAW14897 standard; peptide; 10 AA.  
XX XX  
XX AC AAW14897;  
XX XX  
XX DT 27-NOV-1997 (first entry)  
XX XX  
XX DE Phakellistatin 8.  
XX XX  
XX KW cyclic; decapeptide; phakellistatin; sponge; cytostatic;  
XX KW anticancer.  
XX XX  
XX OS Phakellia costata.  
XX XX  
XX PH Key Location/Qualifiers  
XX FT Modified-site 1  
XX FT /note= "the imino group of this residue forms a  
XX FT peptide bond with the carboxy group of Ile(10),  
XX FT i.e. the residue is a component of a cyclic

FT Modified-site 10 peptide and is not an N-terminal"  
FT /note= "the carboxy group of this residue forms a  
FT peptide bond with the imino group of Pro(1),  
FT i.e. the residue is a component of a cyclic  
FT peptide and is not a C-terminal"  
XX  
PN US5646246-A.  
XX  
XX 08-JUL-1997.  
XX  
XX 14-NOV-1994; 94US-0338383.  
XX  
XX 14-NOV-1994; 94US-0338383.  
XX (UYAR-) UNIV ARIZONA STATE.  
XX  
XX Pettit GR, Xu J;  
XX PI  
XX WPI; 1997-362994/33.  
XX  
XX New cyclic peptide(s) designated phakellistatin -4, -5, -6, -7, -8  
PT and -9 - are isolated from the sponge Phakellia costata and may be  
PT used in treatment of cancer  
XX  
XX Claim 6; Column 55; 29pp; English.  
XX  
XX The patent discloses six new cyclic peptides which have been isolated  
CC from the Western Pacific Ocean sponge Phakellia costata. They are:  
CC cyclo-(Pro-Thr-Pro-Phe-Ile-Phe-Ser) (designated phakellistatin 4),  
CC cyclo-(Pro-Phe-Asn-Ala-Met-Ala-Ile) (designated phakellistatin 5),  
CC cyclo-(Pro-Trp-Leu-Pro-Ile-Pro-Phe) (designated phakellistatin 6),  
CC cyclo-(Pro-Pro-Ile-Phe-Ala-Leu-Pro-Pro-Tyr-Ile) (designated  
CC phakellistatin 7), cyclo-(Pro-Pro-Ile-Phe-Val-Leu-Pro-Pro-Tyr-Ile)  
CC (designated phakellistatin 8) and cyclo-(Pro-Pro-Ile-Phe-Val-Leu-Pro-  
CC Pro-Tyr-Val) (designated phakellistatin 9). The cyclic peptides all  
CC demonstrate in vitro P388 ED50 values of between 0.18 and 4.1 mcg/ml.  
CC They also demonstrate in vitro growth inhibitory activity against  
CC human cancer cell lines. They may thus be used in treatment of cancer.  
CC The present sequence is that of phakellistatin 8 which demonstrates an  
CC in vitro ED50 value against P388 cells of 2.9 mcg/ml.  
XX  
XX Sequence 10 AA;  
SQ

Query Match 57.1%; Score 4; DB 18; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLPP 4  
|||  
Db 5 VLPP 8

RESULT 51  
AAW14898  
ID AAW14898 standard; peptide; 10 AA.  
XX  
XX AAW14898;  
AC  
XX 27-NOV-1997 (first entry)  
DT  
XX  
XX Phakellistatin 9.  
DE  
XX  
XX cyclic; decapeptide; phakellistatin; sponge; cytostatic;  
KW anticancer.  
XX  
XX Phakellia costata.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1  
FT /note= "the imino group of this residue forms a  
FT peptide bond with the carboxy group of Val(10),  
FT i.e. the residue is a component of a cyclic  
FT peptide and is not a C-terminal"

FT Modified-site 10 peptide and is not an N-terminal"  
FT /note= "the carboxy group of this residue forms a  
FT peptide bond with the imino group of Pro(1),  
FT i.e. the residue is a component of a cyclic  
FT peptide and is not a C-terminal"  
XX  
PN US5646246-A.  
XX  
XX 08-JUL-1997.  
XX  
XX 14-NOV-1994; 94US-0338383.  
XX  
XX 14-NOV-1994; 94US-0338383.  
XX (UYAR-) UNIV ARIZONA STATE.  
XX  
XX Pettit GR, Xu J;  
XX PI  
XX WPI; 1997-362994/33.  
XX  
XX New cyclic peptide(s) designated phakellistatin -4, -5, -6, -7, -8  
PT and -9 - are isolated from the sponge Phakellia costata and may be  
PT used in treatment of cancer  
XX  
XX Claim 7; Column 55; 29pp; English.  
XX  
XX The patent discloses six new cyclic peptides which have been isolated  
CC from the Western Pacific Ocean sponge Phakellia costata. They are:  
CC cyclo-(Pro-Thr-Pro-Phe-Ile-Phe-Ser) (designated phakellistatin 4),  
CC cyclo-(Pro-Phe-Asn-Ala-Met-Ala-Ile) (designated phakellistatin 5),  
CC cyclo-(Pro-Trp-Leu-Pro-Ile-Pro-Phe) (designated phakellistatin 6),  
CC cyclo-(Pro-Pro-Ile-Phe-Ala-Leu-Pro-Pro-Tyr-Ile) (designated  
CC phakellistatin 7), cyclo-(Pro-Pro-Ile-Phe-Val-Leu-Pro-Pro-Tyr-Ile)  
CC (designated phakellistatin 8) and cyclo-(Pro-Pro-Ile-Phe-Val-Leu-Pro-  
CC Pro-Tyr-Val) (designated phakellistatin 9). The cyclic peptides all  
CC demonstrate in vitro P388 ED50 values of between 0.18 and 4.1 mcg/ml.  
CC They also demonstrate in vitro growth inhibitory activity against  
CC human cancer cell lines. They may thus be used in treatment of cancer.  
CC The present sequence is that of phakellistatin 9 which demonstrates an  
CC in vitro ED50 value against P388 cells of 4.1 mcg/ml.  
XX  
XX Sequence 10 AA;  
SQ

Query Match 57.1%; Score 4; DB 18; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLPP 4  
|||  
Db 5 VLPP 8

RESULT 52  
AAE05732  
ID AAE05732 standard; peptide; 10 AA.  
XX  
XX AAE05732;  
AC  
XX 24-SEP-2001 (first entry)  
DT  
XX  
XX Complementarity-determining region 3 (CDR3) of MoPhabs #4.  
DE  
XX  
XX CDR3; complementarity-determining region 3; monoclonal phage antibody;  
KW MoPhabs; antigen.  
XX  
XX Synthetic.  
OS  
XX US6265150-B1.  
PN  
XX 24-JUL-2001.  
PD  
XX 26-MAY-1998; 98US-0085072.  
PF

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XX 07-JUN-1995; 95US-0483633.
PR 18-SEP-1997; 97US-0932892.
XX (BECT ) BECTON DICKINSON & CO.
PA (CRUC-) CRUCELL HOLLAND BV.
XX Terstappen LW, Logtenberg T;
PI WPI; 2001-463929/50.
DR WPI; 2001-463929/50.
XX Obtaining a phage particle, useful for obtaining human antibodies
PT against known and novel surface antigens, by incubating a phage library
PT with target cells to allow binding of the antibody fragment to the
PT antigen.
XX Example 6; Column 6; 6pp; English.
XX The invention relates to a method of obtaining a phage particle
CC which has an antibody fragment directed against an antigen associated
CC with the surface of target cells in a heterogeneous cell population.
CC The method involves incubating a library of phage particles with the
CC target cells to allow binding of the antibody fragment expressed on
CC the surface of the phage particles to the antigen associated with
CC the target cells. The method is useful for obtaining human antibodies
CC against known and novel surface antigens in their native configuration,
CC expressed on phenotypically defined subpopulations of cells.
CC The present sequence is complementarity-determining region 3' (CDR3)
CC of monoclonal phage antibodies (Mophabs) used in the exemplification
CC of the invention.
XX SQ Sequence 10 AA;
XX Query Match 57.1%; Score 4; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.8e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LPPN 5
DB 3 LPPN 6
|||||
XX RESULT 53
XX ABJ01356
XX ID ABJ01356 standard; Peptide; 10 AA.
XX AC ABJ01356;
XX DT 19-SEP-2002 (first entry)
XX DE 158PID7 related HLA peptide SEQ ID No 56.
XX KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX HLA.
XX OS Homo sapiens.
XX PN WO200216593-A2.
XX PD 28-SEP-2002.
XX PF 19-SEP-2002 (first entry)
XX DE 158PID7 related HLA peptide SEQ ID No 56.
XX KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX HLA.
XX OS Homo sapiens.
XX PN WO200216593-A2.
XX PD 28-FEB-2002.
XX PF 22-AUG-2001; 2001WO-US26276.
XX PR 22-AUG-2000; 2000US-227098P.
XX PR 10-APR-2001; 2001US-282739P.
XX PA (AGEN-) AGENSYS INC.
XX PI Paris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX PI Challita-eid PM, Jakobovits A;
XX DR WPI; 2002-425659/45.
XX PT New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
or humans)
XX Disclosure; Page 127; 181pp; English.
XX The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention.
XX SQ Sequence 10 AA;
XX Query Match 57.1%; Score 4; DB 23; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.8e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 LPPN 5
DB 5 LPPN 8
|||||
XX RESULT 54
XX ABJ01361
XX ID ABJ01361 standard; Peptide; 10 AA.
XX AC ABJ01361;
XX DT 19-SEP-2002 (first entry)
XX DE 158PID7 related HLA peptide SEQ ID No 61.
XX KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX HLA.
XX OS Homo sapiens.
XX PN WO200216593-A2.
XX PD 28-FEB-2002.
XX PF 22-AUG-2001; 2001WO-US26276.
XX PR 22-AUG-2000; 2000US-227098P.
XX PR 10-APR-2001; 2001US-282739P.
XX PA (AGEN-) AGENSYS INC.
XX PI Paris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX PI Challita-eid PM, Jakobovits A;
XX DR WPI; 2002-425659/45.
XX PT New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
or humans)
XX Disclosure; Page 128; 181pp; English.
XX The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.

```

CC This sequence represents a human leukocyte antigen (HLA) peptide relating  
 CC to the 158P1D7 protein of the invention.

XX Sequence 10 AA;

Query Match 57.1%; Score 4; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
 DB 3 LPPN 6

RESULT 55  
 ABJ01456  
 ID ABJ01456 standard; Peptide; 10 AA.

XX AC ABJ01456;

XX DT 19-SEP-2002 (first entry)

DE 158P1D7 related HLA peptide SEQ ID No 156.

KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;  
 KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;  
 KW HLA.

XX OS Homo sapiens.

XX PN WO200216593-A2.

XX PD 28-FEB-2002.

XX PF 22-AUG-2001; 2001WO-US26276.

XX PR 22-AUG-2000; 2000US-227098P.

XX PR 10-APR-2001; 2001US-282739P.

XX PA (AGEN-) AGENSYS INC.

XX PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;

XX PI Challita-eid PM, Jakobovits A;

XX DR WPI; 2002-425659/45.

XX PT New compositions comprising a gene (designated 158P1D7), its encoded  
 PT protein or their modulators, useful for treating or diagnosing cancers,  
 PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses  
 PT or humans)

XX PS Disclosure; Page 131; 181pp; English.

XX CC The invention relates to a novel nucleic acid, designated 158P1D7. The  
 CC compositions are useful for treating or diagnosing cancers, particularly  
 CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,  
 CC horses or humans). The compositions are also useful for monitoring  
 CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid  
 CC of the invention can be used in gene therapy to treat the said disorders.  
 CC This sequence represents a human leukocyte antigen (HLA) peptide relating  
 CC to the 158P1D7 protein of the invention.

XX SQ Sequence 10 AA;

Query Match 57.1%; Score 4; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
 DB 1 VLPP 4

RESULT 56

ABJ01461

ID ABJ01461 standard; Peptide; 10 AA.

XX AC ABJ01461;

XX DT 19-SEP-2002 (first entry)

DE 158P1D7 related HLA peptide SEQ ID No 161.

KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;  
 KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;  
 KW HLA.

XX OS Homo sapiens.

XX PN WO200216593-A2.

XX PD 28-FEB-2002.

XX PF 22-AUG-2001; 2001WO-US26276.

XX PR 22-AUG-2000; 2000US-227098P.

XX PR 10-APR-2001; 2001US-282739P.

XX PA (AGEN-) AGENSYS INC.

XX PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;

XX PI Challita-eid PM, Jakobovits A;

XX DR WPI; 2002-425659/45.

XX PT New compositions comprising a gene (designated 158P1D7), its encoded  
 PT protein or their modulators, useful for treating or diagnosing cancers,  
 PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses  
 PT or humans)

XX PS Disclosure; Page 131; 181pp; English.

XX CC The invention relates to a novel nucleic acid, designated 158P1D7. The  
 CC compositions are useful for treating or diagnosing cancers, particularly  
 CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,  
 CC horses or humans). The compositions are also useful for monitoring  
 CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid  
 CC of the invention can be used in gene therapy to treat the said disorders.  
 CC This sequence represents a human leukocyte antigen (HLA) peptide relating  
 CC to the 158P1D7 protein of the invention.

XX SQ Sequence 10 AA;

Query Match 57.1%; Score 4; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5

DB 2 LPPN 5

RESULT 57

ABJ01479

ID ABJ01479 standard; Peptide; 10 AA.

XX AC ABJ01479;

XX DT 19-SEP-2002 (first entry)

DE 158P1D7 related HLA peptide SEQ ID No 179.

KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;  
 KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;  
 KW HLA.





CC horses or humans). The compositions are also useful for monitoring  
 CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid  
 CC of the invention can be used in gene therapy to treat the said disorders.  
 CC This sequence represents a human leukocyte antigen (HLA) peptide relating  
 CC to the 158pD7 protein of the invention.

XX Sequence 10 AA;  
 SQ Query Match 57.1%; Score 4; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
 DB 3 LPPN 6

## RESULT 60

ABG75571  
 ID ABG75571 standard; Peptide; 10 AA.

XX AC ABG75571;  
 XX 22-APR-2003 (first entry)

DT CDR3 peptide sequence, #4, used in phage antibody construction.

DE Phage; antibody; antigen; target cell; phage particle;

XX cell-type specific phage antibody library; phage antibody; Phab;

KW monoclonal phage antibody; Mophab; blood cell; foetal bone marrow cell;

KW complementarity determining region 3; CDR3; human.

XX Homo sapiens.

OS Synthetic.

XX US2002132228-A1.

XX 19-SEP-2002.

XX 24-MAY-2001; 2001US-0865048.

XX 07-JUN-1995; 95US-0483633.

XX 26-MAY-1998; 98US-0085072.

XX 18-SEP-1997; 97US-0932892.

XX (TERS/) TERSTAPPEN L W M M.

PA (LOGT/) LOGTENBERG T.

XX Terstappen LWM, Logtenberg T;

XX WPI; 2003-174076/17.

XX Obtaining phage having antibody specific for cell surface antigen of

PT target cells in heterogeneous cell population, by incubating phage

PT antibody library with target cells, and separating phage particles

PT bound target cells

XX Example 6; Page 4; 5pp; English.

XX The invention discloses a method for obtaining a phage comprising an

CC antibody, or its fragment, directed against antigens associated with a

CC target cells surface in a heterogeneous cell population. The method

CC comprises providing a library of antibodies, or their fragments,

CC expressed on the surface of phage particles, incubating the phage

CC antibody library with the target cells, separating the target cells and

CC phage particles associated with them from the phage particles not

CC associated with the target cells and then recovering the phage particles.

CC Also disclosed is a cell-type specific phage antibody library and an

CC antibody, or antibody fragment, obtained using the method. The method is

CC useful for obtaining a selection of phage antibodies (Phabs) and

CC monoclonal phage antibodies (Mophabs). The method is also useful for

CC detecting known and novel structures on various populations of blood and

CC foetal bone marrow cells. The sequence presented is an example of the

CC partly randomised human complementarity determining region 3 (CDR3) used  
 CC in the construction of the antibodies.

XX Sequence 10 AA;  
 SQ Query Match 57.1%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
 DB 3 LPPN 6

## RESULT 61

AAR47937  
 ID AAR47937 standard; Protein; 11 AA.

XX AC AAR47937;  
 XX 25-MAR-2003 (updated)

DT 28-JUL-1994 (first entry)

DE Peptide fragment of galactose contg. glycoprotein H-gal-GP complex.

XX Haemonchus contortus; helminth; arthropod; immunisation; vaccine;

KW glycoprotein; H-gal-GP; Ostertagia; Trichostrongylus; antigen.

XX Haemonchus contortus.

XX Key Location/Qualifiers

FT Misc-difference 6 /note= "Unspecified amino acid."

XX WO9402169-A1.

XX 03-FEB-1994.

XX 20-JUL-1993; 93WO-GB01521.

XX 21-JUL-1992; 92GB-0015505.

XX 19-AUG-1992; 92GB-0017635.

XX (PITM) PITMAN MOORE INC.

XX Knox DP, Liddell S, Murray J, Smith SK, Smith WD;

XX WPI; 1994-048545/06.

XX Metazoan parasite antigens from the intestinal brush border which

PT bind pepstatin - used in vaccines to protect against helminth and

PT arthropod disease

XX Disclosure; Page 35; 109pp; English.

XX An H-gal-GP glycoprotein coding sequence (Clone HG3 (AAQ55918)) is

CC used to produce the glycoprotein which can then be used as an

CC antigen. A vaccine composition comprising the glycoprotein or

CC fragments of it can be used to protect against diseases caused by

CC helminths and arthropods, e.g. cattle ticks and myiasis flies. The

CC antigen may be obtained from Haemonchus, Ostertagia or

CC Trichostrongylus helminths. This peptide sequence is the

CC N-terminal sequence of a fragment of the H-gal-GP complex.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 11 AA;

Query Match 57.1%; Score 4; DB 15; Length 11;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNVG 7

||||

```

Db          7 PNVG 10

RESULT 62
AAW45201
ID  AAW45201 standard; peptide; 11 AA.
XX
XX
AC
XX
DT  19-JAN-2001 (first entry)
XX
DE  Src homology 3 domain binding peptide #8.
XX
XX  Src homology domain 3; SH3; protein-protein interaction; cancer;
KW  signal transduction inhibition; immune suppression-associated disease.
XX
OS  Synthetic.
XX
XX  WO200047607-A1.
XX
XX  17-AUG-2000.
XX
XX  12-FEB-2000; 2000WO-KR00107.
XX
XX  12-FEB-1999; 99AU-0008643.
XX  02-JUN-1999; 99KR-0020282.
XX
XX  (YOON/) YOON J H.
PA  (HANY/) HAN Y T.
XX
XX  Yoon JH, Han YT, Lee KY;
XX
XX  WPI; 2000-533010/48.
XX
XX  Synthetic peptides useful for treating cancers and immunosuppressive
PT  disorders by disrupting interactions of the SH (Src homology) 2 and SH3
PT  motifs of Src family kinase proteins -
XX
XX  Claim 3; Page 34; 40pp; English.
XX
XX  The present sequence is a synthetic peptide which has a high affinity for
CC  the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC  involved in signal transduction pathways, and this peptide can be used to
CC  inhibit these, by disrupting protein-protein interactions, in the
CC  treatment of cancer, particularly hepatocellular carcinoma, cervical
CC  cancer, colon adenocarcinoma and fibrosarcoma, and immune
CC  suppression-associated diseases.
XX
XX  Sequence 11 AA;

Query Match      57.1%; Score 4; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LPPN 5
        ||||
Db      6 LPPN 9

RESULT 64
AAB17502
ID  AAB17502 standard; peptide; 11 AA.
XX
XX  AAB17502;
XX
XX  31-OCT-2000 (first entry)
XX
XX  VIP-mimetic peptide sequence SEQ ID NO:606.
XX
XX  Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW  autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW  immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW  MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW  cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW  vascular endothelial growth factor; matrix metalloproteinase;
KW  asthma; thrombosis; pharmaceutical.
XX
XX  Synthetic.
OS

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---

```

Db          7 PNVG 10

RESULT 62
AAW45201
ID  AAW45201 standard; peptide; 11 AA.
XX
XX
AC
XX
DT  05-MAY-1998 (first entry)
XX
DE  Vasoactive intestinal peptide fragment lipid conjugate #21.
XX
XX  Vasoactive intestinal peptide; VIP; lipophilic conjugate;
KW  male impotence; neurodegenerative disease; sexual dysfunction.
XX
OS  Synthetic.
XX
OS  Mammalia.
XX
XX  Key Location/Qualifiers
FT  Modified-site 1
FT  /note= "Stearoyl-Lys"
FT  Modified-site 11
FT  /note= "C-terminal amide"
XX
XX  WO9740070-A1.
XX
XX  30-OCT-1997.
XX
XX  18-APR-1997; 97WO-IL00129.
XX
XX  23-APR-1996; 96IL-0118003.
XX
XX  (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX  (YEDA ) YEDA RES & DEV CO LTD.
XX
XX  Fridkin M, Gozes I;
XX
XX  WPI; 1997-535777/49.
XX
XX  New conjugates of a peptide coupled to a lipophilic moiety - useful
PT  in the treatment of neurodegenerative diseases and sexual
PT  dysfunctions.
XX
XX  Claim 6; Page 40; 77pp; English.
XX
XX  The present sequence represents a specifically claimed example of a
CC  peptide derived from a fragment of vasoactive intestinal peptide (VIP),
CC  coupled to a lipophilic moiety. The conjugates are useful in treatment of
CC  neurodegenerative diseases, particularly Alzheimer's disease, Down
CC  syndrome, decline in motor or cognitive function due to ischaemia,
CC  stroke, hereditary disease of the central and peripheral nervous system,
CC  decline in motor or cognitive function due to injury of the central or
CC  peripheral nervous system or neuronal disorder associated with blood
CC  circulation and neuronal survival. The compositions are suitable for
CC  nasal administration, particularly as a nasal spray. Some of the
CC  conjugates are also useful in treatment of sexual dysfunctions,
CC  particularly male impotence. The compositions are adapted for transdermal
CC  application, the carrier being 1-glycerol monocaprylate.
XX
XX  Sequence 11 AA;

Query Match      57.1%; Score 4; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LPPN 5
        ||||
Db      4 LPPN 7

RESULT 63
AAB21131

```

XX WO200024782-A2.  
XX PD  
XX  
XX PD  
XX 04-MAY-2000.  
XX PF  
XX 25-OCT-1999; 99WO-US25044.  
XX PR  
XX 23-OCT-1998; 98US-0105371.  
XX PR  
XX 22-OCT-1999; 99US-0428082.  
XX PA  
XX (AMGE-) AMGEN INC.  
XX PI  
XX Feige U, Liu C, Cheetham J, Boone TC;  
XX WPI; 2000-350702/30.  
XX DR  
XX  
XX PT  
XX Novel composition of matter comprising an Fc domain and  
XX PT pharmacologically active peptides, useful for treating cancer and  
XX PT autoimmune diseases -  
XX PS  
XX Claim 39; Page 408; 608pp; English.  
XX CC  
XX The present invention describes composition of matter (I) comprising an  
XX CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
XX CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each  
XX CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,  
XX CC -(L1)c-P1-(L2)d-P2-(L3)e-P\*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4  
XX CC where P1, P2, P3, and P4 = are each independently sequences of  
XX CC pharmacologically active peptides; L1, L2, L3, and L4 = are each  
XX CC independently linkers; and a, b, c, d, e, and f = are each independently  
XX CC 0 or 1, provided that at least 1 of a and b is 1. The composition can  
XX CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive  
XX CC activities. DNAs, vectors and host cells from the present invention can  
XX CC be used for producing pharmaceutical compositions. The compositions are  
XX CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.  
XX CC The use of an Fc domain (rather than a Fab domain) can provide a longer  
XX CC half-life or incorporate functions such as Fc receptor binding, protein  
XX CC A binding, complement fixation, and possibly placental transfer. AAA69443  
XX CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid  
XX CC sequences used in the exemplification of the present invention.  
XX SQ  
XX Sequence 11 AA;  
Query Match 57.1%; Score 4; DB 21; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LPPN 5  
Db ||||  
4 LPPN 7  
RESULT 65  
AAB17522  
ID AAB17522 standard; Peptide; 11 AA.  
XX AC  
XX AAB17522;  
XX DT  
XX 31-OCT-2000 (first entry)  
XX DE  
XX VIP-mimetic peptide sequence SEQ ID NO:626.  
XX KW  
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
XX KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
XX KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;  
XX KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
XX KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
XX KW vascular endothelial growth factor; matrix metalloproteinase;  
XX KW asthma; thrombosis; pharmaceutical.  
XX OS  
XX Synthetic.  
XX XX  
XX WO200024782-A2.  
XX PN

XX 04-MAY-2000.  
XX PD  
XX  
XX PF  
XX 25-OCT-1999; 99WO-US25044.  
XX PR  
XX 23-OCT-1998; 98US-0105371.  
XX PR  
XX 22-OCT-1999; 99US-0428082.  
XX PA  
XX (AMGE-) AMGEN INC.  
XX PI  
XX Feige U, Liu C, Cheetham J, Boone TC;  
XX WPI; 2000-350702/30.  
XX DR  
XX  
XX PT  
XX Novel composition of matter comprising an Fc domain and  
XX PT pharmacologically active peptides, useful for treating cancer and  
XX PT autoimmune diseases -  
XX PS  
XX Claim 39; Page 415; 608pp; English.  
XX CC  
XX The present invention describes composition of matter (I) comprising an  
XX CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
XX CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each  
XX CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,  
XX CC -(L1)c-P1-(L2)d-P2-(L3)e-P\*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4  
XX CC where P1, P2, P3, and P4 = are each independently sequences of  
XX CC pharmacologically active peptides; L1, L2, L3, and L4 = are each  
XX CC independently linkers; and a, b, c, d, e, and f = are each independently  
XX CC 0 or 1, provided that at least 1 of a and b is 1. The composition can  
XX CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive  
XX CC activities. DNAs, vectors and host cells from the present invention can  
XX CC be used for producing pharmaceutical compositions. The compositions are  
XX CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.  
XX CC The use of an Fc domain (rather than a Fab domain) can provide a longer  
XX CC half-life or incorporate functions such as Fc receptor binding, protein  
XX CC A binding, complement fixation, and possibly placental transfer. AAA69443  
XX CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid  
XX CC sequences used in the exemplification of the present invention.  
XX SQ  
XX Sequence 11 AA;  
Query Match 57.1%; Score 4; DB 21; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LPPN 5  
Db ||||  
4 LPPN 7  
RESULT 66  
AAU69073  
ID AAU69073 standard; Peptide; 11 AA.  
XX AC  
XX AAU69073;  
XX DT  
XX 29-JAN-2002 (first entry)  
XX DE  
XX Bacterial conserved peptide motif #22.  
XX KW  
XX Bacteria; invariant peptide motif; antibacterial; drug target;  
XX KW infection.  
XX OS  
XX Bacteria.  
XX XX  
XX WO200174130-A2.  
XX PN  
XX 11-OCT-2001.  
XX PD  
XX  
XX PF  
XX 31-AUG-2000; 2000WO-IN00085.  
XX XX  
XX 30-MAR-2000; 2000US-0539032.  
XX XX

PA (COUL ) COUNCIL SCI & IND RES.  
 XX Brahmachari KS, Dash D;  
 XX WPI; 2001-656954/75.  
 DR  
 XX Computer- based method for identifying invariant peptide motifs which  
 PT are useful as drug targets, especially for broad spectrum  
 PT antibacterials, comprises comparing sequences between species -  
 XX  
 PS Claim 4; Page 21; 29pp; English.  
 XX  
 CC The invention relates to a computer- based method for identifying  
 CC invariant peptide motifs comprising the genome-wise protein sequence  
 CC comparison of several organisms. An overlapping peptide library is  
 CC constructed from all the protein sequences of selected organisms  
 CC available in the database and sorting the peptides, of length N,  
 CC alphabetically according to the one-letter amino acid code. Common  
 CC peptide sequences are matched, located in their original proteins and  
 CC labeled by origin and location. The common sequences are then joined to  
 CC produce long chains of invariant sequences, and their secondary  
 CC structures annotated from a crystal structure database  
 CC Sequences that are not commonly conserved within the genomes of  
 CC pathogenic and non-pathogenic strains are selected and the identified  
 CC motifs are validated as potential targets by searching for them in the  
 CC host genome and rejecting any that are present in the host genome.  
 CC The method is used to identify invariant peptide motifs and potential  
 CC drug targets, particularly in screening for drugs with broad spectrum  
 CC antibacterial activity, also for specific diagnosis of infection. The  
 CC method can also be used to predict toxicity and alternative targets, and  
 CC in a modification, to assign function to proteins of no known function.  
 CC The method requires no a priori assumptions, and so avoids bias, and  
 CC allows rapid and simultaneous genome-wise comparison of many different  
 CC protein sequences. The motifs are identified simply and accurately  
 CC without complicated mathematical calculations. The present sequence  
 CC is a bacterial invariant protein motif of the invention.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 57.1%; Score 4; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PNVG 7  
 Db |||||  
 6 PNVG 9  
 RESULT 67  
 ID AAU97808 standard; Peptide; 11 AA.  
 XX AAU97808;  
 AC AAU97808;  
 XX  
 XX 27-AUG-2002 (first entry)  
 DT Synthetic thrombopoietin (TPO) c-terminal epitope peptide #6.  
 DE  
 XX Thrombopoietin; TPO; immunodominant epitope; cancer; chemotherapy;  
 KW radiation treatment; viral infection; metabolic disorder;  
 KW growth disorder; thrombocytopenia; cytostatic; haemostatic;  
 KW virucide.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200234779-A1.  
 PN  
 XX 02-MAY-2002.  
 PD  
 XX 04-JUN-2001; 2001WO-US40846.  
 PF  
 XX 27-OCT-2000; 2000US-243913P.  
 PR 01-JUN-2001; 2001US-0872702.

(GETH ) GENENTECH INC.  
 XX  
 XX Koren E, Lowe JHN;  
 PI  
 XX WPI; 2002-452421/48.  
 DR  
 XX Modifying a polypeptide, useful for designing or engineering less  
 PT immunogenic molecules intended for use in therapy, by modifying an  
 PT immunodominant epitope identified using an antibodies from a naive  
 PT human or animal population -  
 XX  
 XX Example 3; Page 48; 78pp; English.  
 PS  
 XX The invention describes a method of modifying a polypeptide comprising  
 CC modifying an immunodominant epitope that is identified using an antibody  
 CC or population of antibodies obtained from a naive human or animal  
 CC population. The method is useful for designing and engineering less  
 CC immunogenic molecules. In particular, the method is useful reducing the  
 CC immune response to a polypeptide, while still retaining a substantial  
 CC therapeutic activity of such polypeptide. The modified polypeptide is  
 CC useful in treating cancer and/or patient undergoing chemotherapy or  
 CC radiation treatment, in treating viral infections, metabolic disorders  
 CC or growth disorders. Specifically, the recombinant human thrombopoietin  
 CC is useful for treating thrombocytopenia. The modified polypeptide may be  
 CC used therapeutically in a variety of animal species including human,  
 CC primate, cattle, pigs, poultry or mice. This sequence represents a  
 CC synthetic thrombopoietin (TPO) c-terminal epitope peptide used to create  
 CC antibodies against TPO.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 57.1%; Score 4; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPPN 5  
 Db |||||  
 6 LPPN 9  
 RESULT 68  
 ID ABB73104 standard; Peptide; 11 AA.  
 XX ABB73104;  
 AC ABB73104;  
 XX  
 XX 05-APR-2002 (first entry)  
 DT VIP mimetic peptide SEQ ID NO:606.  
 DE  
 XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;  
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;  
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;  
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;  
 KW antanaemic; anorectic; antiinfectivity; haemostatic; dermatological;  
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
 KW sleep disorder; neurological degenerative disease; anaemia;  
 KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;  
 KW Fanconi's syndrome.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX WO200183525-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX 02-MAY-2001; 2001WO-US14310.  
 PF  
 XX

PR 03-MAY-2000; 2000US-0563286.  
 XX (AMGE-) AMGEN INC.  
 XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;  
 PI WPI; 2002-130313/17.  
 DR Novel vehicle-peptide molecule or its multimers useful for treating  
 XX inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
 PT diabetic retinopathy, obesity, sleep disorders and infertility -  
 XX Claim 39; Page 51; 176pp; English.  
 XX The present invention describes a vehicle-peptide molecule (I) or its  
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,  
 CC antianemic, anorectic, antiinfertility, haemostatic, dermatological and  
 CC neuroprotective activities. (I) can be used as a therapeutic or  
 CC prophylactic agent as well as for screening purposes. (I) is useful for  
 CC diagnosing diseases characterised by dysfunction of their associated  
 CC protein of interest, for identifying normal or abnormal proteins of  
 CC interest, as a part of diagnostic kit to detect the presence of their  
 CC proteins of interest in a biological sample. Additionally, (I) is useful  
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
 CC infertility, and neurological degenerative diseases. (I), comprising  
 CC EPO-mimetic compounds are useful for treating disorders characterised by  
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising  
 CC compounds are useful for treating conditions that involve an existing  
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic  
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,  
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
 CC represent amino acid and nucleic acid sequences used in the  
 CC exemplification of the present invention.  
 XX Sequence 11 AA;  
 SQ  
 Query Match 57.1%; Score 4; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPN 5  
 DB 4 LPN 7  
 RESULT 69  
 ABB73124  
 ID ABB73124 standard; Peptide; 11 AA.  
 XX ABB73124;  
 AC  
 AC  
 DT 05-APR-2002 (first entry)  
 XX VTP mimetic peptide SEQ ID NO:626.  
 DE  
 XX Modified peptide; mimetic; FC domain; fusion; immunoglobulin G; IgG;  
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;  
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;  
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;  
 KW antianemic; anorectic; antiinfertility; haemostatic; dermatological;  
 KW neuroprotective; inflammatory diseases; autoimmune disease; tumour growth;  
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
 KW sleep disorder; neurological degenerative disease; anaemia;  
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
 KW Fanconi's syndrome.  
 XX Homo sapiens.  
 OS Synthetic.

XX WO200183525-A2.  
 XX 08-NOV-2001.  
 XX 02-MAY-2001; 2001WO-US14310.  
 XX 03-MAY-2000; 2000US-0563286.  
 XX (AMGE-) AMGEN INC.  
 XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;  
 XX WPI; 2002-130313/17.  
 XX Novel vehicle-peptide molecule or its multimers useful for treating  
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
 PT diabetic retinopathy, obesity, sleep disorders and infertility -  
 XX Claim 39; Page 51; 176pp; English.  
 XX The present invention describes a vehicle-peptide molecule (I) or its  
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,  
 CC antianemic, anorectic, antiinfertility, haemostatic, dermatological and  
 CC neuroprotective activities. (I) can be used as a therapeutic or  
 CC prophylactic agent as well as for screening purposes. (I) is useful for  
 CC diagnosing diseases characterised by dysfunction of their associated  
 CC protein of interest, for identifying normal or abnormal proteins of  
 CC interest, as a part of diagnostic kit to detect the presence of their  
 CC proteins of interest in a biological sample. Additionally, (I) is useful  
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
 CC infertility, and neurological degenerative diseases. (I), comprising  
 CC EPO-mimetic compounds are useful for treating disorders characterised by  
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising  
 CC compounds are useful for treating conditions that involve an existing  
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic  
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,  
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
 CC represent amino acid and nucleic acid sequences used in the  
 CC exemplification of the present invention.  
 XX Sequence 11 AA;  
 SQ  
 Query Match 57.1%; Score 4; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPN 5  
 DB 4 LPN 7  
 RESULT 70  
 AAB51854  
 ID AAB51854 standard; Protein; 12 AA.  
 XX AAB51854;  
 AC  
 AC  
 DT 16-FEB-2001 (first entry)  
 XX Human secreted protein sequence encoded by gene 28 SEQ ID NO:87.  
 DE  
 XX Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
 KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;  
 KW ophthalmological; vulnary; autoimmune disease; rheumatoid arthritis;  
 KW hyperproliferative disorders; cancer; cardiovascular disorder;  
 KW cardiac arrest; cerebrovascular disorder; nervous system disorder;  
 XX Alzheimer's disease; ocular disorder; wound healing; skin aging.

OS Homo sapiens.  
 XX WO2000061626-A1.  
 XX 19-OCT-2000.  
 XX PF 06-APR-2000; 2000WO-US09066.  
 XX PR 09-APR-1999; 99US-0128698.  
 XX PR 20-JAN-2000; 2000US-0176926.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX (ROSE/) ROSEN C A.  
 XX PI Rosen CA, Ruben SM, Komatsoulis G;  
 XX WPI: 2000-619227/59.  
 XX DR N-PSDB; AAC93506.  
 XX  
 PT New nucleic acid molecules encoding 49 human secreted proteins for  
 PT diagnosing, preventing or ameliorating medical conditions and used for  
 PT food additives or preservatives -  
 XX  
 PS Claim 11; Page 474; 516pp; English.  
 XX  
 CC Polynucleotide sequences AAC93479 - AAC93527 represent cDNA encoding  
 CC human secreted proteins AAB51827 - AAB51875. Sequences AAB51876 -  
 CC AAB51927 represent alternative polypeptides encoded by the genes, and  
 CC amino acid sequences with which they share homology. The genes and  
 CC proteins have activities dependent on the tissues and cells in which they  
 CC are expressed. Examples of their activities include immunosuppressive;  
 CC antarthritic; antirheumatic; antiproliferative; cytostatic; cardiac;  
 CC vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;  
 CC virucide; fungicide; opthalmological; and vulnerary. The secreted  
 CC proteins, polynucleotides, antagonists and agonists may be useful in  
 CC treating, preventing and/or diagnosing diseases and disorders such as  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angioneuroma, nervous system disorders e.g. Alzheimer's disease,  
 CC infections caused by bacteria, viruses and fungi and ocular disorders  
 CC e.g. corneal infection. The polypeptides can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional  
 CC components. Oligonucleotides AAC93470 - AAC93478 and peptide AAB51826 are  
 CC used in the isolation and characterisation of the proteins and  
 CC polynucleotides of the invention.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 57.1%; Score 4; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLPP 4  
 Db 3 VLPP 6  
 RESULT 71  
 ABB05302  
 ID ABB05302 standard; Peptide; 12 AA.  
 XX  
 AC ABB05302;  
 XX  
 DT 04-APR-2002 (first entry)  
 XX  
 DE Polyurethane and not fabric binding peptide P 46 SEQ ID NO:36.  
 XX

KW Human; tumour necrosis factor alpha; TNF-alpha; VEGF; detergent; stain;  
 KW bacteriophage; phage library; vascular endothelial growth factor;  
 KW collar soil; polyurethane; egg; tea; hair; skin; cleaning composition.  
 XX  
 OS Unidentified bacteriophage.  
 XX  
 PN WO200179479-A2.  
 XX 25-OCT-2001.  
 XX  
 PF 11-APR-2001; 2001WO-US11811.  
 XX  
 PR 14-APR-2000; 2000US-197259P.  
 XX  
 XX (GENV ) GENENCOR INT INC.  
 XX  
 XX Estell DA, Murray CJ, Tijerina P, Chen Y;  
 XX WPI: 2002-139323/18.  
 XX  
 DR Screening ligand library comprises allowing binding of ligand with  
 XX anti-target, contacting unbound ligands with selected target to form  
 PT target-bound ligand complex and identifying target bound ligands on the  
 PT complex -  
 XX  
 PS Claim 22; Page 34; 51pp; English.  
 XX  
 CC The present invention describes a method for screening a ligand library  
 CC (LL). The method comprises: (a) contacting the LL with an anti-target  
 CC (AT) to allow the ligands to bind to the AT; (b) separating unbound  
 CC ligands; (c) contacting the unbound ligands with a selected target (T)  
 CC to allow binding of unbound ligands to (T) to form a (T)-bound ligand  
 CC complex (C); (d) separating (C) from ligands which do not bind (T); and  
 CC (e) identifying (T)-bound ligands on (C). The method can be used for  
 CC screening a ligand library, e.g., a library of peptides, polypeptides,  
 CC non-polypeptides or oligonucleotides. A ligand (I) identified by the  
 CC method can be used in a cleaning, therapeutic or personal care  
 CC application. The method is preferably useful for identifying peptide  
 CC useful in cleaning compositions, which involves contacting peptide  
 CC library with AT such as fabric, ceramic, glass, stainless steel or  
 CC plastic; separating unbound AT peptides; contacting unbound AT peptides  
 CC with a target which is a stain such as porphyrin derived stain, tannin  
 CC derived stain, carotenoid pigment derived stain, anthocyanin pigment  
 CC derived stain, soil-based derived stain, oil-based derived stain, and  
 CC human body stain, to allow unbound peptide to bind with the stain to form  
 CC stain-bound peptide complex and identifying the stain-bound peptide on  
 CC the stain-bound peptide complex. A selective targeting method for  
 CC screening a library of ligands that bind to a target may be used to  
 CC identify ligands that bind to a target under harsh conditions. The  
 CC selective targeting method may be used to screen and identify a ligand  
 CC useful for therapeutic intervention, e.g., a library of ligands may be  
 CC screened to identify a tumour-bound ligand. The selective targeting  
 CC method may be used to identify cell type specific surface molecules.  
 CC Preferred anti-targets include one or more different cell types, cells  
 CC in different states, or cells that do not display the surface molecule.  
 CC ABB05232 to ABB05346 represent phage-peptides ligands which are used in  
 CC the exemplification of the present invention.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 57.1%; Score 4; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPPN 5  
 Db 3 LPPN 6  
 RESULT 72  
 ABB04979  
 ID ABB04979 standard; Peptide; 12 AA.  
 XX

AC ABB04979;  
 XX  
 DT 15-MAR-2002 (first entry)  
 XX  
 DE Bovine adenovirus type 3 amino acid sequence SEQ ID NO:34.  
 XX  
 DE Bovine adenovirus 3; BAV3; vaccine; gene therapy; genetic disease;  
 KW haemophilia; thalassaemia; emphysema; Gaucher's disease; cancer;  
 KW cystic fibrosis; Duchenne muscular dystrophy; Duchenne's myopathy;  
 KW Becker's myopathy; viral disease; AIDS; herpesvirus infection;  
 KW cytomegalovirus infection; papillomavirus infection;  
 KW cardiovascular disease.  
 XX  
 OS Mastadenovirus b083.  
 XX  
 XX US6319716-B1.  
 PN  
 XX 20-NOV-2001.  
 PD  
 XX 23-JUN-1998; 98US-0103330.  
 PF  
 XX 23-JUN-1997; 97US-0880234.  
 PR  
 XX (UUSA-) UNIV SASKATCHEWAN.  
 PA  
 XX Tikoo SK, Babiuk LA, Reddy PS, Zakhartchouk A, Baxi M;  
 PI WPI; 2002-105175/14.  
 XX  
 XX Constructing a recombinant bovine adenovirus vector 3 (BAV3) vector,  
 PT useful as vaccine and for gene therapy, comprises linking the  
 PT heterologous sequence to a sequence homologous to BAV3 sequences  
 PT surrounding the insertion site  
 XX  
 XX Example 2; Column 129-130; 181pp; English.  
 PS  
 XX The present invention describes a method for constructing a recombinant  
 CC bovine adenovirus vector 3 (BAV3) vector having a heterologous sequence  
 CC inserted into an insertion site. The method comprises linking the  
 CC heterologous sequence to sequences which are substantially homologous to  
 CC BAV3 sequences surrounding the insertion site, to form an insertion  
 CC cassette. The BAV3 and expression systems can be used for insertion of  
 CC foreign sequences, for providing DNA control sequences, for diagnostic  
 CC transcriptional and translational regulatory sequences, for purposes  
 CC purposes to detect the presence of viral nucleic acids or proteins  
 CC encoded by these regions in a subject or biological sample, for  
 CC providing immunological polypeptides or their fragments, for vaccines,  
 CC and for gene therapy for the treatment of genetic diseases (e.g.,  
 CC haemophilia, thalassaemias, emphysema, Gaucher's disease, cystic  
 CC fibrosis, Duchenne muscular dystrophy, Duchenne's or Becker's  
 CC myopathy), cancers, viral diseases (e.g., AIDS, herpesvirus infection,  
 CC cytomegalovirus infection and papillomavirus infection), and  
 CC cardiovascular diseases. The present sequence represents a BAV3 amino  
 CC acid sequence which is used in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 12 AA;  
 SQ  
 Query Match 57.1%; Score 4; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLPP 4  
 DB 8 VLPP 11  
 RESULT 73  
 AAY20712  
 ID AAY20712 standard; Protein; 13 AA.  
 XX  
 AC AAY20712;  
 XX

DT 22-JUL-1999 (first entry)  
 XX  
 DE Human neurofilament-M wild type protein fragment 54.  
 XX  
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 KW frameshift mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin 1; presenilin 2; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9845322-A2.  
 PN  
 XX 15-OCT-1998.  
 PD  
 XX 02-APR-1998; 98WO-IB00705.  
 PF  
 XX 10-APR-1997; 97US-0043163.  
 PR  
 XX (UYUT-) RIJKSUNIV UTRECHT.  
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
 XX  
 XX Burbach JPH, Grosveid FG, Van Leeuwen FW;  
 PI WPI; 1998-609901/51.  
 XX  
 DR N-PSDB; AAX75759.  
 DR  
 XX  
 XX Diagnosing disease by detecting frameshift mutations in RNA or  
 PT corresponding protein mutations - used to diagnose cancer and  
 PT neurological diseases, particularly Alzheimer's disease, and also  
 PT for treatment and prevention with specific ribozymes or wild-type  
 PT RNA  
 XX  
 PS Disclosure; Figure 8; 258pp; English.  
 XX  
 CC This invention describes a novel method for the diagnosis of a disease  
 CC caused by, or associated with, an RNA molecule that has a frameshift  
 CC mutation. The method is used to diagnose age-related diseases, especially  
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 CC and many others listed) or susceptibility to these disorders. The method  
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
 CC at an early stage. It is based on the observation that disease may be  
 CC caused by mutations in RNA rather than DNA. The invention describes the  
 CC use of neuronal system RNA molecules, specifically proteins including  
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 CC neurofilament-F, presenilin 1, presenilin 2, glial fibrillary acidic  
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 57.1%; Score 4; DB 19; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLPP 4  
 DB 8 VLPP 11  
 RESULT 74



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AAB68459
ID AAB68459 standard; peptide; 13 AA.
XX
AC AAB68459;
XX
DT 23-JUL-2001 (first entry)
XX
DE Mutated peptide derived from the integrase of Ty5-6p.
XX
KW Retrotransposon; polyprotein; integrase; Ty1-copia; silent chromatin;
KW chromosomal integration; chromosomal targeting; Ty5; aging; oncogene.
XX
OS Synthetic.
XX
OS Saccharomyces paradoxus.
XX
FH Key Location/Qualifiers
FT Misc-difference 8
FT /note= "wild type Ser changed to Leu"
XX
XX
PN US6228647-B1.
XX
XX
PD 08-MAY-2001.
XX
XX
PF 15-JAN-1999; 99US-0232446.
XX
XX
PR 15-JAN-1998; 98US-0071383.
XX
XX
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX
PI Voytas DF, Gai X;
XX
XX
DR WPI; 2001-342676/36.
XX
PT Targeting integration of retrotransposon or retrovirus into silent
PT chromatin by transforming a cell with modified integrase having a
PT coding sequence for a peptide portion that interacts with chromatin at
PT desired sites -
XX
XX
PS Disclosure; Column 20; 41pp; English.
XX
XX
CC The present sequence represents a mutated portion of an integrase. The
CC specification describes a method for targeting integration of
CC retrotransposon of Ty1-copia group to desired location on a chromosome.
CC The method uses a modified integrase in a retrotransposon, where the
CC modified integrase contains a coding sequence for a peptide portion
CC which specifically binds to protein bound to the chromosome or to
CC particular nucleic acid sequences on chromosome. The method is useful
CC for targeting integration of a retrotransposon of the Ty1-copia group to
CC a desired location on a chromosome, especially into silent chromatin.
CC The silent chromatin targeting of Ty5 is useful for tagging genes which
CC are affected by aging and for studying oncogenes.
XX
SQ Sequence 13 AA;
Query Match 57.1%; Score 4; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5
DB 8 LPPN 11

RESULT 75
ABP81154
ID ABP81154 standard; peptide; 13 AA.
XX
AC ABP81154;
XX
XX
DT 27-FEB-2003 (first entry)
XX
DE Human TPO peptide with MCH class II binding activity #107.
XX

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KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;
KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.
XX
OS Homo sapiens.
XX
PN WO200268459-A2.
XX
PD 06-SEP-2002.
XX
XX
PF 22-FEB-2002; 2002WO-EP01931.
XX
XX
PR 26-FEB-2001; 2001EP-0104702.
XX
XX
PA (MERE ) MERCK PATENT GMBH.
XX
XX
PI Carr FJ, Carter G;
XX
XX
DR WPI; 2003-103168/09.
XX
XX
PT Modified thrombopoietin molecule for use in pharmaceutical
PT compositions, has same activity of human thrombopoietin, but is
PT non-immunogenic or less immunogenic than other non-modified molecules
PT with same activity -
XX
XX
PS Disclosure; Page 12; 36pp; English.
XX
XX
CC The invention relates to a novel modified molecule having the biological
CC activity of human thrombopoietin (TPO) and being substantially
CC non-immunogenic or less immunogenic than any non-modified molecule having
CC the same biological activity when used in vivo. The invention also
CC discloses T-cell epitope peptides created from non-modified TPO, and
CC having potential MHC class II binding activity. The protein of the
CC invention has immunosuppressive and antiallergic activity. A peptide of
CC the invention is useful in the manufacture of TPO having substantially no
CC or less immunogenicity than any non-modified molecule with the same
CC biological activity when used in vivo. The protein is useful in
CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.
CC allergies and autoimmune disease treatment. The sequences shown in
CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the
CC invention.
XX
SQ Sequence 13 AA;
Query Match 57.1%; Score 4; DB 24; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5
DB 6 LPPN 9

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#### SUMMARIES

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1	7	100.0	7	15 US-10-281-652-17	Sequence 17, Appl
2	5	71.4	11	10 US-09-791-378-140	Sequence 140, App
3	5	71.4	11	10 US-09-826-290-22	Sequence 22, Appl
4	5	71.4	11	10 US-09-826-290-136	Sequence 136, App
5	5	71.4	11	11 US-09-791-393-22	Sequence 22, Appl
6	5	71.4	11	11 US-09-791-393-285	Sequence 285, App
7	5	71.4	11	11 US-09-791-389-22	Sequence 22, Appl
8	5	71.4	11	11 US-09-791-389-265	Sequence 265, App
9	4	57.1	6	15 US-10-028-075B-135	Sequence 135, App
10	4	57.1	6	15 US-10-028-075B-141	Sequence 141, App
11	4	57.1	6	15 US-10-029-206A-135	Sequence 135, App
12	4	57.1	6	15 US-10-029-206A-141	Sequence 141, App
13	4	57.1	7	9 US-09-822-270-6	Sequence 6, Appli
14	4	57.1	7	11 US-09-954-385-46	Sequence 46, Appl
15	4	57.1	7	12 US-10-342-371-6	Sequence 6, Appli

7	15	US-10-028-075B-136	Sequence 136, App
7	15	US-10-028-075B-137	Sequence 137, App
7	15	US-10-028-075B-142	Sequence 142, App
7	15	US-10-028-075B-143	Sequence 143, App
7	15	US-10-029-206A-136	Sequence 136, App
7	15	US-10-029-206A-137	Sequence 137, App
7	15	US-10-029-206A-142	Sequence 142, App
7	15	US-10-029-206A-143	Sequence 143, App
8	15	US-10-028-075B-138	Sequence 138, App
8	15	US-10-028-075B-144	Sequence 144, App
8	15	US-10-029-206A-138	Sequence 138, App
8	15	US-10-029-206A-144	Sequence 144, App
9	12	US-10-277-292-10	Sequence 10, Appl
9	12	US-10-277-292-13	Sequence 13, Appl
9	12	US-10-277-292-33	Sequence 33, Appl
9	12	US-10-277-292-133	Sequence 133, App
9	12	US-10-277-292-211	Sequence 211, App
9	12	US-10-277-292-498	Sequence 498, App
9	12	US-10-277-292-586	Sequence 586, App
9	12	US-10-280-340-10	Sequence 10, Appl
9	12	US-10-280-340-13	Sequence 13, Appl
9	12	US-10-280-340-33	Sequence 33, Appl
9	12	US-10-280-340-133	Sequence 133, App
9	12	US-10-280-340-211	Sequence 211, App
9	12	US-10-280-340-498	Sequence 498, App
9	12	US-10-280-340-586	Sequence 586, App
10	12	US-10-277-292-56	Sequence 56, Appl
10	12	US-10-277-292-61	Sequence 61, Appl
10	12	US-10-277-292-156	Sequence 156, App
10	12	US-10-277-292-161	Sequence 161, App
10	12	US-10-277-292-179	Sequence 179, App
10	12	US-10-277-292-286	Sequence 286, App
10	12	US-10-277-292-636	Sequence 636, App
10	12	US-10-280-340-56	Sequence 56, Appl
10	12	US-10-280-340-61	Sequence 61, Appl
10	12	US-10-280-340-156	Sequence 156, App
10	12	US-10-280-340-161	Sequence 161, App
10	12	US-10-280-340-179	Sequence 179, App
10	12	US-10-280-340-286	Sequence 286, App
10	12	US-10-280-340-636	Sequence 636, App
11	11	US-09-872-702-8	Sequence 8, Appli
12	9	US-09-832-723-36	Sequence 36, Appl
12	12	US-10-303-331-36	Sequence 36, Appl
12	14	US-10-046-938-34	Sequence 34, Appl
12	15	US-10-254-446A-209	Sequence 209, App
14	15	US-10-148-936-6	Sequence 6, Appli
15	11	US-09-880-748-2225	Sequence 2225, Ap
16	12	US-10-161-791-202	Sequence 202, App
16	12	US-10-161-791-406	Sequence 406, App
17	15	US-10-050-704-308	Sequence 308, App
17	15	US-10-138-089-13	Sequence 13, Appl
17	15	US-10-028-075B-133	Sequence 133, App
17	15	US-10-028-075B-139	Sequence 139, App
17	15	US-10-029-206A-133	Sequence 133, App
17	15	US-10-029-206A-139	Sequence 139, App
18	9	US-09-765-527-100	Sequence 100, App
18	9	US-09-864-761-34402	Sequence 34402, A
18	9	US-09-864-761-42763	Sequence 42763, A
20	12	US-09-933-767-852	Sequence 852, App
20	12	US-09-171-432A-41	Sequence 41, Appl
20	12	US-09-171-432A-42	Sequence 42, Appl
20	12	US-10-161-791-153	Sequence 153, App
20	14	US-10-155-059-19	Sequence 19, Appl
20	15	US-10-023-282-852	Sequence 852, App
4	12	US-10-137-867-12	Sequence 12, Appl
4	15	US-10-226-007-3	Sequence 3, Appli
4	15	US-10-028-075B-80	Sequence 80, Appl
4	15	US-10-029-206A-80	Sequence 80, Appl
5	8	US-08-817-832B-11	Sequence 11, Appli
5	9	US-09-054-345-1	Sequence 1, Appli
5	11	US-09-788-006-137	Sequence 137, App
5	11	US-09-788-006-138	Sequence 138, App
3	42.9	US-09-788-006-140	Sequence 140, App

89 3 42.9 5 15 US-10-185-050-231 Sequence 231, App  
 90 3 42.9 5 15 US-10-185-050-233 Sequence 233, App  
 91 3 42.9 5 15 US-10-255-733-1 Sequence 1, Appli  
 92 3 42.9 5 15 US-10-226-007-6 Sequence 6, Appli  
 93 3 42.9 5 15 US-10-028-075B-8 Sequence 8, Appli  
 94 3 42.9 5 15 US-10-029-206A-8 Sequence 8, Appli  
 95 3 42.9 6 9 US-09-821-380-12 Sequence 12, Appl  
 96 3 42.9 6 10 US-09-956-625-17 Sequence 17, Appl  
 97 3 42.9 6 10 US-09-727-963A-71 Sequence 71, Appl  
 98 3 42.9 6 10 US-09-727-963A-80 Sequence 80, Appl  
 99 3 42.9 6 11 US-09-500-700-120 Sequence 120, App  
 100 3 42.9 6 12 US-10-262-522A-12 Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
 US-10-281-652-17  
 ; Sequence 17, Application US/10281652  
 ; Publication No. US20030091606A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STANTON, G. John  
 ; APPLICANT: HUGHES, Thomas K.  
 ; APPLICANT: BOLDOGH, Istvan  
 ; TITLE OF INVENTION: USE OF COLOSTEININ, CONSTITUENT PEPTIDES THEREOF, AND  
 ; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
 ; FILE REFERENCE: 265.00220101  
 ; CURRENT APPLICATION NUMBER: US/10/281,652  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: US/09/641,803  
 ; PRIOR FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 60/149,310  
 ; PRIOR FILING DATE: 1999-08-17  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 17  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-10-281-652-17

Query Match 100.0%; Score 7; DB 15; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPPNVG 7  
 Db 1 VLPPNVG 7

RESULT 2  
 US-09-791-378-140  
 ; Sequence 140, Application US/09791378  
 ; Patent No. US20020142303A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Parekh, Rajesh  
 ; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF  
 ; TITLE OF INVENTION: SCHIZOPHRENIA  
 ; FILE REFERENCE: 9195-061-999  
 ; CURRENT APPLICATION NUMBER: US/09/791,378  
 ; CURRENT FILING DATE: 2001-02-23  
 ; PRIOR APPLICATION NUMBER: 09/750,395  
 ; PRIOR FILING DATE: 2000-12-28  
 ; NUMBER OF SEQ ID NOS: 677  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 140  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-09-791-378-140

Query Match 71.4%; Score 5; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6  
 Db 1 LPPNV 5

RESULT 3  
 US-09-826-290-22  
 ; Sequence 22, Application US/09826290  
 ; Patent No. US20020164668A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Durham, L. Kathryn  
 ; APPLICANT: Friedman, David L.  
 ; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
 ; APPLICANT: Kimmel, Lida H.  
 ; APPLICANT: Parekh, Rajesh Bhikhu  
 ; APPLICANT: Potter, David M.  
 ; APPLICANT: Rohlf, Christian  
 ; APPLICANT: Silber, B. Michael  
 ; APPLICANT: Stiger, Thomas R.  
 ; APPLICANT: Sunderland, P. Trey  
 ; APPLICANT: Townsend, Robert Reid  
 ; APPLICANT: White, Frost  
 ; APPLICANT: Williams, Stephen A.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and  
 ; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of  
 ; TITLE OF INVENTION: Alzheimer's Disease  
 ; FILE REFERENCE: 2572-1-001 N2  
 ; CURRENT APPLICATION NUMBER: US/09/826,290  
 ; CURRENT FILING DATE: 2001-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/194,504  
 ; PRIOR FILING DATE: 2000-04-03  
 ; PRIOR APPLICATION NUMBER: US 60/253,647  
 ; PRIOR FILING DATE: 2000-11-28  
 ; NUMBER OF SEQ ID NOS: 492  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 22  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: homo sapien  
 US-09-826-290-22

Query Match 71.4%; Score 5; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPNV 6  
 Db 1 LPPNV 5

RESULT 4  
 US-09-826-290-136  
 ; Sequence 136, Application US/09826290  
 ; Patent No. US20020164668A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Durham, L. Kathryn  
 ; APPLICANT: Friedman, David L.  
 ; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
 ; APPLICANT: Kimmel, Lida H.  
 ; APPLICANT: Parekh, Rajesh Bhikhu  
 ; APPLICANT: Potter, David M.  
 ; APPLICANT: Rohlf, Christian  
 ; APPLICANT: Silber, B. Michael  
 ; APPLICANT: Stiger, Thomas R.  
 ; APPLICANT: Sunderland, P. Trey  
 ; APPLICANT: Townsend, Robert Reid  
 ; APPLICANT: White, Frost

```

; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Thereof, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-136

Query Match          71.4%; Score 5; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LPPNV 6
Db      1 LPPNV 5

RESULT 5
US-09-791-393-22
; Sequence 22, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-22

Query Match          71.4%; Score 5; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LPPNV 6
Db      1 LPPNV 5

RESULT 6
US-09-791-393-265
; Sequence 265, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian

```

```

; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-265

Query Match          71.4%; Score 5; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LPPNV 6
Db      1 LPPNV 5

RESULT 7
US-09-791-389-22
; Sequence 22, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-22

Query Match          71.4%; Score 5; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LPPNV 6
Db      1 LPPNV 5

RESULT 8
US-09-791-389-265
; Sequence 265, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:

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; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian Alexander
; APPLICANT: Terrett, Jonathan Louise
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-265

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```

Query Match          71.4%; Score 5; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 LPPNV 6
    |||||
DB 1 LPPNV 5

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## RESULT 9

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US-10-028-075B-135
; Sequence 135, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-028-075B-135

```

```

Query Match          57.1%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLPP 4
    |||||
DB 1 VLPP 4

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## RESULT 10

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US-10-028-075B-141
; Sequence 141, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.

```

```

; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
US-10-028-075B-141

```

```

Query Match          57.1%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VLPP 4
    |||||
DB 1 VLPP 4

```

## RESULT 11

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US-10-029-206A-135
; Sequence 135, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-135

```

```

Query Match          57.1%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLPP 4
    |||||
DB 1 VLPP 4

```

## RESULT 12

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US-10-029-206A-141
; Sequence 141, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29

```

; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 141  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/p07434/CGHB PAPAN  
US-10-029-206A-141

Query Match 57.1%; Score 4; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 1 VLPP 4

## RESULT 13

US-09-822-270-6  
; Sequence 6, Application US/09822270  
; Patent No. US20020068697A1  
; GENERAL INFORMATION:  
; APPLICANT: TOURNAIRE, ROSELYNE  
; APPLICANT: DEMANGEL, CAROLINE  
; APPLICANT: DERBIN, CLAUDE  
; APPLICANT: PERRET, GERARD  
; APPLICANT: MAZIE, JEAN-CLAUDE  
; APPLICANT: PLOUET, JEAN  
; APPLICANT: VASSAY, ROGER  
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIA  
; FILE REFERENCE: 205060U0  
; CURRENT APPLICATION NUMBER: US/09/822,270  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 60/193,396  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE  
US-09-822-270-6

Query Match 57.1%; Score 4; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
|||  
Db 1 LPPN 4

## RESULT 14

US-09-954-385-46  
; Sequence 46, Application US/09954385  
; Publication No. US20030100467A1  
; GENERAL INFORMATION:  
; APPLICANT: Ahle, Wolfgang  
; APPLICANT: Baldwin, Toby L.  
; APPLICANT: Van Gastel, Franciscus J.C.  
; APPLICANT: Janssen, Giselle G.  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Wang, Huaming  
; APPLICANT: Wineczky, Deborah S.  
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-Peptide  
; TITLE OF INVENTION: Complexes  
; FILE REFERENCE: GC690

; CURRENT APPLICATION NUMBER: US/09/954,385  
; CURRENT FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 46  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: binding peptide  
US-09-954-385-46

Query Match 57.1%; Score 4; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 2 VLPP 5

## RESULT 15

US-10-342-371-6  
; Sequence 6, Application US/10342371  
; Publication No. US20030171289A1  
; GENERAL INFORMATION:  
; APPLICANT: TOURNAIRE, ROSELYNE  
; APPLICANT: DEMANGEL, CAROLINE  
; APPLICANT: DERBIN, CLAUDE  
; APPLICANT: PERRET, GERARD  
; APPLICANT: MAZIE, JEAN-CLAUDE  
; APPLICANT: PLOUET, JEAN  
; APPLICANT: VASSAY, ROGER  
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIA  
; FILE REFERENCE: 205060U0  
; CURRENT APPLICATION NUMBER: US/10/342,371  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US/09/822,270  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 60/193,396  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE  
US-10-342-371-6

Query Match 57.1%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
|||  
Db 1 LPPN 4

## RESULT 16

US-10-028-075B-136  
; Sequence 136, Application US/10028075B  
; Publication No. US20030113733A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/028,075B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: EP 01203748.7

; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 136  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN  
US-10-028-075B-136

Query Match 57.1%; Score 4; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 1 VLPP 4

RESULT 17  
US-10-028-075B-137  
; Sequence 137, Application US/10028075B  
; Publication No. US20030113733A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/028,075B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 2001-10-04  
; PRIOR APPLICATION NUMBER: EP 01203748.7  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 137  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN  
US-10-028-075B-137

Query Match 57.1%; Score 4; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 2 VLPP 5

RESULT 18  
US-10-028-075B-142  
; Sequence 142, Application US/10028075B  
; Publication No. US20030113733A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/028,075B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 2001-10-04  
; PRIOR APPLICATION NUMBER: EP 01203748.7  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 142  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN  
US-10-028-075B-142

Query Match 57.1%; Score 4; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 1 VLPP 4

RESULT 19  
US-10-028-075B-143  
; Sequence 143, Application US/10028075B  
; Publication No. US20030113733A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/028,075B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 2001-10-04  
; PRIOR APPLICATION NUMBER: EP 01203748.7  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 143  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN  
US-10-028-075B-143

Query Match 57.1%; Score 4; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 2 VLPP 5

RESULT 20  
US-10-029-206A-136  
; Sequence 136, Application US/10029206A  
; Publication No. US20030119720A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Oligopeptide treatment of anthrax  
; FILE REFERENCE: 2183-5222US  
; CURRENT APPLICATION NUMBER: US/10/029,206A  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 09/821,380  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 136  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN  
US-10-029-206A-136

Query Match 57.1%; Score 4; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;



Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 1 VLPP 4

## RESULT 21

US-10-029-206A-137  
; Sequence 137, Application US/10029206A  
; Publication No. US20030119720A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Oligopeptide treatment of anthrax  
; FILE REFERENCE: 2183-5222US  
; CURRENT APPLICATION NUMBER: US/10/029,206A  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/821,380  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 137  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN  
US-10-029-206A-137

Query Match 57.1%; Score 4; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 2 VLPP 5

## RESULT 22

US-10-029-206A-142  
; Sequence 142, Application US/10029206A  
; Publication No. US20030119720A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Oligopeptide treatment of anthrax  
; FILE REFERENCE: 2183-5222US  
; CURRENT APPLICATION NUMBER: US/10/029,206A  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/821,380  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 142  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN  
US-10-029-206A-142

Query Match 57.1%; Score 4; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 1 VLPP 4

## RESULT 23

US-10-029-206A-143  
; Sequence 143, Application US/10029206A  
; Publication No. US20030119720A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Oligopeptide treatment of anthrax  
; FILE REFERENCE: 2183-5222US  
; CURRENT APPLICATION NUMBER: US/10/029,206A  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/821,380  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 143  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN  
US-10-029-206A-143

Query Match 57.1%; Score 4; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 2 VLPP 5

## RESULT 24

US-10-028-075B-138  
; Sequence 138, Application US/10028075B  
; Publication No. US20030113733A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/028,075B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: EP 01203748.7  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 138  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN  
US-10-028-075B-138

Query Match 57.1%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
Db 2 VLPP 5

## RESULT 25

US-10-028-075B-144  
; Sequence 144, Application US/10028075B  
; Publication No. US20030113733A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.  
; APPLICANT: Benner, Robert

```
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
US-10-028-075B-144
```

```
Query Match 57.1%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VLPP 4
Db 2 VLPP 5
```

```
RESULT 26
US-10-029-206A-138
; Sequence 138, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 138
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-138
```

```
Query Match 57.1%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VLPP 4
Db 2 VLPP 5
```

```
RESULT 27
US-10-029-206A-144
; Sequence 144, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
US-10-029-206A-144
```

```
Query Match 57.1%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VLPP 4
Db 2 VLPP 5
```

```
RESULT 28
US-10-277-292-10
; Sequence 10, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-10
```

```
Query Match 57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 LPPN 5
Db 3 LPPN 6
```

```
RESULT 29
US-10-277-292-13
; Sequence 13, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
```

APPLICANT: JAKOBOVITZ, AYA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
TITLE OF INVENTION: OTHER CANCERS  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/277,292  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-13

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LPPN 5  
DB 2 LPPN 5

RESULT 30  
US-10-277-292-33  
Sequence 33, Application US/10277292  
Publication No. US20030199470A1  
GENERAL INFORMATION:  
APPLICANT: FARIS, MARY  
APPLICANT: HUBERT, RENE  
APPLICANT: RAITANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: CHALLITA-EID, PIA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
TITLE OF INVENTION: OTHER CANCERS  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/277,292  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 33  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-33

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LPPN 5  
DB 5 LPPN 8

RESULT 31  
US-10-277-292-133  
Sequence 133, Application US/10277292  
Publication No. US20030199470A1  
GENERAL INFORMATION:  
APPLICANT: FARIS, MARY  
APPLICANT: HUBERT, RENE  
APPLICANT: RAITANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: CHALLITA-EID, PIA  
APPLICANT: JAKOBOVITZ, AYA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
TITLE OF INVENTION: OTHER CANCERS  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/277,292  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 133  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-133

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLPP 4  
DB 4 VLPP 7

RESULT 32  
US-10-277-292-211  
Sequence 211, Application US/10277292  
Publication No. US20030199470A1  
GENERAL INFORMATION:  
APPLICANT: FARIS, MARY  
APPLICANT: HUBERT, RENE  
APPLICANT: RAITANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: CHALLITA-EID, PIA  
APPLICANT: JAKOBOVITZ, AYA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
TITLE OF INVENTION: OTHER CANCERS  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/277,292  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 211  
LENGTH: 9

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-211

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY      2 LPPN 5
      ||||
Db      2 LPPN 5

RESULT 33
US-10-277-292-498
; Sequence 498, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-498

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY      2 LPPN 5
      ||||
Db      1 LPPN 4

RESULT 34
US-10-277-292-586
; Sequence 586, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
```

```
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 586
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-586

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY      2 LPPN 5
      ||||
Db      1 LPPN 4

RESULT 35
US-10-280-340-10
; Sequence 10, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-10

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY      2 LPPN 5
      ||||
Db      3 LPPN 6

RESULT 36
US-10-280-340-13
```

; Sequence 13, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-13

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred.No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
|||  
DB 2 LPPN 5

RESULT 37  
US-10-280-340-33  
; Sequence 33, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-280-340-33

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred.No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
|||  
DB 5 LPPN 8

RESULT 38  
US-10-280-340-133  
; Sequence 133, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 133  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-280-340-133

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred.No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
DB 4 VLPP 7

RESULT 39  
US-10-280-340-211  
; Sequence 211, Application US/10280340  
; Publication No. US20030207835A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/280,340  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US/09/935,430

```
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 211
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-211

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LPN 5
        ||||
DB      2 LPN 5

RESULT 40
US-10-280-340-498
; Sequence 498, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-498

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LPN 5
        ||||
DB      1 LPN 4

RESULT 41
US-10-280-340-586
; Sequence 586, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
```

```
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 586
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-586

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LPN 5
        ||||
DB      1 LPN 4

RESULT 42
US-10-277-292-56
; Sequence 56, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-56

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPN 5  
|||||  
Db 5 LPN 8

## RESULT 43

US-10-277-292-61  
; Sequence 61, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: APAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 61  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-61

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPN 5  
|||||  
Db 3 LPN 6

## RESULT 44

US-10-277-292-156  
; Sequence 156, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: APAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739

; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 156  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-156

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||||  
Db 1 VLPP 4

## RESULT 45

US-10-277-292-161  
; Sequence 161, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: APAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 161  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-161

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPN 5  
|||||  
Db 2 LPN 5

## RESULT 46

US-10-277-292-179  
; Sequence 179, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: APAR, DANIEL  
; APPLICANT: LEVIN, ELANA

APPLICANT: CHALLITA-EID, PIA  
APPLICANT: JAKOBOVITZ, AVA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/277,292  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 179  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-179

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||  
DB 5 VLPP 8  
|||

RESULT 47  
US-10-277-292-286  
Sequence 286, Application US/10277292  
Publication No. US20030199470A1  
GENERAL INFORMATION:  
APPLICANT: FARIAS, MARY  
APPLICANT: HUBERT, RENE  
APPLICANT: RAITANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: CHALLITA-EID, PIA  
APPLICANT: JAKOBOVITZ, AVA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/277,292  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 286  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-286

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
|||

Db 4 VLPP 7  
RESULT 48  
US-10-277-292-636  
Sequence 636, Application US/10277292  
Publication No. US20030199470A1  
GENERAL INFORMATION:  
APPLICANT: FARIAS, MARY  
APPLICANT: HUBERT, RENE  
APPLICANT: RAITANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: CHALLITA-EID, PIA  
APPLICANT: JAKOBOVITZ, AVA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/277,292  
CURRENT FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 636  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-636

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
|||  
DB 3 LPPN 6  
|||

RESULT 49  
US-10-280-340-56  
Sequence 56, Application US/10280340  
Publication No. US20030207835A1  
GENERAL INFORMATION:  
APPLICANT: FARIAS, MARY  
APPLICANT: HUBERT, RENE  
APPLICANT: RAITANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: CHALLITA-EID, PIA  
APPLICANT: JAKOBOVITZ, AVA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
FILE REFERENCE: 51158-20050.00  
CURRENT APPLICATION NUMBER: US/10/280,340  
CURRENT FILING DATE: 2002-10-25  
PRIOR APPLICATION NUMBER: US/09/935,430  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/227,098  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 60/282,739  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 700  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 56

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-56

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5
    ||||
Db 5 LPPN 8

RESULT 50
US-10-280-340-61
; Sequence 61, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-61

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5
    ||||
Db 3 LPPN 6

RESULT 51
US-10-280-340-156
; Sequence 156, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
```

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; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-156

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4
    ||||
Db 1 VLPP 4

RESULT 52
US-10-280-340-161
; Sequence 161, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 161
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-161

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5
    ||||
Db 2 LPPN 5

RESULT 53
```

```
US-10-280-340-179
; Sequence 179, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-179

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLPP 4
        ||||
DB      5 VLPP 8

RESULT 54
US-10-280-340-286
; Sequence 286, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 286
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-286

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLPP 4
        ||||
DB      4 VLPP 7

RESULT 55
US-10-280-340-636
; Sequence 636, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 636
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-636

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LPPN 5
        ||||
DB      3 LPPN 6

RESULT 56
US-09-872-702-8
; Sequence 8, Application US/09872702
; Publication No. US2003007756A1
; GENERAL INFORMATION:
; APPLICANT: Koren, Eugen
; APPLICANT: Lowe, John Hok Nin
; TITLE OF INVENTION: IDENTIFICATION AND MODIFICATION OF IMMUNODOMINANT EPITOPES IN
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 11669.72US01
; CURRENT APPLICATION NUMBER: US/09/872,702
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/243,913
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 11
```

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-872-702-8

Query Match 57.1%; Score 4; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
Db 6 LPPN 9

RESULT 57  
US-09-832-723-36  
; Sequence 36, Application US/09832723  
; Patent No. US20020098524A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Yiyu  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Tijerina, Pilar  
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
; FILE REFERENCE: GC617-2  
; CURRENT APPLICATION NUMBER: US/09/832,723  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: peptide library  
US-09-832-723-36

Query Match 57.1%; Score 4; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
Db 3 LPPN 6

RESULT 58  
US-10-303-331-36  
; Sequence 36, Application US/10303331  
; Publication No. US20030152976A1  
; GENERAL INFORMATION:  
; APPLICANT: Janssen, Giselle G.  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Winetzky, Deborah S.  
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
; FILE REFERENCE: GC617-3  
; CURRENT APPLICATION NUMBER: US/10/303,331  
; CURRENT FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: US 09/832,723  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: peptide library

US-10-303-331-36

Query Match 57.1%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
Db 3 LPPN 6

RESULT 59  
US-10-046-938-34  
; Sequence 34, Application US/10046938  
; Publication No. US20020192185A1  
; GENERAL INFORMATION:  
; APPLICANT: MITTAL, SURESH K.  
; APPLICANT: GRAHAM, FRANK L.  
; APPLICANT: PREVICK, LUDVIK  
; APPLICANT: BABIUK, LORNE A.  
; TITLE OF INVENTION: MAMMALIAN CELL LINES EXPRESSING BOVINE ADENOVIRUS FUNCTIONS  
; FILE REFERENCE: 293102002102  
; CURRENT APPLICATION NUMBER: US/10/046,938  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/435,242  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/815,927  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-13  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/164,294  
; PRIOR FILING DATE: EARLIER FILING DATE: 1993-12-09  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Bovine adenovirus type 3  
US-10-046-938-34

Query Match 57.1%; Score 4; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
Db 8 VLPP 11

RESULT 60  
US-10-254-446A-209  
; Sequence 209, Application US/10254446A  
; Publication No. US20030113714A1  
; GENERAL INFORMATION:  
; APPLICANT: Belcher, Angela M  
; APPLICANT: Smalley, Richard E.  
; APPLICANT: Ryan, Esther  
; APPLICANT: Lee, Seung-Wuk  
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES  
; FILE REFERENCE: 119927-1066  
; CURRENT APPLICATION NUMBER: US/10/254,446A  
; CURRENT FILING DATE: 2003-02-19  
; PRIOR APPLICATION NUMBER: 60/325,664  
; PRIOR FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 245  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 209  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopar  
US-10-254-446A-209

Query Match 57.1%; Score 4; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 VLPP 4  
|||  
Db 1 VLPP 4

RESULT 61  
US-10-148-936-6  
; Sequence 6, Application US/10148936  
; Publication No. US20030113819A1  
; GENERAL INFORMATION:  
; APPLICANT: Horton, Jeffrey  
; APPLICANT: Smith, John  
; APPLICANT: Teear, Michelle  
; APPLICANT: Kendall, Jonathan  
; APPLICANT: Michael, Nigel  
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells  
; FILE REFERENCE: PA9963  
; CURRENT APPLICATION NUMBER: US/10/148,936  
; CURRENT FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/GB00/04593  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: GB 9928674.2  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligomer  
US-10-148-936-6

Query Match 57.1%; Score 4; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 VLPP 4  
|||  
Db 5 VLPP 8

RESULT 62  
US-09-880-748-2225  
; Sequence 2225, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2225  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2225

Query Match 57.1%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 VLPP 4  
|||  
Db 10 VLPP 13

RESULT 63  
US-10-161-791-202  
; Sequence 202, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,972  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 202:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-202

Query Match 57.1%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 VLPP 4  
|||  
Db 8 VLPP 11

RESULT 64  
US-10-161-791-406  
; Sequence 406, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 406:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-406

Query Match 57.1%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
Db 8 VLPP 11

RESULT 65  
US-10-050-704-308  
Sequence 308, Application US/10050704  
Publication No. US20030050442A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 62 Human Secreted Proteins  
FILE REFERENCE: P2039P1  
CURRENT APPLICATION NUMBER: US/10/050,704  
CURRENT FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: 09/684,524  
PRIOR FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: PCT/US00/08979  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: 60/128,693  
PRIOR FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: 60/130,991  
PRIOR FILING DATE: 1999-04-26  
NUMBER OF SEQ ID NOS: 344

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 308  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-050-704-308

Query Match 57.1%; Score 4; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
Db 4 VLPP 7

RESULT 66  
US-10-138-089-13  
Sequence 13, Application US/10138089  
Publication No. US20030092077A1  
GENERAL INFORMATION:  
APPLICANT: Ramarao, Chodavarapu S  
TITLE OF INVENTION: Human Sperm Activator Peptides And Methods of Use Thereof  
FILE REFERENCE: 30705-70810  
CURRENT APPLICATION NUMBER: US/10/138,089  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: 60/288,956  
PRIOR FILING DATE: 2001-05-04  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 13  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-138-089-13

Query Match 57.1%; Score 4; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNVG 7  
Db 7 PNVG 10

RESULT 67  
US-10-028-075B-133  
Sequence 133, Application US/10028075B  
Publication No. US20030113733A1  
GENERAL INFORMATION:  
APPLICANT: Khan, Nisar A.  
APPLICANT: Benner, Robert  
TITLE OF INVENTION: Gene regulator  
FILE REFERENCE: 21831-5223US  
CURRENT APPLICATION NUMBER: US/10/028,075B  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: EP 01203748.7  
PRIOR FILING DATE: 2001-10-04  
NUMBER OF SEQ ID NOS: 175  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 133  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: swissnew/P01229/LSHB HUMAN  
US-10-028-075B-133

Query Match 57.1%; Score 4; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 VLPP 4
      ||||
Db      8 VLPP 11

RESULT 68
US-10-028-075B-139
; Sequence 139, Application US/10028075B
; Publication No. US2003011373A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
US-10-028-075B-139

Query Match      57.1%; Score 4; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLPP 4
      ||||
Db      8 VLPP 11

RESULT 69
US-10-029-206A-133
; Sequence 133, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-133

Query Match      57.1%; Score 4; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLPP 4
      ||||
Db      8 VLPP 11

RESULT 70
US-10-029-206A-139
; Sequence 139, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
US-10-029-206A-139

Query Match      57.1%; Score 4; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLPP 4
      ||||
Db      8 VLPP 11

RESULT 71
US-09-765-527-100
; Sequence 100, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; FUSION PROTEINS AND BPI-DERIVED PEPTIDES
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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NAME/KEY: misc\_feature  
OTHER INFORMATION: "XMP.118"  
SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-09-765-527-100

Query Match 57.1%; Score 4; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNVG 7  
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Db 13 PNVG 16

## RESULT 72

US-09-864-761-34402  
; Sequence 34402, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 34402

LENGTH: 18

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC007685.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 34

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 23  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 18  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.7  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.3  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 20  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 47  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.7  
US-09-864-761-34402

Query Match 57.1%; Score 4; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5

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Db 11 LPPN 14

## RESULT 73

US-09-864-761-42763  
; Sequence 42763, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 42763

LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL035462.12  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.96  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 9.2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3  
US-09-864-761-42763

Query Match 57.1%; Score 4; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLPP 4  
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Db 9 VLPP 12

## RESULT 74

US-09-933-767-852  
Sequence 852, Application US/09933767  
Publication No. US20030181692A1  
GENERAL INFORMATION:  
APPLICANT: NI et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P2  
CURRENT APPLICATION NUMBER: US/09/933,767  
CURRENT FILING DATE: 2001-08-22  
PRIORITY APPLICATION NUMBER: PCT/US01/05614  
PRIORITY FILING DATE: 2001-02-21  
PRIORITY APPLICATION NUMBER: 60/184,836  
PRIORITY FILING DATE: 2000-02-24  
PRIORITY APPLICATION NUMBER: 60/193,170  
PRIORITY FILING DATE: 2000-03-29  
PRIORITY APPLICATION NUMBER: 09/205,258  
PRIORITY FILING DATE: 1998-12-04  
PRIORITY APPLICATION NUMBER: PCT/US98/11422  
PRIORITY FILING DATE: 1998-06-04  
PRIORITY APPLICATION NUMBER: 60/048,885  
PRIORITY FILING DATE: 1997-06-06  
PRIORITY APPLICATION NUMBER: 60/049,375  
PRIORITY FILING DATE: 1997-06-06  
PRIORITY APPLICATION NUMBER: 60/048,881  
PRIORITY FILING DATE: 1997-06-06  
PRIORITY APPLICATION NUMBER: 60/048,880  
PRIORITY FILING DATE: 1997-06-06  
PRIORITY APPLICATION NUMBER: 60/048,896  
PRIORITY FILING DATE: 1997-06-06  
PRIORITY APPLICATION NUMBER: 60/049,020  
PRIORITY FILING DATE: 1997-06-06  
PRIORITY APPLICATION NUMBER: 60/048,876  
PRIORITY FILING DATE: 1997-06-06  
PRIORITY APPLICATION NUMBER: 60/048,895  
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PRIORITY FILING DATE: 1997-06-06  
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PRIORITY FILING DATE: 1997-06-06  
PRIORITY APPLICATION NUMBER: 60/048,893  
PRIORITY FILING DATE: 1997-06-06  
PRIORITY APPLICATION NUMBER: 60/048,900

PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,901  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,892  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,915  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/049,019  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,970  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,972  
PRIOR FILING DATE: 1997-06-06  
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PRIOR APPLICATION NUMBER: 60/049,373  
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PRIOR FILING DATE: 1997-06-06  
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PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,949  
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PRIOR APPLICATION NUMBER: 60/048,974  
PRIOR FILING DATE: 1997-06-06  
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PRIOR FILING DATE: 1997-06-06  
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PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,898  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,962  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,963  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,877  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,878  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/068,054  
PRIOR FILING DATE: 1997-12-18  
PRIOR APPLICATION NUMBER: 60/068,064  
PRIOR FILING DATE: 1997-12-18  
PRIOR APPLICATION NUMBER: 60/068,053  
PRIOR FILING DATE: 1997-12-18  
PRIOR APPLICATION NUMBER: 60/070,923  
PRIOR FILING DATE: 1997-12-18  
PRIOR APPLICATION NUMBER: 60/073,160  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/073,159  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/073,165  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/073,164  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/085,925  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,921  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,923  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,922  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/092,921  
PRIOR FILING DATE: 1998-07-15  
PRIOR APPLICATION NUMBER: 60/094,657  
PRIOR FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1245  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 852  
LENGTH: 20



; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-933-767-852

Query Match 57.1%; Score 4; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
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Db 8 VLPP 11

## RESULT 75

US-09-171-432A-41  
; Sequence 41, Application US/09171432A  
; Publication No. US20030187184A1  
; GENERAL INFORMATION:  
; APPLICANT: Fields, Howard A.  
; APPLICANT: Khudyakov, Yuri E.  
; TITLE OF INVENTION: Antigenically Reactive Regions of the  
; TITLE OF INVENTION: Hepatitis A Virus Polypeptide  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kilpatrick Stockton LLP  
; STREET: 3424 Peachtree Road, N.E.  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30326  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/171,432A  
; FILING DATE: 23-NOV-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greene, Jamie L.  
; REGISTRATION NUMBER: 32,467  
; REFERENCE/DOCKET NUMBER: 03063-0231US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 949-2400  
; TELEFAX: (404) 949-2499  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..20  
; OTHER INFORMATION: /label=YK-1317  
US-09-171-432A-41

Query Match 57.1%; Score 4; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
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Db 14 VLPP 17

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Job time : 14.9255 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 7.63298 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-17

Perfect score: 7  
Sequence: 1 VLPNVG 7

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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pcp.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	4	US-09-641-803-17
2	4	57.1	6	2	US-08-482-228-96
3	4	57.1	6	3	US-08-482-528-96
4	4	57.1	7	4	US-09-822-270-6
5	4	57.1	8	3	US-08-915-498B-17
6	4	57.1	9	1	US-07-946-234A-3
7	4	57.1	9	1	US-08-123-161A-3
8	4	57.1	9	1	US-08-483-278-3
9	4	57.1	10	1	US-08-338-383C-6
10	4	57.1	10	1	US-08-338-383C-6
11	4	57.1	10	3	US-09-085-072-4
12	4	57.1	11	3	US-09-171-654-13
13	4	57.1	12	1	US-07-794-288B-23
14	4	57.1	12	3	US-08-164-292B-34
15	4	57.1	12	3	US-08-945-623-34
16	4	57.1	12	3	US-08-915-927-34
17	4	57.1	12	4	US-09-103-330-34
18	4	57.1	12	4	US-09-435-242-34
19	4	57.1	13	1	US-07-794-288B-22
20	4	57.1	13	3	US-09-232-446B-10
21	4	57.1	14	1	US-07-794-288B-21
22	4	57.1	15	1	US-07-794-288B-20
23	4	57.1	16	1	US-07-794-288B-19
24	4	57.1	16	2	US-08-528-057-12
25	4	57.1	16	3	US-08-915-498B-24
26	4	57.1	16	3	US-08-602-999A-202
27	4	57.1	16	3	US-08-602-999A-406

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29	4	57.1	16	4	US-09-500-124-406	Sequence 406, App
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31	4	57.1	17	1	US-07-794-288B-17	Sequence 17, App
32	4	57.1	18	1	US-07-794-288B-214	Sequence 214, App
33	4	57.1	18	2	US-08-621-803-100	Sequence 100, App
34	4	57.1	18	2	US-09-017-205-27	Sequence 27, App
35	4	57.1	18	2	US-09-017-205-28	Sequence 28, App
36	4	57.1	18	3	US-09-217-353-100	Sequence 100, App
37	4	57.1	19	1	US-07-794-288B-16	Sequence 16, App
38	4	57.1	19	1	US-07-794-288B-126	Sequence 126, App
39	4	57.1	20	1	US-07-794-288B-15	Sequence 15, App
40	4	57.1	20	1	US-07-794-288B-118	Sequence 118, App
41	4	57.1	20	1	US-07-794-288B-125	Sequence 125, App
42	4	57.1	20	3	US-08-602-999A-153	Sequence 153, App
43	4	57.1	20	4	US-09-500-124-153	Sequence 153, App
44	4	57.1	20	4	US-09-081-975-19	Sequence 19, App
45	4	57.1	20	4	US-09-205-258-852	Sequence 852, App
46	3	42.9	3	1	US-07-729-099-5	Sequence 5, App
47	3	42.9	3	1	US-08-257-392-5	Sequence 5, App
48	3	42.9	3	3	US-08-770-035-5	Sequence 5, App
49	3	42.9	3	2	US-08-441-871-27	Sequence 27, App
50	3	42.9	3	3	US-09-039-308A-28	Sequence 28, App
51	3	42.9	5	2	US-08-747-137-91	Sequence 91, App
52	3	42.9	5	4	US-09-646-154-10	Sequence 10, App
53	3	42.9	5	4	US-08-817-832B-11	Sequence 11, App
54	3	42.9	6	1	US-07-956-700B-58	Sequence 58, App
55	3	42.9	6	1	US-08-532-065B-5	Sequence 5, App
56	3	42.9	6	1	US-08-476-537-58	Sequence 58, App
57	3	42.9	6	1	US-08-485-607-58	Sequence 58, App
58	3	42.9	6	2	US-08-317-310A-35	Sequence 35, App
59	3	42.9	6	2	US-08-637-759B-498	Sequence 498, App
60	3	42.9	6	2	US-08-053-451B-124	Sequence 124, App
61	3	42.9	6	2	US-08-726-306A-133	Sequence 133, App
62	3	42.9	6	2	US-08-482-228-97	Sequence 97, App
63	3	42.9	6	2	US-08-475-879-58	Sequence 58, App
64	3	42.9	6	3	US-08-481-985B-132	Sequence 132, App
65	3	42.9	6	3	US-08-871-355A-498	Sequence 498, App
66	3	42.9	6	3	US-08-482-528-97	Sequence 97, App
67	3	42.9	6	3	US-09-039-308A-33	Sequence 33, App
68	3	42.9	6	3	US-09-330-970-21	Sequence 21, App
69	3	42.9	6	3	US-09-330-970-35	Sequence 35, App
70	3	42.9	6	3	US-09-196-934-2	Sequence 2, App
71	3	42.9	6	3	US-09-232-446B-23	Sequence 23, App
72	3	42.9	6	4	US-09-201-945-498	Sequence 498, App
73	3	42.9	6	4	US-09-394-630-14	Sequence 14, App
74	3	42.9	6	4	US-09-433-043B-58	Sequence 58, App
75	3	42.9	6	4	US-09-155-613A-51	Sequence 51, App
76	3	42.9	6	4	US-09-355-160D-11	Sequence 11, App
77	3	42.9	6	4	US-09-584-001C-33	Sequence 33, App
78	3	42.9	6	4	US-09-645-456A-32	Sequence 32, App
79	3	42.9	6	4	US-09-425-324A-32	Sequence 32, App
80	3	42.9	6	5	PCT-US95-13041-35	Sequence 35, App
81	3	42.9	6	5	PCT-US95-13041-35	Sequence 35, App
82	3	42.9	7	1	US-08-044-547-10	Sequence 10, App
83	3	42.9	7	1	US-08-029-333-29	Sequence 29, App
84	3	42.9	7	1	US-07-968-781A-83	Sequence 83, App
85	3	42.9	7	1	US-08-288-728-33	Sequence 33, App
86	3	42.9	7	1	US-08-230-047-40	Sequence 40, App
87	3	42.9	7	1	US-07-932-915-5	Sequence 5, App
88	3	42.9	7	2	US-08-719-758-18	Sequence 18, App
89	3	42.9	7	2	US-08-340-283-38	Sequence 38, App
90	3	42.9	7	2	US-08-537-400-27	Sequence 27, App
91	3	42.9	7	2	US-08-769-745-7	Sequence 7, App
92	3	42.9	7	2	US-08-769-745-26	Sequence 26, App
93	3	42.9	7	2	US-08-709-924-5	Sequence 5, App
94	3	42.9	7	2	US-08-709-925-5	Sequence 5, App
95	3	42.9	7	3	US-09-258-754-160	Sequence 160, App
96	3	42.9	7	3	US-09-258-754-284	Sequence 284, App
97	3	42.9	7	3	US-08-602-999A-9	Sequence 9, App
98	3	42.9	7	3	US-09-119-827-18	Sequence 18, App
99	3	42.9	7	3	US-09-025-819-12	Sequence 12, App
100	3	42.9	7	3	US-09-042-107-160	Sequence 160, App

## ALIGNMENTS

RESULT 1  
US-09-641-803-17  
; Sequence 17, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-17

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPPNVG 7  
|||  
Db 1 VLPPNVG 7

RESULT 2  
US-08-482-228-96  
; Sequence 96, Application US/08482228  
; Patent No. 5968753  
; GENERAL INFORMATION:  
; APPLICANT: Tseng-Law, Janet  
; APPLICANT: Kobori, Joan A.  
; APPLICANT: Al-Abdaly, Fahad A.  
; APPLICANT: Guillermo, Roy  
; APPLICANT: Helgerson, Sam L.  
; APPLICANT: Deans, Robert J.  
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL  
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE  
; NUMBER OF SEQUENCES: 215  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janice Guthrie, Ph.D.  
; STREET: P.O. Box 15210  
; CITY: Irvine  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92713-5210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/482,228  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Guthrie, Janice  
; REGISTRATION NUMBER: 35,170

; REFERENCE/DOCKET NUMBER: IT-4630CIP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 440-5353  
; TELEFAX: (714) 553-1952  
; INFORMATION FOR SEQ ID NO: 96:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-482-228-96

Query Match 57.1%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPNV 6  
|||  
Db 1 PPNV 4

RESULT 3  
US-08-482-528-96  
; Sequence 96, Application US/08482528  
; Patent No. 6017719  
; GENERAL INFORMATION:  
; APPLICANT: Tseng-Law, Janet  
; APPLICANT: Kobori, Joan A.  
; APPLICANT: Al-Abdaly, Fahad A.  
; APPLICANT: Guillermo, Roy  
; APPLICANT: Helgerson, Sam L.  
; APPLICANT: Deans, Robert J.  
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL  
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE  
; NUMBER OF SEQUENCES: 215  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janice Guthrie, Ph.D.  
; STREET: P.O. Box 15210  
; CITY: Irvine  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92713-5210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/482,528  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Guthrie, Janice  
; REGISTRATION NUMBER: 35,170  
; REFERENCE/DOCKET NUMBER: IT-4630CIP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 440-5353  
; TELEFAX: (714) 553-1952  
; INFORMATION FOR SEQ ID NO: 96:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-482-528-96

Query Match 57.1%; Score 4; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPNV 6  
|||  
Db 1 PPNV 4

RESULT 4  
US-09-822-270-6  
; Sequence 6, Application US/09822270  
; Patent No. 6559126  
; GENERAL INFORMATION:  
; APPLICANT: TOURNAIRE, ROSELYNE  
; APPLICANT: DEMANGEL, CAROLINE  
; APPLICANT: DERBIN, CLAUDE  
; APPLICANT: PERRET, GERARD  
; APPLICANT: MAZIE, JEAN-CLAUDE  
; APPLICANT: FLOUET, JEAN  
; APPLICANT: VASSAY, ROGER  
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIA  
; TITLE OF INVENTION: ANGIOGENESIS, POLYNUCLEOTIDES ENCODING SAID PEPTIDES AND METHODS  
; FILE REFERENCE: 205060US0  
; CURRENT APPLICATION NUMBER: US/09/822,270  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 60/193,396  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC PEPTIDE  
US-09-822-270-6  
  
Query Match 57.1%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 LPPN 5  
DB 1 LPPN 4  
  
RESULT 5  
US-08-915-498B-17  
; Sequence 17, Application US/08915498B  
; Patent No. 6132954  
; GENERAL INFORMATION:  
; APPLICANT: James R. Lupski, Robert A. Britton, Donald L.  
; APPLICANT: Court and Bradford S. Powell  
; TITLE OF INVENTION: Methods of Screening for Agents that  
; TITLE OF INVENTION: Delay a Cell Cycle and Compositions Comprising ERA and an Anal  
; TITLE OF INVENTION: of Wild-Type ERA  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
; ADDRESSEE: & No. 6132954ris LLP  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT for WINDOWS 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/915,498B  
; FILING DATE: August 20, 1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/023,353  
; FILING DATE: August 20, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lori Y. Beardsell

; REGISTRATION NUMBER: 34,293  
; REFERENCE/DOCKET NUMBER: BYLR-0037  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-915-498B-17  
  
Query Match 57.1%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 PNVG 7  
DB 3 PNVG 6  
  
RESULT 6  
US-07-946-234A-3  
; Sequence 3, Application US/07946234A  
; Patent No. 5308752  
; GENERAL INFORMATION:  
; APPLICANT: Campbell, Kevin P.  
; APPLICANT: Matsumura, Kiichiro  
; TITLE OF INVENTION: DIAGNOSIS OF AUTOSOMAL MUSCULAR DYSTROPHY  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS  
; STREET: 2 Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/946,234A  
; FILING DATE: 19920914  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: UIRF89-11AAA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)861-6240  
; TELEFAX: (617)861-9540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO ACID  
; MOLECULE TYPE: Peptide  
US-07-946-234A-3  
  
Query Match 57.1%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VLP 4  
DB 6 VLP 9  
  
RESULT 7  
US-08-123-161A-3  
; Sequence 3, Application US/08123161A

Patent No. 5449616  
GENERAL INFORMATION:  
APPLICANT: Campbell, Kevin P.  
APPLICANT: Roberts, Steven L.  
APPLICANT: Anderson, Richard D.  
APPLICANT: Ibraghimov, Oxana B.  
APPLICANT: Yang, Bin  
TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/123,161A  
FILING DATE: 16-SEP-93  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/946,234  
FILING DATE: 14-SEP-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M.  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: UIRF89-11A4  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-08-123-161A-3

Query Match 57.1%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
DB 6 VLPP 9

RESULT 8  
US-08-483-278-3  
Sequence 3, Application US/08483278  
Patent No. 5686073  
GENERAL INFORMATION:  
APPLICANT: Campbell, Kevin P.  
APPLICANT: Ibraghimov, Oxana B.  
APPLICANT: Ervasti, James M.  
APPLICANT: Leveille, Cynthia J.  
TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin M. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,278  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/123,161  
FILING DATE: 16-SEP-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M.  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: UIRF89-11A5  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-08-483-278-3

Query Match 57.1%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
DB 6 VLPP 9

RESULT 9  
US-08-338-383C-5  
Sequence 5, Application US/08338383C  
Patent No. 5646246  
GENERAL INFORMATION:  
APPLICANT: PETTIT, GEORGE R.  
APPLICANT: XU, JUN-PING  
TITLE OF INVENTION: ISOLATION AND STRUCTURE ELUCIDATION  
OF THE HUMAN CANCER CELL GROWTH INHIBITORY CYCLIC  
PEPTIDE  
TITLE OF INVENTION: PHAKELLISTATIN 4, 5, 6, 7, 8 AND 9  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RICHARD R. MYBECK  
STREET: 8010 EAST MORGAN TRAIL, SUITE 10  
CITY: SCOTTSDALE  
STATE: ARIZONA  
COUNTRY: USA  
ZIP: 85258-1234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44-Mb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: DOS 5  
SOFTWARE: Microsoft Word for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/338,383C  
FILING DATE: 11/14/94  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard R. Mybeck  
REGISTRATION NUMBER: 17,886  
REFERENCE/DOCKET NUMBER: 4954  
TELEPHONE: (602)-483-1285  
TELEFAX: (602)-483-7452  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acid residues  
TYPE: amino acid

TOPOLOGY: Cyclic  
MOLECULE TYPE:  
DESCRIPTION: Cyclodecapeptide phakellistatin 8  
HYPOTHETICAL: no  
ANTI-SENSE: no  
FRAGMENT TYPE: circular  
ORIGINAL SOURCE:  
ORGANISM: Phakellia costata  
DEVELOPMENTAL STAGE: Whole organism  
FEATURE:  
NAME/KEY: Phakellistatin 8  
IDENTIFICATION METHOD: by experiment using high  
IDENTIFICATION METHOD: resolution nuclear magnetic resonance, high resolution  
IDENTIFICATION METHOD: mass spectral analysis, MS/MS technique and chiral gas  
IDENTIFICATION METHOD: chromatography  
OTHER INFORMATION: Phakellistatin 8 cell growth  
OTHER INFORMATION: inhibition : P388 (ED50 2.9 mcg/ml)  
US-08-338-383C-5

Query Match 57.1%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
Db 5 VLPP 8

RESULT 10  
US-08-338-383C-6  
Sequence 6, Application US/08338383C  
Patent No. 5646246  
GENERAL INFORMATION:  
APPLICANT: PETTIT, GEORGE R.  
APPLICANT: XU, JUN-PING  
TITLE OF INVENTION: ISOLATION AND STRUCTURE ELUCIDATION  
TITLE OF INVENTION: OF THE HUMAN CANCER CELL GROWTH INHIBITORY CYCLIC  
TITLE OF INVENTION: PHAKELLISTATIN 4, 5, 6, 7, 8 AND 9  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RICHARD R. MYBECK  
STREET: 8010 EAST MORGAN TRAIL, SUITE 10  
CITY: SCOTTSDALE  
STATE: ARIZONA  
COUNTRY: USA  
ZIP: 85258-1234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: DOS 5  
SOFTWARE: Microsoft Word for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/338,383C  
FILING DATE: 11/14/94  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard R. Mybeck  
REGISTRATION NUMBER: 17,886  
REFERENCE/DOCKET NUMBER: 4954  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (602)-483-1285  
TELEFAX: (602)-483-7452  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acid residues  
TYPE: amino acid  
TOPOLOGY: Cyclic  
MOLECULE TYPE: Cyclodecapeptide phakellistatin 9  
HYPOTHETICAL: no  
ANTI-SENSE: no  
FRAGMENT TYPE: circular  
ORIGINAL SOURCE:

ORGANISM: Phakellia costata  
DEVELOPMENTAL STAGE: Whole organism  
FEATURE:  
NAME/KEY: Phakellistatin 9  
IDENTIFICATION METHOD: by experiment using high  
IDENTIFICATION METHOD: resolution nuclear magnetic resonance, high resolution  
IDENTIFICATION METHOD: mass spectral analysis, MS/MS technique and chiral gas  
IDENTIFICATION METHOD: chromatography  
OTHER INFORMATION: Phakellistatin 9 cell growth  
OTHER INFORMATION: inhibition : P388 (ED50 4.1 mcg/ml)  
US-08-338-383C-6

Query Match 57.1%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
Db 5 VLPP 8

RESULT 11  
US-09-085-072-4  
Sequence 4, Application US/09085072  
Patent No. 6265150  
GENERAL INFORMATION:  
APPLICANT: L. Terstappen et al.  
TITLE OF INVENTION: PHAGE ANTIBODIES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann & Baron, LLP  
STREET: 350 Jericho Turnpike  
CITY: Jericho  
STATE: New York  
COUNTRY: USA  
ZIP: 11753  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/085,072  
FILING DATE: 26-MAY-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Feit, Irving N.  
REGISTRATION NUMBER: 28,601  
REFERENCE/DOCKET NUMBER: 890-2 FWC/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-085-072-4

Query Match 57.1%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
Db 3 LPPN 6

RESULT 12  
US-09-171-654-13  
Sequence 13, Application US/09171654A

Patent No. 6239107  
GENERAL INFORMATION:  
APPLICANT: GOZES, Iilana  
APPLICANT: FRIDKIN, Matityahu  
TITLE OF INVENTION: CONJUGATES OF LIPOPHILIC MOIETIES AND FRAGMENTS OF  
TITLE OF INVENTION: VASOACTIVE INTESTINAL PEPTIDE (VIP)  
FILE REFERENCE: GOZES=4  
CURRENT APPLICATION NUMBER: US/09/171,654A  
CURRENT FILING DATE: 1999-04-29  
EARLIER APPLICATION NUMBER: PCT/IL97/00129  
EARLIER FILING DATE: 1997-04-18  
EARLIER APPLICATION NUMBER: IL 118003  
EARLIER FILING DATE: 1996-04-23  
NUMBER OF SEQ ID NOS: 80  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism:Artificial  
FEATURE:  
OTHER INFORMATION: The N-terminus is modified with a stearyl moiety;  
OTHER INFORMATION: the C-terminal residue is amidated.  
US-09-171-654-13

Query Match 57.1%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPPN 5  
DB 4 LPPN 7

RESULT 13  
US-07-794-288D-23  
Sequence 23, Application US/07794288D  
Patent No. 5580953  
GENERAL INFORMATION:  
APPLICANT: ELISABETH ALBRECHT,  
APPLICANT: HOWARD JONES,  
APPLICANT: LAURA S.L. GAETA,  
APPLICANT: KATHRYN S. PRICKETT and  
APPLICANT: KEVIN BEAUMONT  
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: First Interstate World  
STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44  
MEDIUM TYPE: Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version  
OPERATING SYSTEM: 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/794,288D  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/794,288  
FILING DATE: 19-NOV-91  
ATTORNEY/AGENT INFORMATION:

NAME: Duft, Bradford, J.  
REGISTRATION NUMBER: 32,219  
REFERENCE/DOCKET NUMBER: 193/153  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-07-794-288D-23  
Query Match 57.1%; Score 4; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLPP 4  
DB 1 VLPP 4  
RESULT 14  
US-08-164-292B-34  
Sequence 34, Application US/08164292B  
Patent No. 5820868  
GENERAL INFORMATION:  
APPLICANT: MITTAL, SURESH K.  
APPLICANT: GRAHAM, FRANK L.  
APPLICANT: PREVEC, LUDVIK  
APPLICANT: BABIUK, LORNE A.  
TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE  
TITLE OF INVENTION: ADENOVIRUS EXPRESSION VECTOR SYSTEM  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 345 California Street  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94104-2675  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/164,292B  
FILING DATE: 09-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: GRACEY, NANCY J.  
REGISTRATION NUMBER: 28,216  
REFERENCE/DOCKET NUMBER: 29310-20021.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 677-7000  
TELEFAX: (415) 677-7522  
TELEX: 34-0154  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-164-292B-34  
Query Match 57.1%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 VLPP 4  
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|  
Db 8 VLPP 11

RESULT 15  
US-08-845-623-34  
; Sequence 34, Application US/08845623A  
; Patent No. 6001591  
; GENERAL INFORMATION:  
; APPLICANT: BABIUK, LORNE A.  
; APPLICANT: TIKOO, SURESH K.  
; APPLICANT: REDDY, POLICE S.  
; TITLE OF INVENTION: BOVINE ADENOVIRUS 3 GENOME  
; FILE REFERENCE: 293102002120  
; CURRENT APPLICATION NUMBER: US/08/845,623A  
; EARLIER FILING DATE: 1997-04-25  
; EARLIER APPLICATION NUMBER: 08/164,294  
; EARLIER FILING DATE: 1993-12-09  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Bovine adenovirus type 3  
US-08-845-623-34

Query Match 57.1%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
|  
|  
|  
|  
Db 8 VLPP 11

RESULT 16  
US-08-815-927-34  
; Sequence 34, Application US/08815927  
; Patent No. 6086890  
; GENERAL INFORMATION:  
; APPLICANT: MITTAL, SURESH K.  
; APPLICANT: GRAHAM, FRANK L.  
; APPLICANT: PREVIC, LUDVIK  
; APPLICANT: BABIUK, LORNE A.  
; TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE ADENOVIRUS EXPRESSION  
; FILE REFERENCE: 293102002101  
; CURRENT APPLICATION NUMBER: US/08/815,927  
; CURRENT FILING DATE: 1997-03-13  
; EARLIER APPLICATION NUMBER: 08/164,294  
; EARLIER FILING DATE: 1993-12-09  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Bovine adenovirus type 3  
US-08-815-927-34

Query Match 57.1%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
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|  
|  
|  
Db 8 VLPP 11

RESULT 17  
US-09-103-330-34  
; Sequence 34, Application US/09103330A

; Patent No. 6319716  
; GENERAL INFORMATION:  
; APPLICANT: TIKOO, SURESH K.  
; APPLICANT: BABIUK, LORNE A.  
; APPLICANT: REDDY, POLICE S.  
; TITLE OF INVENTION: ISOLATION OF MUTANTS IN THE E3 REGION OF THE  
; FILE REFERENCE: 293102002121  
; CURRENT APPLICATION NUMBER: US/09/103,330A  
; CURRENT FILING DATE: 1998-06-23  
; EARLIER APPLICATION NUMBER: 08/880,234  
; EARLIER FILING DATE: 1997-06-23  
; EARLIER APPLICATION NUMBER: 08/164,292  
; EARLIER FILING DATE: 1993-12-09  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Bovine adenovirus type 3  
US-09-103-330-34

Query Match 57.1%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
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|  
|  
|  
Db 8 VLPP 11

RESULT 18  
US-09-435-242-34  
; Sequence 34, Application US/09435242  
; Patent No. 6379944  
; GENERAL INFORMATION:  
; APPLICANT: MITTAL, SURESH K.  
; APPLICANT: GRAHAM, FRANK L.  
; APPLICANT: PREVIC, LUDVIK  
; APPLICANT: BABIUK, LORNE A.  
; TITLE OF INVENTION: MAMMALIAN CELL LINES EXPRESSING BOVINE ADENOVIRUS FUNCTIONS  
; FILE REFERENCE: 293102002102  
; CURRENT APPLICATION NUMBER: US/09/435,242  
; CURRENT FILING DATE: 1999-11-05  
; EARLIER APPLICATION NUMBER: 08/815,927  
; EARLIER FILING DATE: 1997-03-13  
; EARLIER APPLICATION NUMBER: 08/164,294  
; EARLIER FILING DATE: 1993-12-09  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Bovine adenovirus type 3  
US-09-435-242-34

Query Match 57.1%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
|  
|  
|  
|  
Db 8 VLPP 11

RESULT 19  
US-07-794-288D-22  
; Sequence 22, Application US/07794288D  
; Patent No. 5580953  
; GENERAL INFORMATION:  
; APPLICANT: ELISABETH ALBRECHT,  
; APPLICANT: HOWARD JONES,  
; APPLICANT: LAURA S.L. GAETA,

APPLICANT: KATHRYN S. PRICKETT and  
APPLICANT: KEVIN BEAUMONT  
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: First Interstate World  
STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44  
MEDIUM TYPE: Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version  
OPERATING SYSTEM: 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/794,288D  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/794,288  
FILING DATE: 19-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Duft, Bradford, J.  
REGISTRATION NUMBER: 32,219  
REFERENCE/DOCKET NUMBER: 193/153  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-07-794-288D-22

Query Match 57.1%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
Db 2 VLPP 5

RESULT 20  
US-09-232-446B-10  
Sequence 10, Application US/09232446B  
Patent No. 6228647  
GENERAL INFORMATION:  
APPLICANT: Voytas, Daniel F.  
APPLICANT: Gai, Xiaowu  
TITLE OF INVENTION: Transposable Element Protein that Directs DNA  
TITLE OF INVENTION: Integration to Specific Chromosomal Sites  
FILE REFERENCE: 2-98  
CURRENT APPLICATION NUMBER: US/09/232,446B  
CURRENT FILING DATE: 1999-01-15  
PRIOR APPLICATION NUMBER: US 60/071,383  
PRIOR FILING DATE: 1998-01-15  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10

LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:mutant peptide  
US-09-232-446B-10

Query Match 57.1%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPN 5  
Db 8 LPN 11

RESULT 21  
US-07-794-288D-21  
Sequence 21, Application US/07794288D  
Patent No. 5580953  
GENERAL INFORMATION:  
APPLICANT: ELISABETH ALBRECHT,  
APPLICANT: HOWARD JONES,  
APPLICANT: LAURA S.L. GAETA,  
APPLICANT: KATHRYN S. PRICKETT and  
APPLICANT: KEVIN BEAUMONT  
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: First Interstate World  
STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44  
MEDIUM TYPE: Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version  
OPERATING SYSTEM: 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/794,288D  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/794,288  
FILING DATE: 19-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Duft, Bradford, J.  
REGISTRATION NUMBER: 32,219  
REFERENCE/DOCKET NUMBER: 193/153  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-07-794-288D-21

Query Match

57.1%; Score 4; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 95;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
|||  
Db 3 VLPP 6

## RESULT 22

US-07-794-288D-20  
; Sequence 20, Application US/07794288D  
; Patent No. 5580953

GENERAL INFORMATION:  
; APPLICANT: ELISABETH ALBRECHT,  
; APPLICANT: HOWARD JONES,  
; APPLICANT: LAURA S.L. GAETA,  
; APPLICANT: KATHRYN S. PRICKETT and  
; APPLICANT: KEVIN BEAUMONT  
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LYON & LYON  
; STREET: First Interstate World  
; STREET: Center  
; STREET: 633 West Fifth Street,  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44  
; MEDIUM TYPE: Mb storage  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version  
; OPERATING SYSTEM: 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/794,288D  
; FILING DATE: Herewith

CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/794,288  
; FILING DATE: 19-NOV-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Duft, Bradford, J.  
; REGISTRATION NUMBER: 32,219  
; REFERENCE/DOCKET NUMBER: 193/153  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-07-794-288D-20

Query Match 57.1%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
|||  
Db 4 VLPP 7

## RESULT 23

Best Local Similarity 100.0%; Pred. No. 95;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
|||  
Db 3 VLPP 6

US-07-794-288D-20  
; Sequence 20, Application US/07794288D  
; Patent No. 5580953

GENERAL INFORMATION:  
; APPLICANT: ELISABETH ALBRECHT,  
; APPLICANT: HOWARD JONES,  
; APPLICANT: LAURA S.L. GAETA,  
; APPLICANT: KATHRYN S. PRICKETT and  
; APPLICANT: KEVIN BEAUMONT  
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LYON & LYON  
; STREET: First Interstate World  
; STREET: Center  
; STREET: 633 West Fifth Street,  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44  
; MEDIUM TYPE: Mb storage  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version  
; OPERATING SYSTEM: 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/794,288D  
; FILING DATE: Herewith

CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/794,288  
; FILING DATE: 19-NOV-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Duft, Bradford, J.  
; REGISTRATION NUMBER: 32,219  
; REFERENCE/DOCKET NUMBER: 193/153  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-07-794-288D-20

Query Match 57.1%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
|||  
Db 4 VLPP 7

US-07-794-288D-19  
; Sequence 19, Application US/07794288D  
; Patent No. 5580953

GENERAL INFORMATION:  
; APPLICANT: ELISABETH ALBRECHT,  
; APPLICANT: HOWARD JONES,  
; APPLICANT: LAURA S.L. GAETA,  
; APPLICANT: KATHRYN S. PRICKETT and  
; APPLICANT: KEVIN BEAUMONT  
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LYON & LYON  
; STREET: First Interstate World  
; STREET: Center  
; STREET: 633 West Fifth Street,  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44  
; MEDIUM TYPE: Mb storage  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version  
; OPERATING SYSTEM: 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/794,288D  
; FILING DATE: Herewith

CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/794,288  
; FILING DATE: 19-NOV-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Duft, Bradford, J.  
; REGISTRATION NUMBER: 32,219  
; REFERENCE/DOCKET NUMBER: 193/153  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:  
US-07-794-288D-19

Query Match 57.1%; Score 4; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPP 4  
|||  
Db 5 VLPP 8

## RESULT 24

US-08-528-057-12  
; Sequence 12, Application US/08528057  
; Patent No. 5846715

GENERAL INFORMATION:  
; APPLICANT: PURCELL, Damian F. J.  
; APPLICANT: RUSSELL, Sarah M. C.  
; APPLICANT: MCKENZIE, Ian F. C.  
; TITLE OF INVENTION: CD46 VARIANTS  
; NUMBER OF SEQUENCES: 46

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/528,057
FILING DATE: CONCURRENTLY HERewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/961,686
FILING DATE: 11-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00199
FILING DATE: 10-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK0133/90
FILING DATE: 11-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17227/112 DACO
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-528-057-12

Query Match 57.1%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4
Db 1 VLPP 4

RESULT 25
US-08-915-4988-24
Sequence 24, Application US/089154988
Patent No. 6132954
GENERAL INFORMATION:
APPLICANT: James R. Lupski, Robert A. Britton, Donald L.
APPLICANT: Court and Bradford S. Powell
TITLE OF INVENTION: Methods of Screening for Agents that
TITLE OF INVENTION: Delay a Cell Cycle and Compositions Comprising ERA and an Anal
TITLE OF INVENTION: of Wild-Type ERA
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: & No. 6132954ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/08/915,498B
FILING DATE: August 20, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,353
FILING DATE: August 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0037
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-915-4988-24

Query Match 57.1%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNVG 7
Db 8 PNVG 11

RESULT 26
US-08-602-999A-202
Sequence 202, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leelie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid

```

```
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-202

Query Match          57.1%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4
Db 8 VLPP 11

RESULT 27
US-08-602-999A-406
; Sequence 406, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 16-FEB-1996
; APPLICATION NUMBER: US/08/602,999A
; CLASSIFICATION: 435
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 406:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-406

Query Match          57.1%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4
Db 8 VLPP 11

RESULT 28
US-09-500-124-202
; Sequence 202, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
```

```
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 16-FEB-1996
; APPLICATION NUMBER: US/09/500,124
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 202:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-202

Query Match          57.1%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4
Db 8 VLPP 11

RESULT 29
US-09-500-124-406
; Sequence 406, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
```

CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 406:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-406

Query Match 57.1%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.1e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
DB 8 VLPP 11

RESULT 30  
US-07-794-288D-18  
Sequence 18, Application US/07794288D  
Patent No. 5580953  
GENERAL INFORMATION:  
APPLICANT: ELISABETH ALBRECHT,  
APPLICANT: HOWARD JONES,  
APPLICANT: LAURA S.L. GAETA,  
APPLICANT: KATHRYN S. PRICKETT and  
APPLICANT: KEVIN BEAUMONT  
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: First Interstate World  
STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44  
MEDIUM TYPE: Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version  
OPERATING SYSTEM: 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/794,288D

FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/794,288  
FILING DATE: 19-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Duft, Bradford, J.  
REGISTRATION NUMBER: 32,219  
REFERENCE/DOCKET NUMBER: 193/153  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-07-794-288D-18

Query Match 57.1%; Score 4; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
DB 6 VLPP 9

RESULT 31  
US-07-794-288D-17  
Sequence 17, Application US/07794288D  
Patent No. 5580953  
GENERAL INFORMATION:  
APPLICANT: ELISABETH ALBRECHT,  
APPLICANT: HOWARD JONES,  
APPLICANT: LAURA S.L. GAETA,  
APPLICANT: KATHRYN S. PRICKETT and  
APPLICANT: KEVIN BEAUMONT  
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: First Interstate World  
STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44  
MEDIUM TYPE: Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version  
OPERATING SYSTEM: 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/794,288D  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/794,288  
FILING DATE: 19-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Duft, Bradford, J.  
REGISTRATION NUMBER: 32,219  
REFERENCE/DOCKET NUMBER: 193/153

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-07-794-288D-17

Query Match 57.1%; Score 4; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
Db 7 VLPP 10

RESULT 32  
US-07-794-288D-214  
Sequence 214, Application US/07794288D  
Patent No. 5580953

GENERAL INFORMATION:  
APPLICANT: ELISABETH ALBRECHT,  
APPLICANT: HOWARD JONES,  
APPLICANT: LAURA S.L. GHATA,  
APPLICANT: KATHRYN S. PRICKEIT and  
APPLICANT: KEVIN BEAUMONT  
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: First Interstate World  
STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44  
MEDIUM TYPE: Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version  
OPERATING SYSTEM: 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/794,288D  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/794,288  
FILING DATE: 19-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Duff, Bradford, J.  
REGISTRATION NUMBER: 32,219  
REFERENCE/DOCKET NUMBER: 193/153  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 214:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-07-794-288D-214

Query Match 57.1%; Score 4; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
Db 9 VLPP 12

RESULT 33  
US-08-621-803-100  
Sequence 100, Application US/08621803  
Patent No. 5851802

GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621.803  
FILING DATE: 22-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "XMP.118"  
US-08-621-803-100

Query Match 57.1%; Score 4; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNVG 7  
Db 13 PNVG 16

RESULT 34  
US-09-017-205-27  
Sequence 27, Application US/09017205  
Patent No. 5965357

GENERAL INFORMATION:  
APPLICANT: Marsden, Howard S  
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN

;; TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2  
;; NUMBER OF SEQUENCES: 86  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Nixon & Vandethye PC  
;; STREET: 8th Floor, 1100 No. 5965357th Glebe Road  
;; CITY: Arlington  
;; STATE: Virginia  
;; COUNTRY: USA  
;; ZIP: 22201-4714  
;;  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/017,205  
;; FILING DATE: 02-FEB-1998  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mitchard, Leonard C.  
;; REGISTRATION NUMBER: 29,009  
;; REFERENCE/DOCKET NUMBER: 604-436  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703)816-4000  
;; TELEFAX: (703)816-4100  
;; INFORMATION FOR SEQ ID NO: 27:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide from HSV-2 glycoprotein G  
;; FRAGMENT TYPE: internal  
;;  
US-09-017-205-27

Query Match 57.1%; Score 4; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
DB 15 VLPP 18

RESULT 35  
US-09-017-205-28  
;; Sequence 28, Application US/09017205  
;; Patent No. 5965357  
;; GENERAL INFORMATION:  
;; APPLICANT: Maresden, Howard S  
;; TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN  
;; TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2  
;; NUMBER OF SEQUENCES: 86  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Nixon & Vandethye PC  
;; STREET: 8th Floor, 1100 No. 5965357th Glebe Road  
;; CITY: Arlington  
;; STATE: Virginia  
;; COUNTRY: USA  
;; ZIP: 22201-4714  
;;  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/017,205  
;; FILING DATE: 02-FEB-1998  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mitchard, Leonard C.  
;; REGISTRATION NUMBER: 29,009  
;; REFERENCE/DOCKET NUMBER: 604-436  
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (703)816-4000  
;; TELEFAX: (703)816-4100  
;; INFORMATION FOR SEQ ID NO: 28:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide from HSV-2 glycoprotein G  
;; FRAGMENT TYPE: internal  
;;  
US-09-017-205-28

Query Match 57.1%; Score 4; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
DB 5 VLPP 8

RESULT 35  
US-09-217-352-100  
;; Sequence 100, Application US/09217352  
;; Patent No. 6274344  
;; GENERAL INFORMATION:  
;; APPLICANT: Better, Marc D.  
;; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
;; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides  
;; NUMBER OF SEQUENCES: 265  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
;; STREET: 6300 Sears Tower, 233 South Wacker Drive  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: United States of America  
;; ZIP: 60606-6402  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/217,352  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/621,803  
;; FILING DATE: 22-MAR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Borun, Michael F.  
;; REGISTRATION NUMBER: 25,447  
;; REFERENCE/DOCKET NUMBER: 27129/33199  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312/474-6300  
;; TELEFAX: 312/474-0448  
;; TELEX: 25-3856  
;; INFORMATION FOR SEQ ID NO: 100:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: "XMP.118"  
;;  
US-09-217-352-100

Query Match 57.1%; Score 4; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNVG 7  
DB 13 PNVG 16



## RESULT 37

US-07-794-288D-16  
; Sequence 16, Application US/07794288D  
; Patent No. 5580953  
; GENERAL INFORMATION:  
; APPLICANT: ELISABETH ALBRECHT,  
; APPLICANT: HOWARD JONES,  
; APPLICANT: LAURA S.L. GAETA,  
; APPLICANT: KATHRYN S. PRICKETT and  
; APPLICANT: KEVIN BEAUMONT  
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LYON & LYON  
; STREET: First Interstate World  
; STREET: Center  
; STREET: 633 West Fifth Street,  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44  
; MEDIUM TYPE: Mb storage  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version  
; OPERATING SYSTEM: 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/794,288D  
; FILING DATE: Herewith  
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/794,288  
; FILING DATE: 19-NOV-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Duft, Bradford, J.  
; REGISTRATION NUMBER: 32,219  
; REFERENCE/DOCKET NUMBER: 193/153  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:

US-07-794-288D-16

Query Match 57.1%; Score 4; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4

Db 8 VLPP 11

## RESULT 38

US-07-794-288D-126  
; Sequence 126, Application US/07794288D  
; Patent No. 5580953  
; GENERAL INFORMATION:  
; APPLICANT: ELISABETH ALBRECHT,  
; APPLICANT: HOWARD JONES,

APPLICANT: LAURA S.L. GAETA,  
APPLICANT: KATHRYN S. PRICKETT and  
APPLICANT: KEVIN BEAUMONT  
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: First Interstate World  
STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44  
; MEDIUM TYPE: Mb storage  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version  
; OPERATING SYSTEM: 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/794,288D  
; FILING DATE: Herewith  
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/794,288  
; FILING DATE: 19-NOV-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Duft, Bradford, J.  
; REGISTRATION NUMBER: 32,219  
; REFERENCE/DOCKET NUMBER: 193/153  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 126:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; FEATURE:  
; OTHER INFORMATION:

US-07-794-288D-126

Query Match 57.1%; Score 4; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4

Db 16 VLPP 19

## RESULT 39

US-07-794-288D-15  
; Sequence 15, Application US/07794288D  
; Patent No. 5580953  
; GENERAL INFORMATION:  
; APPLICANT: ELISABETH ALBRECHT,  
; APPLICANT: HOWARD JONES,  
; APPLICANT: LAURA S.L. GAETA,  
; APPLICANT: KATHRYN S. PRICKETT and  
; APPLICANT: KEVIN BEAUMONT  
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
; TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LYON & LYON  
; STREET: First Interstate World

STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44  
MEDIUM TYPE: Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version  
OPERATING SYSTEM: 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/794,288D  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/794,288  
FILING DATE: 19-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Duft, Bradford, J.  
REGISTRATION NUMBER: 32,219  
REFERENCE/DOCKET NUMBER: 193/153  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-07-794-288D-15

Query Match 57.1%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 VLPP 4  
Db 9 VLPP 12

RESULT 40  
US-07-794-288D-118  
Sequence 118, Application US/07794288D  
Patent No. 5580953  
GENERAL INFORMATION:  
APPLICANT: ELISABETH ALBRECHT,  
APPLICANT: HOWARD JONES,  
APPLICANT: LAURA S.L. GAETA,  
APPLICANT: KATHRYN S. PRICKETT and  
APPLICANT: KEVIN BEAUMONT  
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: First Interstate World  
STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44

MEDIUM TYPE: Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version  
OPERATING SYSTEM: 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/794,288D  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/794,288  
FILING DATE: 19-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Duft, Bradford, J.  
REGISTRATION NUMBER: 32,219  
REFERENCE/DOCKET NUMBER: 193/153  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-07-794-288D-118

Query Match 57.1%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 VLPP 4  
Db 17 VLPP 20

RESULT 41  
US-07-794-288D-125  
Sequence 125, Application US/07794288D  
Patent No. 5580953  
GENERAL INFORMATION:  
APPLICANT: ELISABETH ALBRECHT,  
APPLICANT: HOWARD JONES,  
APPLICANT: LAURA S.L. GAETA,  
APPLICANT: KATHRYN S. PRICKETT and  
APPLICANT: KEVIN BEAUMONT  
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: First Interstate World  
STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44  
MEDIUM TYPE: Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version  
OPERATING SYSTEM: 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/794,288D  
FILING DATE: Herewith  
CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/794,288  
;; FILING DATE: 19-NOV-91  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Duft, Bradford J.  
;; REGISTRATION NUMBER: 32,219  
;; REFERENCE/DOCKET NUMBER: 193/153  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 125:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 AMINO ACIDS  
;; TYPE: AMINO ACID  
;; TOPOLOGY: LINEAR  
;; MOLECULE TYPE: PEPTIDE  
;; FEATURE:  
;; OTHER INFORMATION:  
US-07-794-288D-125

Query Match 57.1%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No.1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPp 4  
Db 16 VLPp 19

RESULT 42  
US-08-602-999A-153  
; Sequence 153, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mierock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIS  
; INFORMATION FOR SEQ ID NO: 153:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid

;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-08-602-999A-153

Query Match 57.1%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred.No.1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPp 4  
Db 7 VLPp 10

RESULT 43  
US-09-500-124-153  
; Sequence 153, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mierock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIS  
; INFORMATION FOR SEQ ID NO: 153:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-153

Query Match 57.1%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred.No.1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPp 4  
Db 7 VLPp 10

RESULT 44

US-09-081-975-19  
; Sequence 19, Application US/09081975  
; Patent No. 6451979  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; APPLICANT: Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: 101 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/081,975  
; FILING DATE: 12-MAY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/046,207  
; FILING DATE: 12-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Eisenstein, Ronald I  
; REGISTRATION NUMBER: 30,628  
; REFERENCE/DOCKET NUMBER: 47400  
; TELEPHONE: 617-345-6054  
; TELEFAX: 617-345-1300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-081-975-19

Query Match 57.1%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
QY 2 LPN 5  
Db 16 LPN 19

RESULT 45  
US-09-205-258-852  
; Sequence 852, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,895  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880

; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,896  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,020  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,895  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,884  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,894  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,971  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,882  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,899  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,893  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,900  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,901  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,892  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,915  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,019  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,970  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,972  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,916  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,373  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,875  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,374  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,917  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,949  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,883  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,897  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,898  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,962  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,963  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,877  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,878  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/070,923  
; EARLIER FILING DATE: 1997-12-18  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1227  
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 852  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-852

Query Match 57.1%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4  
Db 8 VLPP 11

## RESULT 46

US-07-729-099-5  
Sequence 5, Application US/07729099  
Patent No. 5403581  
GENERAL INFORMATION:  
APPLICANT: Binger, Mary-Helen  
APPLICANT: Pasamontes, Luis  
TITLE OF INVENTION: Coccidiosis Vaccines  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.  
ZIP: 07110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07729,099  
FILING DATE: 19910712  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Roseman, Catherine R  
REGISTRATION NUMBER: 34,240  
REFERENCE/DOCKET NUMBER: 8514  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-6208  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Eimeria tenella

## US-07-729-099-5

Query Match 42.9%; Score 3; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6  
Db 1 PNV 3

## RESULT 47

US-08-257-392-5  
Sequence 5, Application US/08257392  
Patent No. 5688513  
GENERAL INFORMATION:

APPLICANT: Binger, Mary-Helen  
APPLICANT: Pasamontes, Luis  
TITLE OF INVENTION: Coccidiosis Vaccines  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/257,392  
FILING DATE: 09-JUN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/729,099  
FILING DATE: 12-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Roseman, Catherine R  
REGISTRATION NUMBER: 34,240  
REFERENCE/DOCKET NUMBER: 8514  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-6208  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Eimeria tenella  
US-08-257-392-5

Query Match 42.9%; Score 3; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6  
Db 1 PNV 3

## RESULT 48

US-08-770-035-5  
Sequence 5, Application US/08770035  
Patent No. 6008342  
GENERAL INFORMATION:  
APPLICANT: Binger, Mary-Helen  
APPLICANT: Pasamontes, Luis  
TITLE OF INVENTION: Coccidiosis Vaccines  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

Query Match 42.9%; Score 3; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6  
Db 1 PNV 3

APPLICATION NUMBER: US/08/770,035  
FILING DATE: 09-AUG-1991  
CLASSIFICATION: 07/743614  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715300  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/683400  
FILING DATE: 10-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/621667  
FILING DATE: 03-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Davyl B.  
REGISTRATION NUMBER: 32,637  
REFERENCE/DOCKET NUMBER: 645P5C2D1  
TELEPHONE: 415/225-1249  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
HYPOTHETICAL: YES  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Eimeria tenella  
US-08-770-035-5

Query Match 42.9%; Score 3; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PNV 6  
|||  
Db 1 PNV 3

## RESULT 49

US-08-441-871-27  
Sequence 27, Application US/08441871  
Patent No. 5846765  
GENERAL INFORMATION:  
APPLICANT: Matthews, David J.  
APPLICANT: Wells, James A.  
APPLICANT: Zoller, Mark J.  
TITLE OF INVENTION: Identification of No. 5846765el Substrates  
NUMBER OF SEQUENCES: 152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
FILING DATE: 16-MAY-1995  
APPLICATION NUMBER: US/08/441,871  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/418928  
FILING DATE: 03-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/161692  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/864452  
FILING DATE: 06-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/09133  
FILING DATE: 03-DEC-1991  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743614  
FILING DATE: 09-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715300  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/683400  
FILING DATE: 10-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/621667  
FILING DATE: 03-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Davyl B.  
REGISTRATION NUMBER: 32,637  
REFERENCE/DOCKET NUMBER: 645P5C2D1  
TELEPHONE: 415/225-1249  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-441-871-27

Query Match 42.9%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPP 4  
|||  
Db 1 LPP 3

## RESULT 50

US-09-039-308A-28  
Sequence 28, Application US/09039308A  
Patent No. 6069129  
GENERAL INFORMATION:  
APPLICANT: Sandberg, Lawrence; Roos, Phillip;  
APPLICANT: Mitts, Thomas  
TITLE OF INVENTION: ELASTIN DERIVED COMPOSITION  
TITLE OF INVENTION: AND METHOD OF  
TITLE OF INVENTION: USING SAME  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: REED SMITH SHAW & MCCLAY, LLP  
STREET: PO Box 488  
CITY: Pittsburgh  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 15230  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
COMPUTER: Compaq  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Word 6.0  
CURRENT APPLICATION DATA:  
FILING DATE: March 13, 1998  
APPLICATION NUMBER: US/09/039,308A  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Miller, Raymond A.  
REGISTRATION NUMBER: 42,891  
REFERENCE/DOCKET NUMBER: 97-489  
TELEPHONE: (412) 288-4192  
TELEFAX: (412) 288-3300  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-039-308A-28

Query Match 42.9%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLP 3  
|||  
Db 1 VLP 3

RESULT 51  
US-08-747-137-91  
; Sequence 91, Application US/08747137  
; Patent No. 5945033  
; GENERAL INFORMATION:  
; APPLICANT: YEN, Richard C.K.  
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR  
; THERAPEUTIC AND DIAGNOSTIC USE  
; NUMBER OF SEQUENCES: 184  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,137  
; FILING DATE: 12-NOV-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,546  
; FILING DATE: 14-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,831  
; FILING DATE: 01-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/959,560  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/641,720  
; FILING DATE: 15-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 016197-00084005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
US-08-747-137-91

Query Match 42.9%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPP 4  
|||  
Db 1 LPP 3

US-09-646-154-10  
; Sequence 10, Application US/09646154  
; Patent No. 6429024  
; GENERAL INFORMATION:  
; APPLICANT: KOKUBO, TOHRU  
; APPLICANT: ARAI, KENJI  
; APPLICANT: TOMA, KAZUNORI  
; TITLE OF INVENTION: TEST METHOD FOR IGA NEPHROPATHY  
; FILE REFERENCE: KP-8821  
; CURRENT APPLICATION NUMBER: US/09/646,154  
; CURRENT FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: PCT/JP99/01525  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Bovine sp.  
US-09-646-154-10

Query Match 42.9%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPP 4  
|||  
Db 1 LPP 3

RESULT 53  
US-08-817-832B-11  
; Sequence 11, Application US/08817832B  
; Patent No. 6579691  
; GENERAL INFORMATION:  
; APPLICANT: MANDELKOW, Eckhard, et al.  
; TITLE OF INVENTION: No. 6579691el Protein Kinase (NPK-110)  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 S. Wacker Drive, 6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: US  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,832B  
; FILING DATE: 28-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/04258  
; FILING DATE: 30-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94 11 7122.5  
; FILING DATE: 28-OCT-1994  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 2  
; OTHER INFORMATION: /note="Ser at position 2 is  
; phosphorylated."  
US-08-817-832B-11

US-08-817-832B-11

Query Match 42.9%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
DB 3 LPP 5

RESULT 54

US-07-956-700B-58  
Sequence 58, Application US/07956700B  
Patent No. 5539092  
GENERAL INFORMATION:  
APPLICANT: Robert Haselkorn and Piotr Gornicki  
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
TITLE OF INVENTION: Carboxylase  
NUMBER OF SEQUENCES: 116  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5539092th Clark Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60610

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/956,700B  
FILING DATE: 19921002  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas E. No. 5539092thrup  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD:058  
TELEPHONE: 1-312-744-0090  
TELEFAX: 1-312-755-4489  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: Amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide

US-07-956-700B-58

Query Match 42.9%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
DB 2 LPP 4

RESULT 55

US-08-532-065B-5  
Sequence 5, Application US/08532065B  
Patent No. 5753507  
GENERAL INFORMATION:  
APPLICANT: Ohta, Daiaku  
APPLICANT: Mizutani, Masaharu  
TITLE OF INVENTION: Plant Geraniol/Nerol 10-Hydroxylase and  
TITLE OF INVENTION: DNA Coding Therefor  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5753507artis Corporation

STREET: 59 Route 10  
CITY: East Hanover  
STATE: NJ  
COUNTRY: USA  
ZIP: 07936  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,065B  
FILING DATE: 22-SEP-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide

US-08-532-065B-5

Query Match 42.9%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
DB 2 LPP 4

RESULT 56

US-08-476-537-58  
Sequence 58, Application US/08476537  
Patent No. 5756290  
GENERAL INFORMATION:  
APPLICANT: Robert Haselkorn and Piotr Gornicki  
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
TITLE OF INVENTION: Carboxylase  
NUMBER OF SEQUENCES: 116  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5756290th Clark Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60610

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,537  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/956,700  
FILING DATE: 10/21/92  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas E. No. 5756290thrup  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD:058  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-312-744-0090  
TELEFAX: 1-312-755-4489



INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: Amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
US-08-476-537-58

Query Match 42.9%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
|||  
DB 2 LPP 4

RESULT 57  
US-08-485-607-58  
Sequence 58, Application US/08485607  
Patent No. 5792627  
GENERAL INFORMATION:  
APPLICANT: Robert Haselkorn and Piotr Gornicki  
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
NUMBER OF SEQUENCES: 116  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5792627th Clark Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,607  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/956,700  
FILING DATE: 10/21/92  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas E. No. 5792627thrup  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD:058  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-312-744-0090  
TELEFAX: 1-312-755-4489  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: Amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
US-08-485-607-58

Query Match 42.9%; Score 3; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
|||  
DB 2 LPP 4

RESULT 58  
US-08-317-310A-35

Sequence 35, Application US/08317310A  
Patent No. 5858701  
GENERAL INFORMATION:  
APPLICANT: WHITE, Morris F.  
APPLICANT: SUN, Xiao Jian  
APPLICANT: PIERCE, Jacalyn H.  
TITLE OF INVENTION: THE IRS FAMILY OF GENES  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/317,310A  
FILING DATE: 03-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Louis Myers  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: JDP-022  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-317-310A-35

Query Match 42.9%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
|||  
DB 4 LPP 6

RESULT 59  
US-08-637-759B-498  
Sequence 498, Application US/08637759B  
Patent No. 5876931  
GENERAL INFORMATION:  
APPLICANT: David William Holden  
TITLE OF INVENTION: Identification of Genes  
NUMBER OF SEQUENCES: 501  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabet  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/637,759B  
FILING DATE: 03-MAY-1996

CLASSIFICATION: 435  
PRIOR APPLICATION DATA: PCT/GB95/02875  
APPLICATION NUMBER: 11-DEC-1995  
FILING DATE: 11-DEC-1995  
CLASSIFICATION: 435  
NAME: Pabet, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: RPS 101  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 498:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-637-759B-498

Query Match 42.9%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
Db 4 LPP 6

RESULT 60  
US-08-053-451B-124  
Sequence 124, Application US/08053451B  
Patent No. 5955584  
GENERAL INFORMATION:  
APPLICANT: Chen, Francis W.  
APPLICANT: Ditlow, Charles C.  
APPLICANT: Calenoff, Emanuel  
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC  
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,451B  
FILING DATE: 26-APR-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 7606-033-999  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein

US-08-053-451B-124  
Query Match 42.9%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6  
Db 4 PNV 6

RESULT 61  
US-08-726-306A-133  
Sequence 133, Application US/08726306A  
Patent No. 5958684  
GENERAL INFORMATION:  
APPLICANT: van Leeuwen, Frederik Willem  
APPLICANT: Burbach, Johannes Peter Henri  
APPLICANT: Grosveld, Franklin G.  
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS  
NUMBER OF SEQUENCES: 189  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: 1 Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,306A  
FILING DATE: 02-Oct-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 95/20080.4  
FILING DATE: 02-Oct-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/009,832  
FILING DATE: 01-Jan-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)  
TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 133:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-726-306A-133

Query Match 42.9%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6  
Db 2 PNV 4

RESULT 62  
US-08-482-228-97  
Sequence 97, Application US/08482228  
Patent No. 5968753  
GENERAL INFORMATION:  
APPLICANT: Tseng-Law, Janet

APPLICANT: Kobori, Joan A.  
APPLICANT: Al-Abdaly, Fahad A.  
APPLICANT: Guillermo, Roy  
APPLICANT: Helgeson, Sam L.  
APPLICANT: Deans, Robert J.  
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL  
NUMBER OF SEQUENCES: 215  
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janice Guthrie, Ph.D.  
STREET: P.O. Box 15210  
CITY: Irvine  
STATE: California  
COUNTRY: USA  
ZIP: 92713-5210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,228  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Guthrie, Janice  
REGISTRATION NUMBER: 35,170  
REFERENCE/DOCKET NUMBER: IT-4630CIP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 440-5353  
TELEFAX: (714) 553-1952  
INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-228-97

Query Match 42.9%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6  
|||  
DB 2 PNV 4

RESULT 63  
US-08-475-879-58  
Sequence 58, Application US/08475879  
Patent No. 5972644  
Patent No. 5972644 5786170  
GENERAL INFORMATION:  
APPLICANT: Robert Haselkorn and Piotr Gornicki  
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
TITLE OF INVENTION: Carboxylase  
NUMBER OF SEQUENCES: 116  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5972644 5786170th Clark Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,879  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/956,700  
FILING DATE: 10/21/92  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas E. No. 5972644 5786170thrup  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD:058  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 1-312-744-0090  
TELEFAX: 1-312-755-4489  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: Amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
US-08-475-879-58

Query Match 42.9%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4  
|||  
DB 2 LPP 4

RESULT 64  
US-08-481-985B-132  
Sequence 132, Application US/08481985B  
Patent No. 6011146  
GENERAL INFORMATION:  
APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: Altered Major Histocompatibility Complex  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,985B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0106-04000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:

; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-481-985B-132

Query Match 42.9%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 5 NVG 7  
Db 1 NVG 3

RESULT 65  
US-08-871-355A-498  
; Sequence 498, Application US/08871355A  
; Patent No. 6015669  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/871,355A  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/CB95/02875  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101 CON  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 498:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-871-355A-498

Query Match 42.9%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 2 LPP 4  
Db 4 LPP 6

RESULT 66  
US-08-482-528-97

; Sequence 97, Application US/08482528  
; Patent No. 6017719  
; GENERAL INFORMATION:  
; APPLICANT: Tseng-Law, Janet  
; APPLICANT: Kobori, Joan A.  
; APPLICANT: Al-Abdaly, Fahad A.  
; APPLICANT: Guillermo, Roy  
; APPLICANT: Helgeson, Sam L.  
; APPLICANT: Deans, Robert J.  
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL  
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE  
; NUMBER OF SEQUENCES: 215  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janice Guthrie, Ph.D.  
; STREET: P.O. Box 15210  
; CITY: Irvine  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92713-5210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,528  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Guthrie, Janice  
; REGISTRATION NUMBER: 35,170  
; REFERENCE/DOCKET NUMBER: IT-4630CIP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 440-5353  
; TELEFAX: (714) 553-1952  
; INFORMATION FOR SEQ ID NO: 97:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-482-528-97

Query Match 42.9%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 4 PNV 6  
Db 2 PNV 4

RESULT 67  
US-09-039-308A-33  
; Sequence 33, Application US/09039308A  
; Patent No. 6069129  
; GENERAL INFORMATION:  
; APPLICANT: Sandberg, Lawrence; Roos, Phillip;  
; APPLICANT: Mitts, Thomas  
; TITLE OF INVENTION: ELASTIN DERIVED COMPOSITION  
; TITLE OF INVENTION: AND METHOD OF  
; TITLE OF INVENTION: USING SAME  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: REED SMITH SHAW & MCCLAY, LLP  
; STREET: PO Box 488  
; CITY: Pittsburgh  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 15230  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; COMPUTER: Compaq

OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Word 6.0  
CURRENT APPLICATION NUMBER: US/09/039,308A  
FILING DATE: March 13, 1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Miller, Raymond A.  
REGISTRATION NUMBER: 42,891  
REFERENCE/DOCKET NUMBER: 97-489  
TELEPHONE: (412) 288-4192  
TELEFAX: (412) 288-3300  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-039-308A-33

Query Match 42.9%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
|||  
DB 1 VLP 3

## RESULT 68

US-09-330-970-21  
Sequence 21, Application US/09330970  
Patent No. 6146876  
GENERAL INFORMATION:  
APPLICANT: Robison, Keith E.  
APPLICANT: Kapeller-Libermann, Rosana  
APPLICANT: White, David  
TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide  
TITLE OF INVENTION: Phosphodiesterase  
FILE REFERENCE: 5800-28  
CURRENT APPLICATION NUMBER: US/09/330,970  
CURRENT FILING DATE: 1999-06-11  
EARLIER APPLICATION NUMBER: 09/277,423  
EARLIER FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 21  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-330-970-21

Query Match 42.9%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
|||  
DB 2 VLP 4

## RESULT 69

US-09-330-970-35  
Sequence 35, Application US/09330970  
Patent No. 6146876  
GENERAL INFORMATION:  
APPLICANT: Robison, Keith E.  
APPLICANT: Kapeller-Libermann, Rosana  
APPLICANT: White, David  
TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide  
TITLE OF INVENTION: Phosphodiesterase

FILE REFERENCE: 5800-28  
CURRENT APPLICATION NUMBER: US/09/330,970  
CURRENT FILING DATE: 1999-06-11  
EARLIER APPLICATION NUMBER: 09/277,423  
EARLIER FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 35  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-330-970-35

Query Match 42.9%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLP 3  
|||  
DB 2 VLP 4

## RESULT 70

US-09-196-934-2  
Sequence 2, Application US/09196934  
Patent No. 6191256  
GENERAL INFORMATION:  
APPLICANT: Chen, Li Aug  
APPLICANT: Beutner, Joseph A.  
APPLICANT: Carbone, Ruben G.  
TITLE OF INVENTION: Recombinant Factor VIII Binding Peptides  
FILE REFERENCE: MSB-7251  
CURRENT APPLICATION NUMBER: US/09/196,934  
CURRENT FILING DATE: 1998-11-20  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patencin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-196-934-2

Query Match 42.9%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPN 5  
|||  
DB 3 PPN 5

## RESULT 71

US-09-232-446B-23  
Sequence 23, Application US/09232446B  
Patent No. 6228647  
GENERAL INFORMATION:  
APPLICANT: Voytas, Daniel F.  
APPLICANT: Gai, Xiaowu  
TITLE OF INVENTION: Transposable Element Protein that Directs DNA  
TITLE OF INVENTION: Integration to Specific Chromosomal Sites  
FILE REFERENCE: 2-98  
CURRENT APPLICATION NUMBER: US/09/232,446B  
CURRENT FILING DATE: 1999-01-15  
PRIOR APPLICATION NUMBER: US 60/071,383  
PRIOR FILING DATE: 1998-01-15  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 23  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mutant peptide
; OTHER INFORMATION: sequence
US-09-232-446B-23

Query Match          42.9%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
DB 4 LPP 6

RESULT 72
US-09-201-945-498
; Sequence 498, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 498:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-201-945-498

Query Match          42.9%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
DB 4 LPP 6

RESULT 73
US-09-394-630-14
; Sequence 14, Application US/09394630
; Patent No. 6395306
```

```
; GENERAL INFORMATION:
; APPLICANT: Cui, Xiangmin
; APPLICANT: Lu, Yuefeng
; APPLICANT: Pan Pacific Pharmaceutical, Inc.
; TITLE OF INVENTION: Useful Properties of a Bee Venom Protein and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 019049-000200US
; CURRENT APPLICATION NUMBER: US/09/394,630
; CURRENT FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: US 60/100,172
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:residues 55-60
; OTHER INFORMATION: of SEQ ID NO:2 obtained through protein sequencing
US-09-394-630-14

Query Match          42.9%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PNV 6
DB 1 PNV 3

RESULT 74
US-09-433-043B-58
; Sequence 58, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-58

Query Match          42.9%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPP 4
DB 2 LPP 4

RESULT 75
US-09-155-613A-51
; Sequence 51, Application US/09155613A
; Patent No. 6420120
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
```

; APPLICANT: Karayan, Lucie  
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses  
; FILE REFERENCE: 032751-036  
; CURRENT APPLICATION NUMBER: US/09/155,613A  
; CURRENT FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: PCT/FR98/00184  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: FR 97/01005  
; PRIOR FILING DATE: 1997-01-30  
; PRIOR APPLICATION NUMBER: FR 97/11166  
; PRIOR FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Phagotope  
US-09-155-613A-51

Query Match 42.9%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NVG 7  
|||  
Db 2 NVG 4

Search completed: November 25, 2003, 20:16:14  
Job time : 9.63298 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 9.20213 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-18  
Perfect score: 10  
Sequence: 1 VYPFTGPIPN 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

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Minimum DB seq length: 3
Maximum DB seq length: 20
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### Post-processing: Listing first 100 summaries

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Database :      PIR_76:*
1:  _pir1:*
2:  _pir2:*
3:  _pir3:*
4:  _pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	4	40.0	18	2	A59137	protein Pil - gold
2	3	30.0	6	2	JN0861	peptidyl-dipeptidase
3	3	30.0	6	2	A61049	halo-toxin - Pseud
4	3	30.0	8	2	PT0368	Ig gamma chain C r
5	3	30.0	9	2	S70332	endosperm protein,
6	3	30.0	9	2	A26363	cardioactive pepti
7	3	30.0	9	2	S39766	cardioactive pepti
8	3	30.0	9	2	S27233	cardioactive pepti
9	3	30.0	9	2	S29767	cardioactive pepti
10	3	30.0	11	1	XAV1BH	bradykinin-potent
11	3	30.0	11	2	A58838	hemolysin - Porphy
12	3	30.0	11	2	PS0259	39K protein 3225 -
13	3	30.0	12	2	E45691	probable minor cap
14	3	30.0	12	2	S92213	28K protein 4412 -
15	3	30.0	12	2	A28955	polysialoglycoprot
16	3	30.0	12	2	S23168	Z protein - guinea
17	3	30.0	12	2	PQ0786	NADH2 dehydrogenas
18	3	30.0	13	2	A35245	histone H1a - mous
19	3	30.0	13	2	A26599	carboxylesterase (
20	3	30.0	13	2	B28955	polysialoglycoprot
21	3	30.0	13	2	S13273	polysialoglycoprot
22	3	30.0	14	2	PA0111	protein QA100054 -
23	3	30.0	15	2	A54397	ubiquitin-carrier
24	3	30.0	15	2	B61457	alpha-glucosidase
25	3	30.0	15	2	PL0154	glycoprotein - log
26	3	30.0	15	2	S08282	cytochrome P450K-2
27	3	30.0	16	2	A42291	tail fiber protein
28	3	30.0	16	2	S16376	L-serine dehydrata
29	3	30.0	16	2	S22040	cob protein - comm

## ALIGNMENTS

RESULT 1  
 A59137  
 protein p11 - golden needle mushroom (fragment)  
 C:Species: Flammulina velutipes (golden needle mushroom)  
 C>Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 12-Nov-1999  
 C:Accession: A59137  
 R:Sakamoto, Y.; Ando, A.; Tanai, Y.; Miura, K.  
 Submitted to the Protein Sequence Database, November 1999  
 A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr  
 A:Reference number: A59137  
 A:Accession: A59137  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-18 <SA>  
 Query Match 40.0%; Score 4; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PFTG 6  
 Db 15 PFTG 18  
 ||||  
 RESULT 2  
 JN0861  
 peptidyl-diesterase A inhibitory peptide C111 - striped bonito  
 C:Species: Sarda orientalis (striped bonito)  
 C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C:Accession: JN0861  
 R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
 A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe  
 A:Reference number: JN0859; MUID:94080036; PMID:7764272  
 A:Accession: JN0861  
 A:Molecule type: protein  
 A:Residues: 1-6 <MAT>  
 A:Experimental source: liver  
 C:Comment: The carboxyl end is essential for the protein's expression of angiotensin I-c  
 C:Superfamily: bradykinin-potentiating peptide  
 C:Keywords: angiotensin-converting enzyme inhibitor  
 Query Match 30.0%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVP 3  
 Db 2 VVP 4  
 ||||  
 RESULT 3  
 A61049  
 halo-toxin - Pseudomonas syringae pv. mori  
 C:Species: Pseudomonas syringae pv. mori  
 A:Note: host mulberry tree  
 C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Jan-1997  
 C:Accession: A61049  
 R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.  
 Chem. Lett. 00, 679-680, 1989  
 A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri  
 A:Reference number: A61049  
 A:Accession: A61049  
 A:Molecule type: protein  
 A:Residues: 1-6 <KAJ>  
 A:Note: sequence confirmed by synthesis  
 C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry  
 C:Keywords: toxin  
 Query Match 30.0%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVP 3  
 Db 2 VVP 4  
 ||||  
 RESULT 4  
 PT0368  
 Ig gamma chain C region (gamma-1) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Aug-1996  
 C:Accession: PT0368  
 R:Milili, M.; Fougereau, M.; Guglielmi, P.; Schiff, C.  
 Mol. Immunol. 28, 753-761, 1991  
 A:Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.  
 A:Reference number: PT0368; MUID:91312348; PMID:1906981  
 A:Accession: PT0368  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <MIL>  
 A:Experimental source: fetal liver  
 C:Keywords: immunoglobulin  
 Query Match 30.0%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GPI 8  
 Db 4 GPI 6  
 ||||  
 RESULT 5  
 S70332  
 endosperm protein, 10K - rye (fragment)  
 C:Species: Secale cereale (rye)  
 C>Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
 C:Accession: S70332  
 R:Roche, A.; Calero, M.; Soriano, F.; Mendez, E.  
 Biochim. Biophys. Acta 1295, 13-22, 1996  
 A:Title: Identification of major rye secalins as coeliac immunoreactive proteins.  
 A:Reference number: S70327; MUID:96283789; PMID:8679669  
 A:Accession: S70332  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <ROC>  
 Query Match 30.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 TGP 7  
 Db 1 TGP 3  
 ||||  
 RESULT 6  
 A26363  
 cardioactive peptide - green crab (fragment)  
 C:Species: Carcinus maenas (green crab, common shore crab)  
 C>Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 18-Jun-1993  
 C:Accession: A26363  
 R:Stangier, J.; Hilbich, C.; Beyreuther, K.; Keller, R.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 575-579, 1987  
 A:Title: Unusual cardioactive peptide (CCAP) from pericardial organs of the shore crab  
 A:Reference number: A26363  
 A:Accession: A26363  
 A:Molecule type: protein  
 A:Residues: 1-9 <STA>  
 Query Match 30.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 TGP 7  
 Db 1 TGP 3  
 ||||

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
|||  
Db 6 FTG 8

RESULT 7  
S39766  
cardioactive peptide CCAP - yellow mealworm  
C:Species: Tenebrio molitor (yellow mealworm)  
C:Date: 07-Oct-1994 #sequence\_revision 12-Apr-1996 #text\_change 07-May-1999  
C:Accession: S39766  
R:Furuya, K.; Liao, S.; Reynolds, S.E.; Ota, R.B.; Hackett, M.; Schooley, D.A.  
Biol. Chem. Hoppe-Seyler 374, 1065-1074, 1993  
A:Title: Isolation and identification of a cardioactive peptide from Tenebrio molitor and  
A:Reference number: S39766; MUID:94176032; PMID:8129851  
A:Accession: S39766  
A:Molecule type: protein  
A:Residues: 1-9 <FUR>  
C:Keywords: neuropeptide

Query Match 30.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
|||  
Db 6 FTG 8

RESULT 8  
S27233  
cardioactive peptide CCAP - tobacco hornworm  
C:Species: Manduca sexta (tobacco hornworm)  
C:Date: 09-Jun-1994 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996  
C:Accession: S27233  
R:Cheung, C.C.; Loi, P.K.; Sylwester, A.W.; Lee, T.D.; Tublitz, N.J.  
FBAS Lett. 313, 165-168, 1992  
A:Title: Primary structure of a cardioactive neuropeptide from the tobacco hawkmoth, Man  
A:Reference number: S27233; MUID:93050243; PMID:1426284  
A:Accession: S27233  
A:Molecule type: protein  
A:Residues: 1-9 <CHE>  
C:Keywords: neuropeptide

Query Match 30.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
|||  
Db 6 FTG 8

RESULT 9  
S39767  
cardioactive peptide CCAP - Spodoptera eridania  
C:Species: Spodoptera eridania  
C:Date: 07-Oct-1994 #sequence\_revision 12-Apr-1996 #text\_change 07-May-1999  
C:Accession: S39767  
R:Furuya, K.; Liao, S.; Reynolds, S.E.; Ota, R.B.; Hackett, M.; Schooley, D.A.  
Biol. Chem. Hoppe-Seyler 374, 1065-1074, 1993  
A:Title: Isolation and identification of a cardioactive peptide from Tenebrio molitor an  
A:Reference number: S39766; MUID:94176032; PMID:8129851  
A:Accession: S39767  
A:Molecule type: protein  
A:Residues: 1-9 <FUR>  
C:Keywords: neuropeptide

Query Match 30.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
|||  
Db 6 FTG 8

RESULT 10  
XAVIBH  
bradykinin-potentiating peptide - halys viper  
N:Alternate names: Bpp  
C:Species: Agkistrodon halys (halys viper)  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 05-Aug-1994  
C:Accession: JC0002  
R:Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.  
Peptides 6, 339-342, 1985  
A:Title: Structure-function studies on the bradykinin potentiating peptide from Chinese  
A:Reference number: JC0002; MUID:86177022; PMID:3008123  
A:Accession: JC0002  
A:Molecule type: protein  
A:Residues: 1-11 <CHI>  
C:Comment: Because this peptide both inhibits the activity of the angiotensin-converting  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyro  
F:Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.0%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIP 9  
|||  
Db 8 PIP 10

RESULT 11  
A58838  
hemolysin - Porphyromonas gingivalis (fragment)  
C:Species: Porphyromonas gingivalis  
C:Date: 29-Sep-1999 #sequence\_revision 29-Sep-1999 #text\_change 29-Sep-1999  
C:Accession: A58838  
R:Deshpande, R.  
submitted to the Protein Sequence Database, April 1998  
A:Reference number: A58838  
A:Accession: A58838  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <DES>

Query Match 30.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IPN 10  
|||  
Db 3 IPN 5

RESULT 12  
PS0259  
39K protein 3225 - rice (strain Nihonbare) (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
C:Accession: PS0259  
R:Tsuigita, A.; Kamo, M.  
submitted to JIPID, April 1993  
A:Reference number: PS0209  
A:Accession: PS0259  
A:Molecule type: protein  
A:Residues: 1-11 <TSU>  
C:Comment: molecular weight 39K, pI 5.7.

Query Match 30.0%; Score 3; DB 2; Length 11;

Query Match 30.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPI 8  
|||  
Db 6 GPI 8

RESULT 13  
E45691  
probable minor capsid protein R117a [similarity] - Lactobacillus delbrueckii subsp. lactis  
C:Species: Lactobacillus delbrueckii subsp. lactis phage LL-H  
C:Date: 24-Feb-1994 #sequence\_revision 25-Apr-1997 #text\_change 28-Jul-2000  
C:Accession: E45691  
R:Vasala, A.; Dupont, L.; Baumann, M.; Ritzenthaler, P.; Alatosava, T.  
J. Virol. 67, 3061-3068, 1993  
A:Title: Molecular comparison of the structural proteins encoding gene clusters of two  
A:Reference number: A45691; MUID:93267750; PMID:8497043  
A:Accession: E45691  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-12 <VAS>  
A>Note: sequence extracted from NCBI backbone (NCBIN:132363, NCBI:P:132373)

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIP 9  
|||  
Db 4 PIP 6

RESULT 14  
PS0213  
28K protein 4412 - rice (strain Nihonbare) (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
C:Accession: PS0213  
R:Tsuigita, A.; Kamo, M.  
submitted to JIPID, April 1993  
A:Reference number: PS0209  
A:Accession: PS0213  
A:Molecule type: protein  
A:Residues: 1-12 <TSU>  
A:Experimental source: callus  
C:Comment: molecular weight 28K, pI 4.6.

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
|||  
Db 6 FTG 8

RESULT 15  
A28955  
poly(al)oglycoprotein repeating unit - whitespotted char  
C:Species: Salvelinus leucomaenis pluvius (whitespotted char)  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 31-Dec-1993  
C:Accession: A28955  
R:Kitajima, K.; Sorimachi, H.; Inoue, S.; Inoue, Y.  
Biochemistry 27, 7141-7145, 1988  
A:Title: Comparative structures of the apopoly(al)oglycoproteins from unfertilized and  
A:Reference number: A90537; MUID:89062454; PMID:3196707  
A:Accession: A28955  
A:Molecule type: protein  
A:Residues: 1-12 <KIT>  
C:Keywords: glycoprotein

Query Match 30.0%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
|||  
Db 9 TGP 11

RESULT 16  
S23168  
Z protein - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
C:Accession: S23168  
R:Nicollier, M.; Roblin, S.; Cypriani, B.; Remy-Martin, J.P.; Adeesi, G.L.  
Eur. J. Biochem. 205, 1137-1144, 1992  
A:Title: Purification and characterization of a binding protein related to the Z class  
A:Reference number: S23168; MUID:92249319; PMID:1576997  
A:Accession: S23168  
A:Molecule type: protein  
A:Residues: 1-12 <NIC>  
A:Experimental source: liver  
C:Function:  
C:Description: binds dehydroepiandrosterone sulfate, estrone sulfate, oleic acid, cholester  
C:Keywords: liver; steroid binding

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
|||  
Db 3 FTG 5

RESULT 17  
PQ0786  
NADH2 dehydrogenase (EC 1.6.99.3) 26K chain - fava bean mitochondrion (fragment)  
N:Alternate names: complex I 26K chain; NADH-ubiquinone reductase 26K chain  
C:Species: mitochondrion Vicia faba (fava bean)  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 03-Jun-2002  
C:Accession: PQ0786  
R:Letierme, S.; Boutry, M.  
Plant Physiol. 102, 435-443, 1993  
A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH  
A:Reference number: PQ0775; MUID:94151437; PMID:8108509  
A:Accession: PQ0786  
A:Molecule type: protein  
A:Residues: 1-12 <LET>  
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the ti  
ranging from 5K to 75K.  
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by  
C:Genetics:  
A:Genome: mitochondrion  
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIP 9  
|||  
Db 5 PIP 7

RESULT 18  
A35245  
histone H1a - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 31-Oct-1997  
C:Accession: A35245  
R:Ajiro, K.; Shibata, K.; Nishikawa, Y.  
J. Biol. Chem. 265, 6494-6500, 1990

A:Title: Subtype-specific cyclic AMP-dependent histone H1 phosphorylation at the different  
A:Reference number: A35245; MUID:90202935; PMID:1690730  
A:Accession: A35245  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <AJI>  
C:Superfamily: histone H1  
C:Keywords: chromosomal protein; nucleosome

Query Match 30.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
|||  
Db 3 TGP 5

## RESULT 19

A26999  
C:Species: Caenorhabditis elegans  
C:Title: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 07-Feb-1997

A:Reference number: A26999  
A:Accession: A26999  
A:Molecule type: protein  
A:Residues: 1-13 <MCG>  
C:Keywords: carboxylic ester hydrolase; intestine

Query Match 30.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPI 8  
|||  
Db 1 GPI 3

## RESULT 20

B28955  
C:Species: Oncorhynchus masou ishikawai (Ishikawa's cherry salmon)

C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 31-Dec-1993  
C:Accession: B28955  
R:Kitajima, K.; Sorimachi, H.; Inoue, S.; Inoue, Y.  
Biochemistry 27, 7141-7145, 1988  
A:Title: Comparative structures of the apolysialoglycoproteins from unfertilized and fertilized eggs of Oncorhynchus masou ishikawai  
A:Reference number: A90537; MUID:89062454; PMID:3196707  
A:Accession: B28955  
A:Molecule type: protein  
A:Residues: 1-13 <KIT>  
C:Keywords: glycoprotein

Query Match 30.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
|||  
Db 9 TGP 11

## RESULT 21

S13273  
N:Alternate names: PSGP  
C:Species: Oncorhynchus nerka (sockeye salmon)

C:Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 05-Dec-1998  
C:Accession: S13273

R:Song, Y.; Kitajima, K.; Inoue, Y.

Arch. Biochem. Biophys. 283, 167-172, 1990  
A:Title: New tandem-repeating peptide structures in polysialoglycoproteins from the unfertilized eggs of Oncorhynchus masou ishikawai  
A:Reference number: S13273; MUID:91053178; PMID:2241168

A:Accession: S13273  
A:Molecule type: protein  
A:Residues: 1-13 <SON>  
A:Experimental source: egg  
C:Keywords: glycoprotein

Query Match 30.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
|||  
Db 9 TGP 11

## RESULT 22

PA0111  
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 07-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 06-Jun-1997  
C:Accession: PA0111  
R:Kamo, M.; Kawakami, T.; Tsugita, A.  
submitted to JIPID, March 1995  
A:Reference number: PA0109  
A:Accession: PA0111  
A:Molecule type: protein  
A:Residues: 1-14 <KAM>  
A:Experimental source: root

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
|||  
Db 1 TGP 3

## RESULT 23

A54397  
ubiquitin-carrier protein E2-F1 - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 11-Jan-2000  
C:Accession: A54397  
R:Blumenfeld, N.; Gonen, H.; Mayer, A.; Smith, C.E.; Siegel, N.R.; Schwartz, A.L.; Cieciorka, J.  
Biochemistry 26, 9574-9581, 1994  
A:Title: Purification and characterization of a novel species of ubiquitin-carrier protein  
A:Reference number: A54397; MUID:94193635; PMID:8144544  
A:Accession: A54397  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <BLU>  
A:Experimental source: reticulocyte  
A:Note: sequence extracted from NCBI backbone (NCBI:146038)  
C:Superfamily: human ubiquitin-protein ligase E2

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPF 4  
|||  
Db 9 YPF 11

## RESULT 24

B61457  
C:Species: Tetrahymena pyriformis  
alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)

C>Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-Dec-1999  
 C:Accession: B61457  
 R:Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.  
 J. Protozool. 36, 562-567, 1989  
 A:Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification  
 A:Reference number: A61457; MUID:90095988; PMID:2689637  
 A:Accession: B61457  
 A:Molecule type: protein  
 A:Residues: 1-15 <BAN>  
 C:Genetics:  
 A:Genetic code: SGC5  
 C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monom

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFT 5  
 |||  
 Db 4 PFT 6  
 |||

RESULT 25  
 PL0154  
 glycoprotein - loggerhead (fragment)  
 C:Species: Caretta caretta (loggerhead)  
 C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 11-May-2000  
 C:Accession: PL0154  
 R:Radhakrishna, G.; Chin, C.C.Q.; Wold, F.; Weldon, P.J.  
 Comp. Biochem. Physiol. B 94, 375-378, 1989  
 A:Title: Glycoproteins in Rathke's gland secretions of loggerhead (Caretta caretta) and  
 A:Reference number: PL0154; MUID:90075703; PMID:2591198  
 A:Accession: PL0154  
 A:Molecule type: protein  
 A:Residues: 1-15 <RAD>  
 A:Experimental source: Rathke's gland  
 C:Keywords: glycoprotein

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPI 8  
 |||  
 Db 13 GPI 15  
 |||

RESULT 26  
 S08282  
 cytochrome P450K-2 - rat (tentative sequence) (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 31-Mar-2000  
 C:Accession: S08282  
 R:Imaoka, S.; Nagashima, K.; Funae, Y.  
 Arch. Biochem. Biophys. 276, 473-480, 1990  
 A:Title: Characterization of three cytochrome P450s purified from renal microsomes of un  
 A:Reference number: S08282; MUID:90165442; PMID:2306108  
 A:Accession: S08282  
 A:Molecule type: protein  
 A:Residues: 1-15 <IMA>  
 C:Keywords: heme; monooxygenase

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
 |||  
 Db 9 TGP 11  
 |||

RESULT 27  
 A42291

tail fiber protein I - phage P2 (fragment)  
 C:Species: phage P2  
 C>Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 30-Sep-1993  
 C:Accession: A42291  
 R:Haggard-Ljungquist, E.; Halling, C.; Calendar, R.  
 J. Bacteriol. 174, 1462-1477, 1992  
 A:Title: DNA sequences of the tail fiber genes of bacteriophage P2: evidence for horizon  
 A:Reference number: A42291; MUID:92165720; PMID:1531648  
 A:Accession: A42291  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-16 <HAG>  
 A:Cross-references: GB:M64677

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYP 3  
 |||  
 Db 13 VYP 15  
 |||

RESULT 28  
 S16376  
 L-serine dehydratase beta chain - Peptostreptococcus asaccharolyticus  
 C:Species: Peptostreptococcus asaccharolyticus  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
 C:Accession: S16376  
 R:Grabowski, R.; Buckel, W.  
 Eur. J. Biochem. 199, 89-94, 1991  
 A:Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat  
 A:Reference number: S16224; MUID:91293139; PMID:2065681  
 A:Accession: S16376  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-16 <EUR>

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPI 8  
 |||  
 Db 8 GPI 10  
 |||

RESULT 29  
 S22040  
 cob protein - common sunflower  
 C:Species: Helianthus annuus (common sunflower)  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Sep-1997  
 C:Accession: S22040  
 R:Koehler, R.H.  
 submitted to the EMBL Data Library, October 1991  
 A:Reference number: S22040  
 A:Accession: S22040  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-16 <KOE>  
 A:Cross-references: EMBL:X62592; NID:g12990; PID:g12991

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IPN 10  
 |||  
 Db 1 IPN 3  
 |||

RESULT 30  
 PH1351

```

Ig heavy chain DJ region (clone C100-109B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1351
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1351
A:Molecule type: DNA
A:Residues: 1-16 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match      30.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GPI 8
Db      5 GPI 7

RESULT 31
PH1790
T cell receptor alpha chain V region (clone 2PBL V alpha 24-6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1790
R:Porcellì, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood lymphocytes
A:Reference number: PH1754; MUID:93301595; PMID:8391057
A:Accession: PH1790
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-16 <POR>

Query Match      30.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GPI 8
Db      7 GPI 9

RESULT 32
PA0004
plastocyanin - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 15-Mar-1996
C:Accession: PA0004
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Taugita, A.
Submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
A:Reference number: PA0001
A:Accession: PA0004
A:Molecule type: protein
A:Residues: 1-17 <KAM>
A:Experimental source: stem
C:Superfamily: plastocyanin
C:Keywords: copper; electron transfer

Query Match      30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 IPN 10
Db     15 IPN 17

```

```

RESULT 33
SS9481
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
C:Species: Phaseolus vulgaris (kidney bean)
C:Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
C:Accession: SS9481
R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A:Title: Specificity in the immobilisation of cell wall proteins in response to different elicitors
A:Reference number: SS9481; MUID:96011753; PMID:7548825
A:Accession: SS9481
A:Molecule type: protein
A:Residues: 1-17 <WOJ>
C:Keywords: glycoprotein; hydroxyproline
F:6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match      30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VYP 3
Db     13 VYP 15

RESULT 34
SI7274
ribosomal protein YML35, mitochondrial, questionable - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
A:Variety: strain 07173
C:Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997
C:Accession: SI7274
R:Grohmann, L.; Graack, H.R.; Kruft, V.; Choi, T.; Goldschmidt-Reisin, S.; Kitakawa, M.
FEBS Lett. 284, S1-S6, 1991
A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast
A:Reference number: SI7255; MUID:91285106; PMID:2060626
A:Accession: SI7274
A:Molecule type: protein
A:Residues: 1-17 <GRO>
C:Comment: A coding region for this protein could not be identified in the genome of Saccharomyces cerevisiae
C:Genetics:
A:Genome: nuclear
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match      30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VYP 3
Db     13 VYP 15

RESULT 35
EZ3734
insulin-like growth factor-binding protein 3 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
C:Accession: EZ3734
R:Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N.
Mol. Endocrinol. 5, 938-948, 1991
A:Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-3
A:Reference number: A23734; MUID:92049376; PMID:1719383
A:Accession: EZ3734
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <SHI>

Query Match      30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 TGP 7

```

Db |||  
7 TGP 9

RESULT 36  
PT0286  
Ig heavy chain CDR3 region (clone 4-100B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0286  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0286  
A:Molecule type: DNA  
A:Residues: 1-18 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPF 4  
|||  
9 YPF 11

Db

RESULT 37  
B57789  
kidney stone matrix protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 23-Feb-1996  
C:Accession: B57789  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, February 1996  
A:Description: The proteins of gallbladder stones.  
A:Reference number: A57789  
A:Accession: B57789  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <BN>  
A:Experimental source: urate calcium oxalate kidney stone

Query Match 30.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
|||  
7 FTG 9

Db

RESULT 38  
EW5MCN  
cinnamycin - Streptovorticillium cinnamoneum  
N:Alternate names: lanthiopeptin; lantibiotic Ro 09-0198  
C:Species: Streptovorticillium cinnamoneum  
C:Date: 30-Sep-1993 #sequence\_revision 12-May-1994 #text\_change 07-May-1999  
C:Accession: A45767  
R:Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase, K.  
J. Antibiot. 42, 837-845, 1989  
A:Title: Lanthiopeptin, a new peptide antibiotic. Production, isolation and properties of  
A:Reference number: A45767; MUID:89291558; PMID:2544544  
A:Accession: A45767  
A:Molecule type: protein  
A:Residues: 1-19 <NAR>  
R:Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.  
Tetrahedron Lett. 29, 4771-4772, 1988  
A:Title: Lanthiopeptin, a new peptide effective against Herpes simplex virus: structural  
A:Reference number: A53359  
A:Contents: annotation; strain L337-2

C:Superfamily: cinnamycin precursor  
C:Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine  
F:1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F:4-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental  
F:5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F:6-11/Cross-link: (2Xi,9S)-lysinoalanine (Ser-Lys) #status experimental  
F:15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 30.0%; Score 3; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFT 5  
|||  
9 PFT 11

Db

RESULT 39  
S69153  
Neb-colloostatin - flesh fly (Sarcophaga bullata)  
C:Species: Sarcophaga bullata  
C:Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 19-May-2000  
C:Accession: S69153  
R:Bylemans, D.; Proost, P.; Samijn, B.; Borovsky, D.; Grauwels, L.; Huybrechts, R.; van  
Eur. J. Biochem. 228, 45-49, 1995  
A:Title: Neb-colloostatin, a second folliculastatin of the grey fleshfly, Neobellieria b  
A:Reference number: S69153; MUID:95188911; PMID:7883009  
A:Accession: S69153  
A:Molecule type: protein  
A:Residues: 1-19 <BYL>

Query Match 30.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPI 8  
|||  
12 GPI 14

Db

RESULT 40  
C60692  
proline-rich protein ms4B - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 30-Sep-1993  
C:Accession: C60692  
R:Spitzman, A.I.; Bennick, A.  
Arch. Oral Biol. 34, 117-130, 1989  
A:Title: Isolation and characterization of six proteins from rabbit parotid saliva belo  
A:Reference number: A60692; MUID:89391780; PMID:2783045  
A:Accession: C60692  
A:Molecule type: protein  
A:Residues: 1-19 <SPI>  
A:Note: 4-Leu was also found  
C:Keywords: glycoprotein; saliva

Query Match 30.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
|||  
4 TGP 6

Db

RESULT 41  
B44920  
2-halobenzoate 1,2-dioxygenase component A alpha chain - Pseudomonas cepacia (fragment)  
C:Species: Pseudomonas cepacia  
C:Date: 01-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 03-Mar-1995  
C:Accession: B44920  
R:Fetzner, S.; Muller, R.; Lingens, F.  
J. Bacteriol. 174, 279-290, 1992



A:Title: Purification and some properties of 2-halobenzoate 1,2-dioxygenase, a two-comp  
 A:Reference number: A44920; MUID:92104974; PMID:1370284  
 A:Contents: 2CBS  
 A:Accession: B44920  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <FRT>  
 A:Note: sequence extracted from NCBI backbone (NCBI:75378)

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
 |||  
 Db 8 TGP 10

## RESULT 42

B43594  
 fimbrial protein mrpA - Proteus mirabilis (fragment)  
 C:Species: Proteus mirabilis  
 C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993  
 C:Accession: B43594  
 R:Bahrani, F.K.; Johnson, D.E.; Robbins, D.; Mobley, H.L.T.  
 Infect. Immun. 59, 3574-3580, 1991  
 A:Title: Proteus mirabilis flagella and MR/P fimbriae: isolation, purification, N-termir  
 A:Reference number: A43594; MUID:91372967; PMID:1680106  
 A:Accession: B43594  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <BAH>

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
 |||  
 Db 9 FTG 11

## RESULT 43

C57789  
 gallbladder stone matrix protein, 13K - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 23-Feb-1996  
 C:Accession: C57789  
 R:Binette, J.P.; Binette, M.B.  
 submitted to the Protein Sequence Database, February 1996  
 A:Description: The proteins of gallbladder stones.  
 A:Reference number: A57789  
 A:Accession: C57789  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <BIN>

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
 |||  
 Db 17 FTG 19

## RESULT 44

A60801  
 acrosome stabilizing factor large chain - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: A60801  
 R:Wilson, W.L.; Oliphant, G.

Biol. Reprod. 37, 159-169, 1987  
 A:Title: Isolation and biochemical characterization of the subunits of the rabbit sperm  
 A:Reference number: A60801; MUID:88000873; PMID:3651543  
 A:Accession: A60801  
 A:Molecule type: protein  
 A:Residues: 1-20 <WIL>  
 C:Comment: spermatozoa must undergo capacitation and the acrosome reaction to become ca;  
 C:Keywords: glycoprotein; semen

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPI 8  
 |||  
 Db 15 GPI 17

## RESULT 45

A41717  
 p100 protein - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 23-Mar-1993  
 C:Accession: A41717  
 R:Traub, L.M.; Sagi-Eisenberg, R.  
 J. Biol. Chem. 266, 24642-24649, 1991  
 A:Title: Purification of p100, a protein antigenically related to the signal transducin  
 A:Reference number: A41717; MUID:92105130; PMID:1722209  
 A:Accession: A41717  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <TRA>

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IPN 10  
 |||  
 Db 15 IPN 17

## RESULT 46

A58903  
 metalloproteinase AP34 (EC 3.4.24.-) - Aeromonas caviae (fragment)  
 C:Species: Aeromonas caviae  
 C:Date: 31-Dec-2001 #sequence\_revision 31-Dec-2001 #text\_change 31-Dec-2001  
 C:Accession: A58903  
 R:Toma, C.  
 submitted to the Protein Sequence Database, November 1998  
 A:Description: Metalloprotease AP34.  
 A:Reference number: A58903  
 A:Accession: A58903  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <TOM>  
 C:Keywords: hydrolase; metalloproteinase

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
 |||  
 Db 4 TGP 6

## RESULT 47

A43391  
 TRH-like tripeptide - alfalfa  
 C:Species: Medicago sativa (alfalfa)  
 C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C:Accession: A43391

R;Lackey, D.B.  
 J. Biol. Chem. 267, 17508-17511, 1992  
 A>Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglutamic acid  
 A:Reference number: A43391; MUID:92388092; PMID:1517203  
 A:Accession: A43391

A:Molecule type: protein  
 A:Residues: 1-3 <LAC>  
 C:Keywords: amidated carboxyl end; pyroglutamic acid  
 F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F.3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 20.0%; Score 2; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YP 3  
 ||  
 Db 2 YP 3

RESULT 48  
 PT0636  
 T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 A:Accession: PT0636  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991

A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0636

A>Status: translation not shown  
 A:Molecule type: mRNA

A:Residues: 1-3 <FEE>  
 A:Experimental source: newborn thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
 ||  
 Db 2 TG 3

RESULT 49  
 A32039  
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 18-Aug-2000  
 A:Accession: A32039  
 R;Horvath, A.; Kastin, A.J.  
 J. Biol. Chem. 264, 2175-2179, 1989

A>Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor  
 A:Reference number: A32039; MUID:89123285; PMID:2563371  
 A:Accession: A32039

A:Molecule type: protein  
 A:Residues: 1-4 <HOR>

A:Experimental source: brain  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end

F.4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YP 3  
 ||  
 Db .1 YP 2

RESULT 50  
 PT0240

IG heavy chain CRD3 region (clone 2-100B) - human (fragment)

C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 A:Accession: PT0240

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991

A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0240

A:Molecule type: DNA

A:Residues: 1-4 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YP 3  
 ||  
 Db 1 YP 2

RESULT 51  
 PT0675  
 T-cell receptor beta chain V-D-J region (140-1AC) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 A:Accession: PT0675

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0675

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FEE>

A:Experimental source: day 18 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7  
 ||  
 Db 3 GP 4

RESULT 52  
 E60274  
 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)

C:Species: Mycobacterium tuberculosis

C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993

A:Accession: E60274

R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A>Title: Isolation and partial characterization of major protein antigens in the culture

A:Reference number: A60274; MUID:91099989; PMID:1898899

A:Accession: E60274

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 <NAG>

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YP 3  
 ||  
 Db 2 YP 3

## RESULT 53

PQ0009

angiotensin-converting enzyme inhibitor (FLP-2) - common fig

N:Alternate names: ficus latex peptide 2

C:Species: Ficus carica (common fig)

C&gt;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995

C:Accession: PQ0009

R:Maruyama, S.; Miyoshi, S.; Tanaka, H.

Agric. Biol. Chem. 53, 2763-2767, 1989

A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A:Reference number: PQ0008

A:Accession: PQ0009

A:Molecule type: protein

A:Residues: 1-5 &lt;MAR&gt;

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YP 3

||

DB 2 YP 3

## RESULT 54

B37988

acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)

C:Species: Physarum polycephalum

C&gt;Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993

C:Accession: B37988

R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og

J. Biol. Chem. 265, 19898-19903, 1990

A:Title: Purification and characterization of a novel intracellular acid proteinase from

A:Reference number: A37988; MUID:91060608; PMID:2246266

A:Accession: B37988

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 &lt;MUR&gt;

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PI 8

||

DB 4 PI 5

## RESULT 55

JS0319

subesophageal ganglion pentapeptide - house cricket

C:Species: Acheta domesticus (house cricket)

C&gt;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000

C:Accession: JS0319

R:Wicker, C.; Wicker, C.

Comp. Biochem. Physiol. C 88, 185-187, 1987

A:Title: Isolation and structure of a peptide isolated from the subesophageal ganglion

A:Reference number: JS0319

A:Accession: JS0319

A:Molecule type: protein

A:Residues: 1-5 &lt;WIC&gt;

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4

||

DB 4 PF 5

## RESULT 56

PT0267

Ig heavy chain CRD3 region (clone 3-94A) - human (fragment)

C:Species: Homo sapiens (man)

C&gt;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0267

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0267

A:Molecule type: DNA

A:Residues: 1-5 &lt;YAM&gt;

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7

||

DB 3 GP 4

## RESULT 57

JT0520

Ig kappa chain V-III region (SD1) - human (fragment)

C:Species: Homo sapiens (man)

C&gt;Date: 23-Oct-1992 #sequence\_revision 23-Oct-1992 #text\_change 16-Aug-1996

C:Accession: JT0520

R:Anker, R.; Conley, M.E.; Pollok, B.A.

J. Exp. Med. 179, 2103-2119, 1989

A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglob

A:Reference number: JT0511; MUID:89279157; PMID:2786547

A:Accession: JT0520

A:Molecule type: mRNA

A:Residues: 1-5 &lt;ANK&gt;

A&gt;Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements

A&gt;Note: a stop codon terminates the sequence in the V region

C:Keywords: heterotetramer; immunoglobulin

F:1-5/Domain: V kappa region &lt;VRE&gt;

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7

||

DB 4 GP 5

## RESULT 58

CS3284

T-cell receptor beta 2 chain D region, Dbeta2 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C&gt;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C:Accession: CS3284

R:Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A:Title: Evolutionarily conserved organization and sequences of germline diversity and

A:Reference number: A53284; MUID:91342695; PMID:1678859

A:Accession: CS3284

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 &lt;HAR&gt;

A:Cross-references: GB:S60737; NID:g233916; PIDN:AA819519.1; PID:g233919

A&gt;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60740)

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 5 TG 6  
||  
2 TG 3

Db

RESULT 59

PT0644

T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0644

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0644

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 4 FT 5  
||  
4 FT 5

Db

RESULT 60

PT0686

T-cell receptor beta chain V-D-J region (120-1R and 154-2D) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Sep-1997

C:Accession: PT0615; PT0686

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0615

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:Experimental source: newborn thymus, strain BALB/c, clone 120-1R

A:Accession: PT0686

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-5 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-2D

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY 5 TG 6  
||  
4 TG 5

Db

RESULT 61

PT0669

T-cell receptor beta chain V-D-J region (121-3BH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0669

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0669

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:Experimental source: day 4 postnatal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7  
||  
4 GP 5

Db

RESULT 62

PT0590

T-cell receptor beta chain V-D-J region (141-1B) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0590

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0590

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:Experimental source: day 19 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
||  
4 TG 5

Db

RESULT 63

A44916

mosquitocidal toxin 21 - Bacillus sphaericus (fragment)

C:Species: Bacillus sphaericus

C>Date: 01-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995

C:Accession: A44916

R:Thanabalu, T.; Hindley, J.; Berry, C.

J. Bacteriol. 174, 5051-5056, 1992

A:Title: Proteolytic processing of the mosquitocidal toxin from Bacillus sphaericus SS11

A:Reference number: A44916; MUID:92332441; PMID:1352768

A:Accession: A44916

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-6 <THA>

A:Experimental source: SS11-1

A>Note: sequence extracted from NCBI backbone (NCBIF:108973)

Query Match 20.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 FN 10  
||  
5 FN 6

Db

RESULT 64

S14159

paraesporal crystal protein CryIC - Bacillus thuringiensis (fragment)

## N:Alternate names: delta-endotoxin

C:Species: Bacillus thuringiensis  
 C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 18-Jul-1997  
 C:Accession: S14159  
 R:Convents, D.; Charlet, M.; van Damme, J.; Lasters, I.; Lauwereys, M.  
 Eur. J. Biochem. 195, 631-635, 1991  
 A:Title: Two structural domains as a general fold of the toxic fragment of the Bacillus  
 A:Reference number: S14087; MUID:91153300; PMID:1847865  
 A:Accession: S14159  
 A:Molecule type: protein  
 A:Residues: 1-6 <CON>

Query Match 20.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
 ||  
 Db 3 TG 4

## RESULT 65

## PQ0008

## angiotensin-converting enzyme inhibitor (FLP-1) - common fig

N:Alternate names: ficus latex peptide 1  
 C:Species: Ficus carica (common fig)  
 C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995  
 C:Accession: PQ0008  
 R:Maruyama, S.; Miyoshi, S.; Tanaka, H.  
 Agric. Biol. Chem. 53, 2763-2767, 1989

A:Title: Angiotensin 1-converting enzyme inhibitors derived from Ficus carica.  
 A:Reference number: PQ0008  
 A:Accession: PQ0008  
 A:Molecule type: protein

A:Residues: 1-6 <MAR>

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PI 8  
 ||  
 Db 4 PI 5

## RESULT 66

## B61512

## variant surface glycoprotein MITat 1.1 - Trypanosoma brucei (fragment)

C:Species: Trypanosoma brucei  
 C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-May-1999  
 C:Accession: B61512  
 R:Holder, A.A.; Cross, G.A.M.  
 Mol. Biochem. Parasitol. 2, 135-150, 1981  
 A:Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-termi  
 A:Reference number: A61512; MUID:81172836; PMID:6163983  
 A:Accession: B61512

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-6 <HOL>

C:Keywords: glycoprotein

Query Match 20.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
 ||  
 Db 4 TG 5

## RESULT 67

## I51317

## bHLH transcription factor inhibitor - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
 C:Accession: I51317  
 R:Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.  
 Mech. Dev. 50, 119-130, 1995  
 A:Title: Id gene activity during Xenopus embryogenesis.  
 A:Reference number: I51316; MUID:95344988; PMID:7619724  
 A:Accession: I51317  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-6 <ZHA>  
 A:Cross-references: GB:S79038; NID:G1042006; PIDN:AAD14294.1; PID:G4261994  
 C:Genetics:  
 A:Gene: XidIb

Query Match 20.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4  
 ||  
 Db 5 PF 6

## RESULT 68

## PT0518

## T-cell receptor beta chain V-D-J region (100-4B) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0518  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0518  
 A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEE>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
 ||  
 Db 5 TG 6

## RESULT 69

## PT0630

## T-cell receptor beta chain V-D-J region (111-1C) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0630  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0630  
 A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
||  
Db 5 TG 6

## RESULT 70

PT0643  
T-cell receptor beta chain V-D-J region (111-1E) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0643

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0643

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
||  
Db 3 TG 4

## RESULT 71

PT0619  
T-cell receptor beta chain V-D-J region (120-2CN) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0619; PT0563; PT0598

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0619

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEE>

A:Experimental source: newborn thymus, strain BALB/c, clone 120-2CN

A:Accession: PT0563

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEE>

A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 136-3A

A:Accession: PT0598

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEE>

A:Experimental source: newborn thymus, strain BALB/c, clone 111-1Q

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
||  
Db 5 TG 6

## RESULT 72

PT0662  
T-cell receptor beta chain V-D-J region (121-3BA) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0662

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0662

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEE>

A:Experimental source: day 4 postnatal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
||  
Db 4 TG 5

## RESULT 73

PT0668  
T-cell receptor beta chain V-D-J region (121-3BB) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0668

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0668

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FEE>

A:Experimental source: day 4 postnatal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
||  
Db 5 TG 6

## RESULT 74

PT0723  
T-cell receptor beta chain V-D-J region (135-1AF) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0723

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0723

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-6 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 20.0%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
||  
Db 4 TG 5

## RESULT 75

I49421  
laminin B1 - western wild mouse (fragment)  
C;Species: Mus spretus (western wild mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C;Accession: I49421  
R;KO, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maizaki, Y.; Nadeau, J.H.  
Mamm. Genome 5, 349-355, 1994  
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
A;Reference number: I48934; MUID:94319082; PMID:8043949  
A;Accession: I49421  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-6 <RES>  
A;Cross-references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829

Query Match 20.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VY 2  
||  
Db 1 VY 2

Search completed: November 25, 2003, 18:28:25  
Job time : 10.2021 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 4.84043 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-18

Perfect score: 10

Sequence: 1 VYPFTGPIPN 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705. residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	30.0	8	1 VGLG HSV2B	P81780 herpes simp
2	3	30.0	9	1 CCAP_CARMA	P38556 carcinius ma
3	3	30.0	9	1 MGMT_BOVIN	P29177 bos taurus
4	3	30.0	11	1 BPP_AGRHP	P04562 agkistrodon
5	3	30.0	11	1 TINI_HOFTI	P82651 hoplobatrach
6	3	30.0	14	1 TAT_HVIW2	P12509 human immun
7	3	30.0	14	1 TAT_HVI28	P12511 human immun
8	3	30.0	15	1 RKGG_CARCR	P21586 caretta car
9	3	30.0	15	1 UC29_MAIZE	P80635 zea mays (m
10	3	30.0	17	1 PNOG_PIG	P55791 sus scrofa
11	3	30.0	17	1 RM35_YEAST	P36530 saccharomyc
12	3	30.0	19	1 COOT_SARBU	Q09148 sarcophaga
13	3	30.0	19	1 DURA_STRGV	P36504 streptococ
14	2	20.0	5	1 RE31_LITRU	P82072 litoria rub
15	2	20.0	5	1 RE32_LITRU	P82073 litoria rub
16	2	20.0	5	1 SUGA_ACHDO	P19991 acheta dome
17	2	20.0	6	1 EI01_LITRU	P82096 litoria rub
18	2	20.0	7	1 CHOX_ALCSP	P16101 alcaligenes
19	2	20.0	7	1 FARI_HELTI	P41871 helisoma tr
20	2	20.0	7	1 FARA_PANRE	P41875 panagrellus
21	2	20.0	7	1 MNPI_LEPDE	P42984 leptotars
22	2	20.0	7	1 TY51_LITRU	P82065 litoria rub
23	2	20.0	7	1 UN06_PINPS	P81675 pinus pinas
24	2	20.0	8	1 AKHC_GRYBI	P14086 gryllus bim
25	2	20.0	8	1 AKH_LIBAU	P25418 libellula a
26	2	20.0	8	1 AKH_TABAT	P14595 tabanus atr
27	2	20.0	8	1 AL15_CARMA	P81818 carcinius ma
28	2	20.0	8	1 AL15_CARMA	P81819 carcinius ma
29	2	20.0	8	1 ALL5_CALVO	P41841 calliphora
30	2	20.0	8	1 ALL8_CARMA	P81811 carcinius ma
31	2	20.0	8	1 ALL9_CARMA	P81812 carcinius ma
32	2	20.0	8	1 ANG2_BOTJA	Q10582 bothrops ja
33	2	20.0	8	1 FARI_PANRE	P41872 panagrellus

RESULT 1

#### ALIGNMENTS

34	2	20.0	8	1	FAR7_ASCSU	P43171 ascaris suu
35	2	20.0	8	1	HTF1_PERAM	P04548 periplaneta
36	2	20.0	8	1	HTF2_PERAM	P04549 periplaneta
37	2	20.0	8	1	HTF_TENMO	P25419 tenebrio mo
38	2	20.0	8	1	LMT2_LOCOMI	P22396 locusta mig
39	2	20.0	8	1	LPK_LEUMA	P13049 leucophaea
40	2	20.0	8	1	ORWY_ORCLI	P82455 orconectes
41	2	20.0	8	1	PPK2_PERAM	P82692 periplaneta
42	2	20.0	8	1	PPK3_PERAM	P82618 periplaneta
43	2	20.0	8	1	RS7_MYCIT	P33564 mycobacteri
44	2	20.0	8	1	UPAA_HUMAN	P30096 homo sapien
45	2	20.0	8	1	AL11_CARMA	P81814 carcinius ma
46	2	20.0	9	1	FAR2_PANRE	P41873 panagrellus
47	2	20.0	9	1	FAR4_CALVO	P41859 calliphora
48	2	20.0	9	1	FAR9_ASCSU	P43172 ascaris suu
49	2	20.0	9	1	FARA_CALVO	P41865 calliphora
50	2	20.0	9	1	ISOT_CVPCA	P42993 cyprinus ca
51	2	20.0	9	1	KNL3_BOMVA	P83058 bombina var
52	2	20.0	9	1	LITR_PHYRO	P08946 phyllomedus
53	2	20.0	9	1	LMT3_LOCOMI	P41489 locusta mig
54	2	20.0	9	1	OXYT_BUFRE	P42995 bufo regula
55	2	20.0	9	1	OXYT_BISFO	P42998 eisenia foe
56	2	20.0	9	1	OXYT_OCTVU	P80027 octopus vul
57	2	20.0	9	1	PPK1_PERAM	P82691 periplaneta
58	2	20.0	10	1	TKL1_LOCOMI	P16223 locusta mig
59	2	20.0	10	1	AH3_PRUSE	P29261 prunus sero
60	2	20.0	10	1	ANG1_BOTJA	Q10581 bothrops ja
61	2	20.0	10	1	ANGT_BOVIN	P01017 bos taurus
62	2	20.0	10	1	ANGT_CHICK	P01018 gallus gall
63	2	20.0	10	1	BPP2_BOTIN	P30422 bothrops in
64	2	20.0	10	1	BPP2_BOTJA	P30426 bothrops in
65	2	20.0	10	1	BPP8_BOTIN	P31351 vipera aspi
66	2	20.0	10	1	BPP_VIPAS	P82086 litoria cit
67	2	20.0	10	1	CA12_LITCI	P56264 litoria xan
68	2	20.0	10	1	CABR_LITXA	P80432 rattus norv
69	2	20.0	10	1	COXO_RAT	P80982 thunnus obe
70	2	20.0	10	1	COXO_THUOB	P81012 schizaphis
71	2	20.0	10	1	ESTA_SCHGA	P82660 panagrellus
72	2	20.0	10	1	FAR6_PANRE	P37043 gallus gall
73	2	20.0	10	1	GON2_CHICK	P80243 bacillus su
74	2	20.0	10	1	GS09_BACSU	P18110 romalea mic
75	2	20.0	10	1	HTF1_ROMMI	P11385 carausius m
76	2	20.0	10	1	HTF2_CARMO	P14596 tabanus atr
77	2	20.0	10	1	HTF_TABAT	P41488 locusta mig
78	2	20.0	10	1	LPK2_LOCOMI	P81533 microplitis
79	2	20.0	10	1	MP2_MICOC	P81863 pardachirus
80	2	20.0	10	1	PAP1_PARMA	P80901 methanobact
81	2	20.0	10	1	PORB_METTM	P80525 fasciola he
82	2	20.0	10	1	PPCK_FASHE	P56923 rana tempor
83	2	20.0	10	1	TENK_RANTE	P08610 phyllomedus
84	2	20.0	10	1	TKN_PHYBI	P42634 aedes aegypt
85	2	20.0	10	1	TKS1_AEDAE	P42635 aedes aegypt
86	2	20.0	10	1	TKS2_AEDAE	P81740 leucophaea
87	2	20.0	10	1	TRP8_LEUMA	P32118 homo sapien
88	2	20.0	10	1	UPA4_HUMAN	P80599 bacillus su
89	2	20.0	10	1	URAI_HUMAN	P32118 homo sapien
90	2	20.0	10	1	VEG6_BACSU	P09037 crinia geor
91	2	20.0	11	1	ANGT_CRIGE	P30423 bothrops in
92	2	20.0	11	1	BPP3_BOTIN	P30424 bothrops in
93	2	20.0	11	1	BPP4_BOTIN	P01021 agkistrodon
94	2	20.0	11	1	BPPB_AGGKIA	P12797 megascolia
95	2	20.0	11	1	BRK_MEGFL	P82087 litoria cit
96	2	20.0	11	1	CA21_LITCI	P82088 litoria cit
97	2	20.0	11	1	CA22_LITCI	P82089 litoria cit
98	2	20.0	11	1	CA31_LITCI	P82090 litoria cit
99	2	20.0	11	1	CA32_LITCI	P82091 litoria cit
100	2	20.0	11	1	CA41_LITCI	

```
VGLG_HSV2B
ID VGLG_HSV2B STANDARD; PRT; 8 AA.
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GG, GI, AND GE.
CC -!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 8 AA; 683 MW; 7847686772C865B8 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPI 8
DB 6 GPI 8

RESULT 2
CCAP_CARMA STANDARD; PRT; 9 AA.
ID CCAP_CARMA
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579 (1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexata;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168 (1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074 (1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
```

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CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC INTO THE HEMOLYMPH.
CC PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6
DB 6 FTG 8

RESULT 3
MGMT_BOVIN STANDARD; PRT; 9 AA.
ID MGMT_BOVIN
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
DE methylguanine-DNA methyltransferase) (Fragment).
DN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase.";
RL Nucleic Acids Res. 18:17-21 (1990).
CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
CC IRREVERSIBLY INACTIVATED.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIP 9
DB 2 PIP 4

RESULT 4
BPP_AKGHP STANDARD; PRT; 11 AA.
ID BPP_AKGHP
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
OS enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydus.
OX NCBI_TaxID=8714;
RN [1]_SEQUENCE.
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: JC0002; XAVIDH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277685777 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 7 PIP 9
    |||
DB 8 PIP 10

RESULT 5
TINI_HOPII
ID TINI_HOPII STANDARD; PRT; 11 AA.
AC P82651;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-1.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]_SEQUENCE.
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=1031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 2 10
FT MOD RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 7 PIP 9
    |||
DB 8 PIP 10

us-09-641-801-18.oligo.rsp

Db 6 PIP 8

RESULT 6
TAT_HVIW2
ID TAT_HVIW2 STANDARD; PRT; 14 AA.
AC P12509;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
RN [1]_SEQUENCE.
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS.";
RL Science 232:1548-1553(1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC -----
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CC -----
DR EMBL; M12507; AAB12991.1; -.
RW HIV; M12507; TAT$WMJ2.
KW AIDS.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1467 MW; 37CC737BF6F67AA8 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 5 TGP 7
    |||
DB 10 TGP 12

RESULT 7
TAT_HVI28
ID TAT_HVI28 STANDARD; PRT; 14 AA.
AC P12511;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
RN [1]_SEQUENCE.
RP SEQUENCE FROM N.A.
RX MEDLINE=86281278; PubMed=3395517;
RA Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,

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RA Gallo R.C.;  
 RT "Nucleotide sequence analysis of the env gene of a new Zairian  
 RL isolate of HIV-1.";  
 CC AIDS Res. Hum. Retroviruses 4:165-173(1988).  
 CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE  
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND  
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR  
 CC PROMOTER.  
 CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.  
 CC -!- MISCELLANEOUS: THE 2-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD  
 CC ZAIREAN MALE.  
 CC -----  
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 CC -----  
 CC EMBL; J03653; AAA44685.1; -;  
 DR HIV; J03653; TATSJY1.  
 KW Transcription regulation; Activator; RNA-binding; Nuclear protein;  
 KW AIDS.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;  
 Query Match 30.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 TGP 7  
 DB 10 TGP 12  
 RESULT 8  
 RKGG\_CARCR STANDARD; PRT; 15 AA.  
 ID RKGG\_CARCR  
 AC P21586;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE Rathke's gland glycoprotein (Fragment).  
 OS Carretta caretta (Loggerhead).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Testudines; Cryptodira; Chelonioidea; Cheloniidae; Carretta.  
 CC NCBI\_TaxID=8467;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Rathke's gland;  
 RX MEDLINE=90075703; PubMed=2591198;  
 RA Radhakrishna G.; Chin C.C.Q.; Mold F.; Weidon P.J.;  
 RT "Glycoproteins in Rathke's gland secretions of loggerhead (Carretta  
 RT caretta) and Kemp's ridley (Lepidochelys kempi) sea turtles.";  
 RL Comp. Biochem. Physiol. 94B:375-378(1989).  
 CC -!- FUNCTION: RATHKE'S GLAND SECRETIONS MAY FUNCTION AS PHEROMONES,  
 CC AS PREDATOR REPELLENTS, OR CONTRIBUTE TO THE MAINTENANCE OF THE  
 CC TURTLE SHELL.  
 CC -!- SIMILARITY: WITH RATHKE'S GLAND GLYCOPROTEIN FROM KEMP'S RIDLEY  
 CC SEA TURTLE.  
 CC PIR; P0154; P0154.  
 KW Glycoprotein.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1477 MW; CC893BAAA1B1B5ED CRC64;  
 Query Match 30.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GPI 8  
 DB 11  
 RESULT 9  
 UC29\_MAIZE STANDARD; PRT; 15 AA.  
 ID UC29\_MAIZE  
 AC P80635;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)  
 DE (fragment).  
 DE Zea mays (Maize).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 CC NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P.; Riccardi F.; Morin C.; Damerval C.; Huet J.-C.;  
 RA Fernollet J.-C.; Zivy M.; de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9, ITS MW IS: 37.6 kDa.  
 CC Maize-2DPAGE; P80635; COLEOPTILE.  
 DR MaizeDB; 123960; -;  
 DR NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;  
 Query Match 30.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PIP 9  
 DB 6 PIP 8  
 RESULT 10  
 PNOC\_PIG STANDARD; PRT; 17 AA.  
 ID PNOC\_PIG  
 AC P55791;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Nociceptin (Orphanin FQ).  
 GN PNOC.  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 CC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hypothalamus;  
 RX MEDLINE=96055113; PubMed=7481766;  
 RA Reinscheid R.K.; Nethacker H.-P.; Bourson A.; Ardati A.;  
 RA Henningsen R.A.; Bunzow J.R.; Grandy D.K.; Langan H.; Monsma F.J. Jr.;  
 RA Civelli O.;  
 RT "Orphanin FQ: a neuropeptide that activates an opioidlike G protein-  
 RT coupled receptor.";  
 RL Science 270:792-794(1995).  
 CC -!- FUNCTION: NOCICEPTIN IS THE LIGAND OF THE OPIOID RECEPTOR-LIKE  
 CC RECEPTOR (OPRL1). IT MAY ACT AS A TRANSMITTER IN THE BRAIN BY  
 CC MODULATING NOCICEPTIVE AND LOCOMOTOR BEHAVIOR. MAY BE INVOLVED IN  
 CC NEURONAL DIFFERENTIATION AND DEVELOPMENT. WHEN ADMINISTERED  
 CC INTRACEREBROVENTRICULARLY INTO MICE, THIS PEPTIDE INDUCES  
 CC HYPERALGESIA AND DECREASES LOCOMOTOR ACTIVITY.  
 CC -!- SUBCELLULAR LOCATION: SECRETED INTO THE ENDOPLASMIC RETICULUM.  
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY IN THE BRAIN AND SPINAL CORD.

DB 13 GPI 15  
 RESULT 9  
 UC29\_MAIZE STANDARD; PRT; 15 AA.  
 ID UC29\_MAIZE  
 AC P80635;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)  
 DE (fragment).  
 DE Zea mays (Maize).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 CC NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P.; Riccardi F.; Morin C.; Damerval C.; Huet J.-C.;  
 RA Fernollet J.-C.; Zivy M.; de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9, ITS MW IS: 37.6 kDa.  
 CC Maize-2DPAGE; P80635; COLEOPTILE.  
 DR MaizeDB; 123960; -;  
 DR NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;  
 Query Match 30.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PIP 9  
 DB 6 PIP 8  
 RESULT 10  
 PNOC\_PIG STANDARD; PRT; 17 AA.  
 ID PNOC\_PIG  
 AC P55791;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Nociceptin (Orphanin FQ).  
 GN PNOC.  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 CC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hypothalamus;  
 RX MEDLINE=96055113; PubMed=7481766;  
 RA Reinscheid R.K.; Nethacker H.-P.; Bourson A.; Ardati A.;  
 RA Henningsen R.A.; Bunzow J.R.; Grandy D.K.; Langan H.; Monsma F.J. Jr.;  
 RA Civelli O.;  
 RT "Orphanin FQ: a neuropeptide that activates an opioidlike G protein-  
 RT coupled receptor.";  
 RL Science 270:792-794(1995).  
 CC -!- FUNCTION: NOCICEPTIN IS THE LIGAND OF THE OPIOID RECEPTOR-LIKE  
 CC RECEPTOR (OPRL1). IT MAY ACT AS A TRANSMITTER IN THE BRAIN BY  
 CC MODULATING NOCICEPTIVE AND LOCOMOTOR BEHAVIOR. MAY BE INVOLVED IN  
 CC NEURONAL DIFFERENTIATION AND DEVELOPMENT. WHEN ADMINISTERED  
 CC INTRACEREBROVENTRICULARLY INTO MICE, THIS PEPTIDE INDUCES  
 CC HYPERALGESIA AND DECREASES LOCOMOTOR ACTIVITY.  
 CC -!- SUBCELLULAR LOCATION: SECRETED INTO THE ENDOPLASMIC RETICULUM.  
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY IN THE BRAIN AND SPINAL CORD.

CC -!- SIMILARITY: BELONGS TO THE OPIOIDS NEUROPEPTIDES PRECURSORS  
CC FAMILY.

DR InterPro: IPR006024; Opioid neupept.  
DR PROSITE: PS01252; OPIOIDS PRECURSOR; PARTIAL.  
KW Opioid peptide; Neurotransmitter; Neuropeptide.  
SQ SEQUENCE 17 AA; 1809 MW; 36363A785F8768409 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
|||  
DB 4 FTG 6

## RESULT 11

## RM35\_YEAST

ID RM35\_YEAST STANDARD; PRT; 17 AA.

AC P36530;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE Mitochondrial 60S ribosomal protein L35 (YML35) (Fragment).

GN MRP35.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE.

RX MEDLINE=91285106; PubMed=2060626;

RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,

RA Kitakawa M.;

RT "Extended N-terminal sequencing of proteins of the large ribosomal

RT subunit from yeast mitochondria.";

RL FEBS Lett. 284:51-56(1991).

DR PIR; S17274; S17274.

DR SGD; S0002730; MRPL35.

KW Ribosomal protein; Mitochondrion.

FT NON\_TER 17 17

SQ SEQUENCE 17 AA; 1826 MW; 6CE89CB415483EE8 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYP 3  
|||  
DB 13 VYP 15

## RESULT 12

## COOT\_SARBU

ID COOT\_SARBU STANDARD; PRT; 19 AA.

AC Q09148;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE NEB-collocostatin (Folliculostatin).

OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

OC Sarcophagidae; Sarcophaga.

OX NCBI\_TaxID=7385;

RN [1]

RP SEQUENCE.

RX MEDLINE=95188911; PubMed=7883009;

RA Bylenans D., Proost P., Samijn B., Borovsky D., Grauwels L.,

RA Huybrechts R., van Damme J., van Beeumen J., de Loof A.;

RT "Neb-collocostatin, a second folliculostatin of the grey fleshfly,

RT Neobellieria bullata.";

RL Eur. J. Biochem. 228:45-49(1995).

CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO  
CC INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC  
CC FOLLICLES.

CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.

CC -!- CAUTION: NEB-COLOOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM  
CC COLLAGEN IV.

DR PIR; S69153; S69153.

SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CEB8251 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPI 8  
|||  
DB 12 GPI 14

## RESULT 13

## DURA\_STRGV

ID DURA\_STRGV STANDARD; PRT; 19 AA.

AC P36504;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Lantibiotic duramycin (Leucopeptin) (Antibiotic PA48009).

OS Streptovorticillum griseovorticillatum.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomycetes.

OX NCBI\_TaxID=68215;

RN [1]

RP SEQUENCE, AND STRUCTURE BY NMR.

RC STRAIN=PA-48009;

RX MEDLINE=91107438; PubMed=2272918;

RA Hayashi F., Negashima K., Terui Y., Kawamura Y., Matsumoto K.,

RA Itazaki H.;

RT "The structure of PA48009: the revised structure of duramycin.";

RL J. Antibiot. 43:1421-1430(1990).

RN [2]

RP SEQUENCE.

RX MEDLINE=91107436; PubMed=2125590;

RA Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J.,

RA Raschdorf P., Peter H.H.;

RT "Duramycins B and C, two new lantionine containing antibiotics as

RT inhibitors of phospholipase A2. Structural revision of duramycin and

RT cinnamycin.";

RL J. Antibiot. 43:1403-1412(1990).

CC -!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.

CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of  
CC Thr, and Ser into dehydrated AA and the formation of thioether  
CC bonds with cysteine or the formation of dialkylamine bonds with  
CC lysine. This is followed by membrane translocation and cleavage of  
CC the modified precursor.

CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.

KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.

FT CROSSLNK 1 18 Beta-methylanthionine (Cys-Thr).

FT CROSSLNK 4 14 Lanthionine (Ser-Cys).

FT CROSSLNK 5 11 Beta-methylanthionine (Cys-Thr).

FT CROSSLNK 6 19 Lysinoalanine (Ser-Lys).

SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFT 5  
|||  
DB 9 PFT 11

## RESULT 14

## RE31\_LITRU

ID RE31\_LITRU STANDARD; PRT; 5 AA.

```
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians."
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD RES 5 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;
Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 FT 5
DB 4 FT 5
RESULT 15
RE32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 FT 5
DB 4 FT 5
```

```
RESULT 16
SUGA_ACHDO STANDARD; PRT; 5 AA.
ID SUGA_ACHDO
AC P19991;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Suboesophageal ganglion pentapeptide.
OS Acheta domesticus (House cricket).
OC Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Acheta.
OX NCBI_TaxID=6997;
RN [1]
RP SEQUENCE.
RA Wicker C., Wicker C.;
RT "Isolation and structure of a peptide isolated from the
RT suboesophageal ganglion of Acheta domesticus (orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987).
CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
CC -!- GANGLIA.
CC PIR; JS0319; JS0319.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;
Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PF 4
DB 4 PF 5
RESULT 17
EI01_LITRU STANDARD; PRT; 6 AA.
ID EI01_LITRU
AC P82056;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 6 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
Query Match 20.0%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PI 8
DB 3 PI 4
RESULT 18
CHOX_ALCSP STANDARD; PRT; 7 AA.
ID CHOX_ALCSP
```

AC P16101;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-APR-1990 (Rel. 14, Last annotation update)  
DE Choline oxidase (EC 1.1.3.17) (Fragment).  
OS Alkaligenes sp.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Alcaligenaceae; Alcaligenes.  
OX NCBI\_TaxID=512;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81006769; PubMed=6997283;  
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;  
RT "Identification and properties of the prosthetic group of choline  
RT oxidase from *Alcaligenes* sp.";  
RL J. Biochem. 88:197-203(1980).  
CC -1- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).  
DR PIR, A15398; A15398.  
KW Oxidoreductase.  
FT NON\_TER 7  
SQ SEQUENCE 7 AA; 839 MW; 7415B1B457644AC0 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 PN 10  
DB 3 PN 4  
  
RESULT 19  
FAR1 HELTI  
ID FAR1 HELTI STANDARD; PRT; 7 AA.  
AC P41871;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide GDPFLRF-amide.  
OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC Lymnaeidae; Planorbidae; Helisoma.  
OX NCBI\_TaxID=27815;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRFamide-related peptides from the kidney of the snail, *Helisoma*  
RT trivolvis";  
RL Peptides 15:31-36(1994).  
CC -1- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING  
CC -1- THE KIDNEY, MANTLE AND SKIN.  
CC -1- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 PF 4  
DB 3 PF 4  
  
RESULT 20  
FAR4 PANRE  
ID FAR4 PANRE STANDARD; PRT; 7 AA.  
AC P41875;

DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE FMRFamide-like neuropeptide PF4 (KPNFIRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RX MEDLINE=95323026; PubMed=7716079;  
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,  
RA Thim L., Kubrak T.M., Martin R.A., Geary T.G.;  
RT "Isolation and preliminary biological characterization of  
RT KPNFIRFamide, a novel FMRFamide-related peptide from the free-living  
RT nematode, *Panagrellus redivivus*.";  
RL Peptides 16:87-93(1995).  
CC -1- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT  
CC MUSCLE TENSION INCREASE.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 PN 10  
DB 2 PN 3  
  
RESULT 21  
MNPI LEPDE  
ID MNPI LEPDE STANDARD; PRT; 7 AA.  
AC P42984;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Myotropic neuropeptide 1 (Led-MNP-I).  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Phytophaga; Chrysomelidae; Chrysomelinae;  
OC Chrysomelini; Leptinotarsa.  
OX NCBI\_TaxID=7539;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Head;  
RX MEDLINE=95380343; PubMed=7651886;  
RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,  
RA Grauwels L., van Leuven F., de Loof A.;  
RT "Identification, characterization, and immunological localization of  
RT a novel myotropic neuropeptide in the Colorado potato beetle,  
RT Leptinotarsa decemlineata";  
RL Peptides 16:365-374(1995).  
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE  
CC OVIDUCT.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 GP 7  
DB 4 GP 5

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RESULT 22
TV51_LITRU          STANDARD;          PRT;          7 AA.
AC P82065;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OC NCBI_TaxID=104895;
RN [1]_TaxID=104895;
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowle J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:953-963 (1996).
CC -!- FUNCTION: May act as a neuromodulator or neurotransmitter.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=965; METHOD=PAB.
KW Amphibian defense peptide; Amidation; Neuropeptide;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match          20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IP 9
DB 2 IP 3

RESULT 23
UN06_PINPS          STANDARD;          PRT;          7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OC NCBI_TaxID=71647;
RN [1]_TaxID=71647;
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344391;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108 (1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC -!- PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match          20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4

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DB 6 PF 7

RESULT 24
AKHG_GRYBI          STANDARD;          PRT;          8 AA.
ID AKHG_GRYBI
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OC NCBI_TaxID=6999, 7007;
RN [1]_TaxID=6999, 7007;
RP SEQUENCE.
RC SPECIES=G. bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914 (1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R. microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688 (1988).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A28004; A28004.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH, 1.
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match          20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6
DB 6 TG 7

RESULT 25
AKH_LIBAU           STANDARD;          PRT;          8 AA.
ID AKH_LIBAU
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OC NCBI_TaxID=6966;
RN [1]_TaxID=6966;
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;

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GAEDE G.;  
 RT "The putative ancestral peptide of the adipokinetic/red-pigment-  
 RT concentrating hormone family isolated and sequenced from a  
 RT dragonfly.";  
 RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).  
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; S10596; S10596.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 978 MW; 865A771A9C452D6 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FT 5  
 DB 4 FT 5

RESULT 26  
 AKH\_TABAT  
 ID AKH\_TABAT STANDARD; PRT; 8 AA.  
 AC P14595;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)  
 DE (DCC I).  
 OS Tabanus atratus (Horse fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;  
 OC Tabanus.  
 OX NCBI\_TaxID=7207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=90046758; PubMed=2813385;  
 RA Jaffe H., Raina A.K., Riley C.T., Frazer B.A., Nachman R.J.,  
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;  
 RT "Primary structure of two neuro peptide hormones with adipokinetic and  
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse  
 RT flies (Diptera).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).  
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A33995; A33995.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FT 5  
 DB 4 FT 5

RESULT 27  
 AL15\_CARMA  
 ID AL15\_CARMA STANDARD; PRT; 8 AA.  
 AC P81818;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 15.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuro peptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GP 7  
 DB 2 GP 3

RESULT 28  
 AL16\_CARMA  
 ID AL16\_CARMA STANDARD; PRT; 8 AA.  
 AC P81819;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 16.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuro peptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GP 7  
 DB 2 GP 3

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RESULT 29
ALL5 CALVO
ID ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RN Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RA "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RN J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR: E47393; E47393.
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD RES 3 3 HYDROXYLATION (20%).
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7
DB 1 GP 2

RESULT 30
ALL8 CARMA
ID ALL8_CARMA STANDARD; PRT; 8 AA.
AC P8181;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 8.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RN Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 781 MW; 7C2879CDBC8476878 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7
DB 2 GP 3

RESULT 31
ALL9 CARMA
ID ALL9_CARMA STANDARD; PRT; 8 AA.
AC P81812;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 9.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RN Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 781 MW; 7C2879CDBC8476878 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7
DB 2 GP 3

RESULT 32
ANG2 BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RX TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=88299801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RA "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RT
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RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
KW PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match          20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VY 2
DB 3 VY 4

RESULT 33
FAR1_PANRE STANDARD; PRT; 8 AA.
AC P41872;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRPamide-like neuropeptide PFI (SDPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]_TaxID=6233;
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RA Garrison R.D., Williams J.F., Friedman A.R.;
RA "Two FMRPamide-like peptides from the free-living nematode
RT Panagrellus redivivus."
RL Peptides 13:209-214(1992).
CC -!- FUNCTION: MYOACTIVE.
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
CC CAUDALLY TO THE BASE OF THE PHARYNX.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match          20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PN 10
DB 3 PN 4

RESULT 34
FAR7_ASCSU STANDARD; PRT; 8 AA.
AC P43171;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRPamide-like neuropeptide AF7.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RA "Eight novel FMRPamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
```

```

RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match          20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7
DB 2 GP 3

RESULT 35
HTF1_PERAM STANDARD; PRT; 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
OS Periplaneta americana (American cockroach),
OS Periplaneta decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]_TaxID=6978;
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RA "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry."
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RA "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana."
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RA "The metabolic neuropeptides of the corpus cardiacum from the potato
RT beetle and the American cockroach are identical."
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RA "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
```

CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A44960; A44960.  
 DR PIR; A49823; A49823.  
 DR PIR; S08995; S08995.  
 DR INTERPRO; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PN 10  
 ||  
 DB 6 PN 7

## RESULT 36

ID HTF2\_PERAM STANDARD; PRT; 8 AA.  
 AC P04549;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypertrehalosemic factor II (Neuropeptide M-II) (Periplanetin CC-2)  
 DE (PeA-CAH-II) (LeD-CC-II) (Hypertrehalosemic neuropeptide II).  
 OS Periplaneta americana (American cockroach),  
 OS Lepidoptera decemlineata (Colorado potato beetle), and  
 OS Blatta orientalis (Oriental cockroach).  
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978, 7539, 6976;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=85046530; PubMed=6548628;  
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,  
 RA Rinehart K.L. Jr.;  
 RT "Structures of two cockroach neuropeptides assigned by fast atom  
 RT bombardment mass spectrometry."  
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
 RN [2]

RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=84298179; PubMed=6591205;  
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,  
 RA Miller C.A., Schooley D.A.;  
 RT "Isolation and primary structure of two peptides with  
 RT cardioacceleratory and hyperglycemic activity from the corpora  
 RT cardiaca of Periplaneta americana."  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90160053; PubMed=2576128;  
 RA Gaede G., Kellner R.;  
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato  
 RT beetle and the American cockroach are identical."  
 RL Peptides 10:1287-1289(1989).  
 RN [4]

RP SEQUENCE.  
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90253659; PubMed=2340112;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from  
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
 RT atom bombardment mass spectrometry."

RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
 CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT  
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; B44960; B44960.  
 DR PIR; B49823; B49823.  
 DR PIR; S08996; S08996.  
 DR INTERPRO; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FT 5  
 ||  
 DB 4 FT 5

## RESULT 37

ID HTF\_TENMO STANDARD; PRT; 8 AA.  
 AC P25419;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Hypertrehalosemic factor (HOTH) (Hypertrehalosemic neuropeptide).  
 OS Tenbrionid molitor (Yellow mealworm), and  
 OS Zophobas rugipes.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
 OC Tenebrionidae; Tenebrio.  
 OX NCBI\_TaxID=7067, 7075;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=T.molitor, and Z.rugipes;  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=90341081; PubMed=2381871;  
 RA Gaede G., Rosinski G.;  
 RT "The primary structure of the hypertrehalosemic neuropeptide from  
 RT tenebrionid beetles: a novel member of the AKH/RPCH family."  
 RL Peptides 11:455-459(1990).  
 CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT  
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A43976; A43976.  
 DR PIR; B43976; B43976.  
 DR INTERPRO; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PN 10  
 ||  
 DB 6 PN 7

## RESULT 38

LMT2\_LOCM1  
 ID LMT2\_LOCM1 STANDARD; PRT; 8 AA.  
 AC P22396;

DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE Locustamytotropin 2 (LOM-MT-2).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
 RT "Isolation, identification and synthesis of locustamytotropin II, an  
 RT additional neuropeptide of Locusta migratoria. Member of the  
 RT cephalomyotropic peptide family.";  
 RL Insect Biochem. 20:479-484(1990).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC -1- (MYOTROPIC ACTIVITY).  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 8  
 FT SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;  
 SQ  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FT 5  
 Db 4 FT 5  
 RESULT 39  
 LPK\_LEUMA STANDARD; PRT; 8 AA.  
 ID LPK\_LEUMA  
 AC P13049;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leucopyrokinin (LPK) (LEM-PK).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberoidea; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=86269041; PubMed=3015140;  
 RA Nachman R.J., Holman G.M., Cook B.J.;  
 RT "Active fragments and analogs of the insect neuropeptide  
 RT leucopyrokinin: structure-function studies.";  
 RL Biochem. Biophys. Res. Commun. 137:936-942(1986).  
 RN [2]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RX MEDLINE=87052651; PubMed=2877794;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Primary structure and synthesis of a blocked myotropic  
 RT neuropeptide isolated from the cockroach, Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 85C:219-224(1986).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC -1- (MYOTROPIC ACTIVITY).  
 CC -1- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS  
 CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE  
 CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST  
 CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE  
 CC PENTAPEPTIDE FRAGMENT FTPLR.  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR PIR; A23967; A23967.  
 DR InterPro; IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1  
 FT SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;  
 SQ  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FT 5  
 Db 4 FT 5  
 RESULT 40  
 ORMY\_ORCLI STANDARD; PRT; 8 AA.  
 ID ORMY\_ORCLI  
 AC P82455;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Orcomyotropin (OMT).  
 OS Orconectes limosus (Spinycheek crayfish).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Astacidea; Cambaridae; Orconectes.  
 OX NCBI\_TaxID=28379;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.  
 RC TISSUE=Hindgut;  
 RX MEDLINE=20411310; PubMed=10952880;  
 RA Dirksen H., Burdick S., Sauter A., Keller R.;  
 RT "Two orconectins and the novel octapeptide orcomytotropin in the hindgut  
 RT of the crayfish Orconectes limosus: identified myostimulatory  
 RT neuropeptides originating together in neurones of the terminal  
 RT abdominal ganglion.";  
 RL J. Exp. Biol. 203:2807-2818(2000).  
 CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND  
 CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED  
 CC BY ABDOMINAL GANGLIONIC NEURONS.  
 CC -1- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.  
 KW Amidation; Neuropeptide.  
 FT MOD\_RES 8  
 FT SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;  
 SQ  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FT 5  
 Db 4 FT 5  
 RESULT 41  
 PPK2\_PERAM STANDARD; PRT; 8 AA.  
 ID PPK2\_PERAM  
 AC P82652;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=97353923; PubMed=9210163;  
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;

RT "Isolation and structural elucidation of two pyrokinins from the  
 RT reticerebral complex of the American cockroach.";  
 RL Peptides 18:473-478 (1997).  
 RN [2]

TISSUE SPECIFICITY.  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRlamides in the nervous system of  
 RT the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363 (2000).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro: IPR001484; Pyrokinin.  
 DR PROSITE: PS00539; PYROKININ; FALSE NEG.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4

DB 3 PF 4

## RESULT 42

PPK3 PERAM  
 ID FPK3 PERAM STANDARD; PRT; 8 AA.  
 AC P82618;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Pteriplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]\_TaxID=6978;  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=retrocerebral complex;  
 RX MEDLINE=99212469; PubMed=10196736;  
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
 RT "Differential distribution of pyrokinin-isoforms in cerebral and  
 RT abdominal neurohemal organs of the American cockroach.";  
 RL Insect Biochem. Mol. Biol. 29:139-144 (1999).  
 RN [2]

TISSUE SPECIFICITY.  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRlamides in the nervous system of  
 RT the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363 (2000).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4

DB 3 PF 4

Db 3 PF 4

## RESULT 43

RS7\_MYCIT  
 ID RS7 MYCIT STANDARD; PRT; 8 AA.  
 AC P33564;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 30S ribosomal protein S7 (Fragment).  
 GN RPSG.

OS Mycobacterium intracellulare.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1767;  
 RN [1]

SEQUENCE FROM N.A.  
 RX MEDLINE=93197130; PubMed=8451173;  
 RA Nair J., Rouse D.A., Morris S.L.;  
 RT "Nucleotide sequence analysis of the ribosomal S12 gene of  
 RT Mycobacterium intracellulare.";  
 RL Nucleic Acids Res. 21:1039-1039 (1993).  
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds  
 CC directly to 16S rRNA where it nucleates assembly of the head  
 CC domain of the 30S subunit. Is located at the subunit interface  
 CC close to the decoding center, probably blocks exit of the E-site  
 CC rRNA (by similarity).  
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9  
 CC and S11 (by similarity).  
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.

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 CC -----  
 CC EMBL; L08171; AAA25376.1; -.  
 CC PIR; S35538; S35538.  
 CC HAMAP; MF 00480; -; 1.  
 CC InterPro: IPR000235; Ribosomal S7.  
 CC PROSITE; PS00052; RIBOSOMAL\_S7; PARTIAL.  
 KW Ribosomal protein; RNA-binding; rRNA-binding; tRNA-binding.  
 FT INIT MET 0 0 BY SIMILARITY.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7

DB 4 GP 5

## RESULT 44

UPAA HUMAN  
 ID UPAA HUMAN STANDARD; PRT; 8 AA.  
 AC P30066;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochrasser D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.  
DR SWISS-2DPAGE; P30096; HUMAN.  
FT NON TER 1 1  
FT VARIANT 5 5 F -> P.  
FT NON TER 8 8 /FTID=VAR\_000004.  
FT SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;  
SQ  
Query Match 20.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YP 3  
Db 6 YP 7

RESULT 45  
AL11 CARMA  
ID AL11 CARMA STANDARD; PRT; 9 AA.  
AC P81874;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinostat 11.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 9 9  
FT SEQUENCE 9 AA; 927 MW; 832D79CDB46D861 CRC64;  
SQ  
Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 TG 6  
Db 2 TG 3

RESULT 46  
FAR2 PANRE  
ID FAR2 PANRE STANDARD; PRT; 9 AA.  
AC P41873;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRamide-like neuropeptide PF2 (SADPNFLRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.

OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93027659; PubMed=1408999;  
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
RA Garrison R.D., Williams J.F., Friedman A.R.;  
RT "Two FMRamide-like peptides from the free-living nematode  
RT Panagrellus redivivus.";  
RL Peptides 13:209-214(1992).  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
CC -!- CAUDALLY TO THE BASE OF THE PHARYNX.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 9 9  
FT SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;  
SQ  
Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 PN 10  
Db 4 PN 5

RESULT 47  
FAR4 CALVO  
ID FAR4 CALVO STANDARD; PRT; 9 AA.  
AC P41859;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CallifMRamide 4.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated callifMRamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; D41978; D41978.  
KW Neuropeptide; Amidation.  
FT MOD RES 9 9  
FT SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;  
SQ  
Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 PN 10  
Db 2 PN 3

RESULT 48  
FAR9 ASCSU  
ID FAR9 ASCSU STANDARD; PRT; 9 AA.  
AC P43172;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)

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DE FMRamide-like neuropeptide AF9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
OC Ascarididae; Ascaris.
ON NCBI_TaxID=6253;
RX SEQUENCE.
RP MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum."
RL Peptides 16:491-500 (1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176977 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7
DB 3 GP 4

RESULT 49
FARA_CALVO STANDARD; PRT; 9 AA.
AC P41865;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 10.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
ON NCBI_TaxID=27454;
RX SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330 (1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC PIR; A44787;
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
FT UNSURE 1 1 OR S OR A.
SQ SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PN 10
DB 2 PN 3

RESULT 50
ISOT_CYPCA STANDARD; PRT; 9 AA.
AC P42993;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

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DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Isotocin.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
ON NCBI_TaxID=7962;
RX SEQUENCE.
RP TISSUE=Pituitary;
RC Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishes."
RL Comp. Biochem. Physiol. 14:245-254 (1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A61364; A61364.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PI 8
DB 7 PI 8

RESULT 51
KNL3_BOMVA STANDARD; PRT; 9 AA.
ID KNL3_BOMVA
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
ON NCBI_TaxID=8348;
RX SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RP TISSUE=Skin secretion;
RC Chen T.B., Orr D.F., Bjournson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens."
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FT 5
DB 5 FT 6

RESULT 52
LITR_PHYTO

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ID LITR_PHYRO STANDARD; PRT; 9 AA.
AC P08946;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rhodei-litorin.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=85127560; PubMed=3838283;
RA Barta D., Ersamer G.F., Simmaco M., Bossa F., Melchiorri P.,
RA Ersamer V.;
RT "Rhodei-litorin: a new peptide from the skin of Phyllomedusa rohdei.";
RL FEBS Lett. 182:53-56(1985).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
CC PIR: S07241; S07241.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT MOD_RES 9 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1090 MW; 4ECC1E81ADC377 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6
DB 5 TG 6

RESULT 53
LMT3_LOCMI STANDARD; PRT; 9 AA.
ID LMT3 LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6
DB 5 TG 6

RESULT 54
OXYT_EUFRE STANDARD; PRT; 9 AA.
ID OXYT_EUFRE STANDARD; PRT; 9 AA.
AC P42958;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Seritocin ([Ser5,Ile8]-oxytocin).
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
OC Bufo.
OX NCBI_TaxID=8390;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: Devoid of oxytocic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000381; Neurohyp_horm.
DR Pfam; PF02220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 983 MW; 17FF476EAS6D04B CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PI 8
DB 7 PI 8

RESULT 55
OXYT_EISFO STANDARD; PRT; 9 AA.
ID OXYT_EISFO STANDARD; PRT; 9 AA.
AC P42958;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=94121660; PubMed=8292046;
RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
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ID LITR_PHYRO STANDARD; PRT; 9 AA.
AC P08946;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rhodei-litorin.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=85127560; PubMed=3838283;
RA Barta D., Ersamer G.F., Simmaco M., Bossa F., Melchiorri P.,
RA Ersamer V.;
RT "Rhodei-litorin: a new peptide from the skin of Phyllomedusa rohdei.";
RL FEBS Lett. 182:53-56(1985).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
CC PIR: S07241; S07241.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT MOD_RES 9 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1090 MW; 4ECC1E81ADC377 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6
DB 5 TG 6

RESULT 53
LMT3_LOCMI STANDARD; PRT; 9 AA.
ID LMT3 LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6
DB 5 TG 6

RESULT 54
OXYT_EUFRE STANDARD; PRT; 9 AA.
ID OXYT_EUFRE STANDARD; PRT; 9 AA.
AC P42958;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Seritocin ([Ser5,Ile8]-oxytocin).
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
OC Bufo.
OX NCBI_TaxID=8390;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: Devoid of oxytocic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000381; Neurohyp_horm.
DR Pfam; PF02220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 983 MW; 17FF476EAS6D04B CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PI 8
DB 7 PI 8

RESULT 55
OXYT_EISFO STANDARD; PRT; 9 AA.
ID OXYT_EISFO STANDARD; PRT; 9 AA.
AC P42958;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=94121660; PubMed=8292046;
RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
```

CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE  
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH  
CC NEPHRIDIAL FUNCTION.  
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR PIR; PC2021; PC2021.  
DR InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; FALSE\_NEG.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 996 MW; D4EEB76B45412C9 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6  
DB 8 TG 9

RESULT 56  
OXYT\_OCTVU  
ID OXYT OCTVU STANDARD; PRT; 9 AA.  
AC P80027;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Cephalotocin.  
OS Octopus vulgaris (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=6645;  
RN [1]

RP TISSUE=Nerve endings;  
RC MEDLINE=92270139; PubMed=1589145;  
RX Reich G.;  
RA "A new peptide of the oxytocin/vasopressin family isolated from  
RT nerves of the cephalopod Octopus vulgaris.";  
RL Neurosci. Lett. 134:191-194(1992).  
CC -1- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA  
CAVA.

CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
CC InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1072 MW; 17FF476B45409DB CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PI 8  
DB 7 PI 8

RESULT 57  
PPKL\_PERAM  
ID PPKL PERAM STANDARD; PRT; 9 AA.  
AC P82691;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-1 (Pea-PK-1) (FXPR-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;

OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=97353923; PubMed=9210163;  
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;  
RT "Isolation and structural elucidation of two pyrokinins from the  
RT retrocerebral complex of the American cockroach.";  
RL Peptides 18:473-478(1997).  
RN [2]

RP TISSUE SPECIFICITY.  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
RT the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
(MYOTROPIC ACTIVITY).  
CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -1- MASS SPECTROMETRY: MW=1010.4; METHOD=MALDI.  
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1011 MW; 885C176059C87DC1 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IP 9  
DB 6 IP 7

RESULT 58  
TKL1\_LOCM1  
ID TKL1 LOCM1 STANDARD; PRT; 9 AA.  
AC P16223;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Locustatachykinin I (TK-I).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Brain;  
RX MEDLINE=90184489; PubMed=23111766;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Locustatachykinin I and II, two novel insect neuropeptides with  
RT homology to peptides of the vertebrate tachykinin family.";  
RL FEBS Lett. 261:397-401(1990).  
CC -1- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE  
OVIDUCT AND FOREGUT.

CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7  
DB 1 GP 2

RESULT 59  
 ID AH3 PRUSE STANDARD; PRT; 10 AA.  
 AC P29261;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase isozyme II) (AH II) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -1- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-glucose.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR EMBRYONAL TISSUES.  
 CC -1- PTM: GLYCOSYLATED.  
 CC Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 KW NON\_TER 10 10  
 FT SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;  
 SQ  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PI 8  
 DB 4 PI 5

RESULT 60  
 ID ANGL BOTJA STANDARD; PRT; 10 AA.  
 AC Q10581;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Angiotensin-like peptide I (Fragment).  
 OS Bothrops jararaca (Jararaca).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=96208932; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the plasma of the snake Bothrops jararaca.";  
 RL Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 10 10  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1308 MW; CEP50DD761F2DB42 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 PI 8  
 DB 4 PI 5

RESULT 61  
 ID ANGT BOVIN STANDARD; PRT; 10 AA.  
 AC P01017;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)] (Fragment).  
 DE (Fragment).  
 GN AGT OR SERPIN8.  
 OS Bos taurus (Bovine).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RA Elliott D.F., Peart W.S.;  
 RT "The amino acid sequence in a hypertensin.";  
 RL Biochem. J. 65:246-254(1957).  
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the plasma.  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A90345; A90345.  
 DR PDB; 3ER5; 15-JUL-92.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.  
 FT PEPTIDE 1 10  
 FT PEPTIDE 1 8  
 FT PEPTIDE 2 8  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VY 2  
 DB 3 VY 4

RESULT 62  
 ID ANGT CHICK STANDARD; PRT; 10 AA.  
 AC P01018;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)] (Fragment).  
 DE (Fragment).  
 GN AGT OR SERPIN8.  
 OS Gallus gallus (Chicken), and  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.  
OX NCBI\_TaxID=9031, 93934;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Chicken;  
RX MEDLINE=74127845; PubMed=4361802;  
RA Nakayama T., Nakajima T., Sokabe H.;  
RT "Comparative studies on angiotensins. 3. Structure of fowl  
angiotensin and its identification by DNS-method.";  
RL Chem. Pharm. Bull. 21:2085-2087(1973).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=C.c.japonica;  
RX MEDLINE=90284684; PubMed=2191893;  
RA Takei Y., Hasegawa Y.;  
RT "Vasopressor and depressor effects of native angiotensins and  
inhibition of these effects in the Japanese quail.";  
RL Gen. Comp. Endocrinol. 79:12-22(1990).  
CC -|- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
BALANCE OF BODY FLUIDS.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.  
CC -|- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR PIR; A60624; A60624.  
DR PIR; A90917; A90917.  
DR InterPro; IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT PEPTIDE 2 8 ANGIOTENSIN III.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VY 2  
||  
3 VY 4  
DB

RESULT 63  
BPP2\_BOTIN STANDARD; PRT; 10 AA.  
AC P30422;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting  
enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -|- FUNCTION: This peptide both inhibits the activity of the  
angiotensin-converting enzyme and enhances the action of  
bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.

DR PIR; B37196; B37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1  
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 IP 9  
||  
8 IP 9  
DB

RESULT 64  
BPP2\_BOTJA STANDARD; PRT; 10 AA.  
AC P01022;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme  
inhibitor V-6-II).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=72118526; PubMed=4334402;  
RA Ondetti M.A., Williams N.J., Sabo E.F., Plusec J., Weaver E.R.,  
RA Kocy O.;  
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops  
jararaca. Isolation, elucidation of structure, and synthesis.";  
RL Biochemistry 10:4033-4039(1971).  
CC -|- FUNCTION: This peptide both inhibits the activity of the  
angiotensin-converting enzyme and enhances the action of  
bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; A01255; XAVI6B.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1  
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 IP 9  
||  
8 IP 9  
DB

RESULT 65  
BPP8\_BOTIN STANDARD; PRT; 10 AA.  
AC P30426;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting  
enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;

RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RL peptides from Bothrops insularis snake venom."; J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; H37196; H37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;  
  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 9 PN 10  
 DB 6 PN 7  
  
 RESULT 66  
 BPP\_VIPAS STANDARD; PRT; 10 AA.  
 AC P31351;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Vipera aspis (Aspic viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Vipera.  
 OX NCBI\_TaxID=8706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90382616; PubMed=2169439;  
 RA Komori Y., Sugihara H.;  
 RT "Characterization of a new inhibitor for angiotensin converting  
 RL enzyme from the venom of Vipera aspis aspis.";  
 RL Int. J. Biochem. 22:767-771(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A60377; XASNPC.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1062 MW; 3B827C327686773 CRC64;  
  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 GP 7  
 DB 5 GP 6  
  
 RESULT 67  
 CA12\_LITCI STANDARD; PRT; 10 AA.  
 AC P82086;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 1.2/1.2Y4.  
 OS Litoria citropa (Australian blue mountains tree frog), and  
 OS Litoria splendida (Magnificent tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=94770, 30345;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEINS 1.2 AND 1.2Y4).  
 RC SPECIES=L.citropa; TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT montana tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry.";  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 RN [2]  
 RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).  
 RC SPECIES=L.splendida; TISSUE=Skin secretion;  
 RX MEDLINE=20069371; PubMed=10601876;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;  
 RT "Differences in the skin peptides of the male and female Australian  
 RT tree frog Litoria splendida. The discovery of the aquatic male sex  
 RT pheromone splendipherin, together with Phe8 caerulein and the  
 RT antibiotic peptide caerin 1.10.";  
 RL Eur. J. Biochem. 267:269-275(2000).  
 CC -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 1.2Y4 differs from isoform 1.2 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1366; METHOD=Electrospray.  
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 DR InterPro; IPRO01651; Gastrin.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1306 MW; 99DBFCD37861BB5A CRC64;  
  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 TG 6  
 DB 5 TG 6  
  
 RESULT 68  
 CAER\_LITXA STANDARD; PRT; 10 AA.  
 AC P56264;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Caerulein.  
 OS Litoria xanthomera (Orange-thighed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=79697;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97374000; PubMed=9230483;  
 RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,  
 RA Ramsay S.L.;  
 RT "New caerin antibacterial peptides from the skin glands of the  
 RT Australian tree frog Litoria xanthomera.";  
 RL J. Pept. Sci. 3:181-185(1997).  
 CC -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1354; METHOD=PAB.

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CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro: IPR001651; Gastrin.
RX PROSITE: PS00259; GASTRIN; 1.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
FT PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT MOD_RES 4 4
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1290 MW; 99DBF3837861BB5A CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TG 6
DB 5 TG 6

RESULT 69
COCO_RAT
ID COXO_RAT STANDARD; PRT; 10 AA.
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1)
DE (VIIIA) (Fragment).
DE COX7C OR COX7C1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricyochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
DR PIR; S65388; S65388.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7
DB 6 GP 7

RESULT 70
COCO_THUOB
ID COXO_THUOB STANDARD; PRT; 10 AA.
AC P80982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

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OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricyochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
DR PIR; S77990; S77990.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP 7
DB 6 GP 7

RESULT 71
ESTA_SCHGA
ID ESTA_SCHGA STANDARD; PRT; 10 AA.
AC P81012;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
DE (Fragment).
OS Schizaphis graminum (Aphid).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Aphididae; Aphidini; Schizaphis.
OX NCBI_TaxID=13262;
RN [1]
RP SEQUENCE.
RX MEDLINE=97468499; PubMed=9327586;
RA Siegfried B.D., Ono M., Swanson J.J.;
RT "Purification and characterization of a carboxylesterase associated
RT with organophosphate resistance in the greenbug, Schizaphis graminum
RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR InterPro: IPR002018; CarbesteraseB.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW Hydrolase; Serine esterase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1025 MW; 018ABE587865A2C0 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PI 8
DB 2 PI 3

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RESULT 72  
 ID FAR6 PANRE STANDARD; PRT; 10 AA.  
 AC P8260;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE FMRPamide-like neuropeptide PF6 (NGAPQPFVRF-amide).  
 OS Panagrellus redivivus.  
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimidae; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]  
 RN SEQUENCE, FUNCTION, AND AMIDATION.  
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
 RA Maule A.G.;  
 RT "Isolation, characterization and pharmacology of RMRPamide-related  
 RT peptides (FarPe) from free-living nematode, Panagrellus redivivus.";  
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: MYOACTIVE.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;  
  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 3 PF 4  
 ||  
 DB 6 PF 7  
  
 RESULT 73  
 GON2\_CHICK STANDARD; PRT; 10 AA.  
 AC P37043; P20408; P81750;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadolibetin II (Gonadotropin-releasing hormone II) (GNRH-II)  
 DE (LH-RH II) (Luliberin II).  
 OS Gallus gallus (Chicken).  
 OS Alligator mississippiensis (American alligator).  
 OS Squalus acanthias (Spiny dogfish).  
 OS Hydrolagus colliei (Spotted ratfish) (Pacific ratfish), and  
 OS Clupea pallasi (Pacific herring).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031, 8496, 7797, 7873, 30724;  
 RN [1]  
 RN SEQUENCE.  
 RC SPECIES=Chicken; TISSUE=Hypothalamus;  
 RX MEDLINE=84222059; PubMed=6427779;  
 RA Miyamoto K., Hasegawa Y., Nomura M., Igarashi M., Kangawa K.,  
 RA Matsuo H.;  
 RT "Identification of the second gonadotropin-releasing hormone in  
 RT chicken hypothalamus: evidence that gonadotropin secretion is  
 RT probably controlled by two distinct gonadotropin-releasing hormones  
 RT in avian species.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3874-3878 (1984).  
 RN [2]  
 RN SEQUENCE.  
 RC SPECIES=A. mississippiensis; TISSUE=Brain;  
 RX MEDLINE=91352338; PubMed=1892082;  
 RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,  
 RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure of two forms of gonadotropin-releasing hormone

from brains of the American alligator (Alligator mississippiensis).";  
 Regul. Pept. 33:105-116(1991).  
 RN [3]  
 RN SEQUENCE.  
 RP SPECIES=S. acanthias; TISSUE=Brain;  
 RX MEDLINE=92335300; PubMed=1631133;  
 RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,  
 RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;  
 RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in  
 RT dogfish brain provides insight into GNRH evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).  
 RN [4]  
 RN SEQUENCE.  
 RP SPECIES=H. colliei; TISSUE=Brain;  
 RX MEDLINE=91340067; PubMed=1678723;  
 RA Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,  
 RA Lee T.;  
 RT "Primary structure of gonadotropin-releasing hormone from the brain  
 RT of a holoccephalan (ratfish: Hydrolagus colliei).";  
 RL Gen. Comp. Endocrinol. 82:152-161(1991).  
 RN [5]  
 RN SEQUENCE, AND FUNCTION.  
 RP SPECIES=C. pallasi; TISSUE=Brain, and Pituitary;  
 RX MEDLINE=20114351; PubMed=10650929;  
 RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,  
 RA Chang J.P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure and function of three gonadotropin-releasing  
 RT hormones, including a novel form, from an ancient teleost, herring.";  
 RL Endocrinology 141:505-512(2000).  
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the GNRH family.  
 DR PIR; A61126; A61126.  
 DR PIR; B46030; B46030.  
 DR PIR; B60066; RHA02.  
 DR InterPro; IPR002012; GNRH.  
 DR Pfam; PF00446; GNRH; 1.  
 DR PROSITE; PS00473; GNRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1254 MW; 284B2E437871F5A3 CRC64;  
  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 YP 3  
 ||  
 DB 8 YP 9  
  
 RESULT 74  
 GS09\_BACSU STANDARD; PRT; 10 AA.  
 ID GS09\_BACSU  
 AC P80243;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE General stress protein 9 (GSP9) (Fragment).  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RN SEQUENCE.  
 RC STRAIN=168 / IS58;  
 RX MEDLINE=94282319; PubMed=8012595;  
 RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,  
 RA Schmid R., Mach H., Hecker M.;  
 RT "Analysis of the induction of general stress proteins of Bacillus  
 RT subtilis.";  
 RL Microbiology 140:741-752(1994).  
 CC -1- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE

CC LIMITATION AND OXYGEN LIMITATION.  
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.  
KW Heat shock. 10 10  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1168 MW; 99766442D5A2C05A CRC64;  
Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VY 2  
Db 7 VY 8

RESULT 75  
HTF1\_ROMMI STANDARD; PRT; 10 AA.  
AC P18110;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE RO I (Hypertrehalosaemic factor).  
OS Romalea microptera (lubber grasshopper).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Romaleidae; Romalea.  
OX NCBI\_TaxID=7007;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=89145002; PubMed=3226948;  
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from  
RL the lubber grasshopper, Romalea microptera.";  
RL Peptides 9:681-688(1988).  
CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT  
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH (TREHALOSE IS  
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYPH OF INSECTS).  
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
CC InterPro: IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;  
Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 FT 5  
Db 4 FT 5

Search completed: November 25, 2003, 18:17:36  
Job time : 5.84043 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 24.0957 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-18

Perfect score: 10

Sequence: 1 VYFTGPIPN 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	40.0	19	10	P82245
2	3	30.0	8	2	Q49534 mycoplasma
3	3	30.0	9	12	Q71066 canine dist
4	3	30.0	10	4	Q9P229
5	3	30.0	10	10	Q9F593 silene pent
6	3	30.0	10	11	Q91W23
7	3	30.0	12	6	Q9N2B9
8	3	30.0	12	6	Q9N2B8
9	3	30.0	12	6	Q9N2C0
10	3	30.0	12	10	Q9SYT4
11	3	30.0	12	10	Q9FSA9
12	3	30.0	13	8	Q8WEK0
13	3	30.0	13	10	Q9FSA8
14	3	30.0	13	10	Q9F594
15	3	30.0	13	12	P90442
16	3	30.0	14	2	Q8KSE3

Q8J1G5	14	3	30.0	3	30.0	14	3	Q8J1G5
Q9F595	14	10	30.0	3	30.0	14	10	Q9F595
Q9F5B1	14	10	30.0	3	30.0	14	10	Q9F5B1
Q9F591	14	10	30.0	3	30.0	14	10	Q9F591
P83291	14	10	30.0	3	30.0	14	10	P83291
Q8JDM3	14	15	30.0	3	30.0	14	15	Q8JDM3
Q8JDM7	14	15	30.0	3	30.0	14	15	Q8JDM7
Q8JDM0	14	15	30.0	3	30.0	14	15	Q8JDM0
Q9R4M8	15	2	30.0	3	30.0	15	2	Q9R4M8
O05463	15	2	30.0	3	30.0	15	2	O05463
Q9UC22	15	4	30.0	3	30.0	15	4	Q9UC22
P81831	15	5	30.0	3	30.0	15	5	P81831
Q9F5A5	15	10	30.0	3	30.0	15	10	Q9F5A5
Q9F5B2	15	10	30.0	3	30.0	15	10	Q9F5B2
Q9F598	15	10	30.0	3	30.0	15	10	Q9F598
Q9F513	15	10	30.0	3	30.0	15	10	Q9F513
Q9F5A0	15	10	30.0	3	30.0	15	10	Q9F5A0
Q9F599	15	10	30.0	3	30.0	15	10	Q9F599
Q9F515	15	10	30.0	3	30.0	15	10	Q9F515
Q9F514	15	10	30.0	3	30.0	15	10	Q9F514
Q9F580	15	10	30.0	3	30.0	15	10	Q9F580
Q9F5B0	15	10	30.0	3	30.0	15	10	Q9F5B0
Q9QV00	15	11	30.0	3	30.0	15	11	Q9QV00
Q9Q594	15	13	30.0	3	30.0	15	13	Q9Q594
Q9F1S7	16	2	30.0	3	30.0	16	2	Q9F1S7
Q9F1S4	16	2	30.0	3	30.0	16	2	Q9F1S4
Q9TWK1	16	5	30.0	3	30.0	16	5	Q9TWK1
Q8MB2	16	6	30.0	3	30.0	16	6	Q8MB2
Q34699	16	8	30.0	3	30.0	16	8	Q34699
Q8HU42	16	8	30.0	3	30.0	16	8	Q8HU42
Q8HU29	16	8	30.0	3	30.0	16	8	Q8HU29
O55091	17	3	30.0	3	30.0	17	3	O55091
P83488	17	3	30.0	3	30.0	17	3	P83488
Q9UCT3	17	4	30.0	3	30.0	17	4	Q9UCT3
Q9TWB9	17	5	30.0	3	30.0	17	5	Q9TWB9
O46473	17	6	30.0	3	30.0	17	6	O46473
Q9TRY8	17	6	30.0	3	30.0	17	6	Q9TRY8
Q9QUW6	17	11	30.0	3	30.0	17	11	Q9QUW6
Q9QY2	17	15	30.0	3	30.0	17	15	Q9QY2
Q9QY1	17	15	30.0	3	30.0	17	15	Q9QY1
Q9R4C3	18	2	30.0	3	30.0	18	2	Q9R4C3
Q9BU72	18	4	30.0	3	30.0	18	4	Q9BU72
Q28069	18	6	30.0	3	30.0	18	6	Q28069
Q9F5B3	18	10	30.0	3	30.0	18	10	Q9F5B3
Q39829	18	10	30.0	3	30.0	18	10	Q39829
Q8R170	18	11	30.0	3	30.0	18	11	Q8R170
Q9R4D8	19	2	30.0	3	30.0	19	2	Q9R4D8
Q9TWG5	19	5	30.0	3	30.0	19	5	Q9TWG5
Q9TWJ8	19	5	30.0	3	30.0	19	5	Q9TWJ8
Q9S8G6	19	10	30.0	3	30.0	19	10	Q9S8G6
Q64977	19	12	30.0	3	30.0	19	12	Q64977
Q905J2	19	15	30.0	3	30.0	19	15	Q905J2
Q905E0	19	15	30.0	3	30.0	19	15	Q905E0
Q905I8	19	15	30.0	3	30.0	19	15	Q905I8
Q90RF4	19	15	30.0	3	30.0	19	15	Q90RF4
Q90RE9	19	15	30.0	3	30.0	19	15	Q90RE9
Q90RG9	19	15	30.0	3	30.0	19	15	Q90RG9
Q53345	20	2	30.0	3	30.0	20	2	Q53345
Q9R5Q5	20	2	30.0	3	30.0	20	2	Q9R5Q5
Q53346	20	2	30.0	3	30.0	20	2	Q53346
Q9R5T4	20	2	30.0	3	30.0	20	2	Q9R5T4
O13594	20	3	30.0	3	30.0	20	3	O13594
Q9UCB3	20	4	30.0	3	30.0	20	4	Q9UCB3
Q9UC71	20	4	30.0	3	30.0	20	4	Q9UC71
Q9TR41	20	6	30.0	3	30.0	20	6	Q9TR41
Q9TCY9	20	6	30.0	3	30.0	20	6	Q9TCY9
Q9TR87	20	6	30.0	3	30.0	20	6	Q9TR87
Q9S8X5	20	10	30.0	3	30.0	20	10	Q9S8X5
P82163	20	10	30.0	3	30.0	20	10	P82163
Q63667	20	11	30.0	3	30.0	20	11	Q63667
Q9QVG2	20	11	30.0	3	30.0	20	11	Q9QVG2

90 Q8V9H3 chicken ane  
 91 Q47505 escherichia  
 92 Q50556 actinobacil  
 93 Q98866 spinacia ol  
 94 Q07624 rous sarcom  
 95 Q986D5 escherichia  
 96 Q9RG49 buchnera ap  
 97 Q9AGP4 arthrobaacte  
 98 Q4463 rhizobiales  
 99 Q9X3K1 prochloroco  
 100 Q934E4 thiobacilli

## ALIGNMENTS

RESULT 1  
 ID P82245 PRELIMINARY; PRT; 19 AA.  
 AC P82245;  
 DT 01-JUN-2000 (TREMBlrel. 14, Created)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE Chloroplast 50S ribosomal protein L28 (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC STRAIN=cv. ALVARO; TISSUE=Leaf;  
 RX MEDLINE=20435798; PubMed=10874046;  
 RT Yamaguchi K., Subramanian A.R.;  
 RT "The plastid ribosomal proteins. Identification of all the proteins in  
 the 50 S subunit of an organelle ribosome (chloroplast).";  
 RL J. Biol. Chem. 275:28466-28482(2000).  
 CC - FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
 CC - SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC - TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC - MASS SPECTROMETRY: MW=8991.8; METHOD=ELECTROSPRAY.  
 CC - MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 13 KDA.  
 CC - SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.  
 KW Ribosomal protein; Chloroplast; rRNA-binding.  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2230 MW; 4849481933F1F486B CRC64;  
 Query Match 40.0%; Score 4; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PFTG 6  
 DB 5 PFTG 8  
 RESULT 2  
 ID Q49534 PRELIMINARY; PRT; 8 AA.  
 AC Q49534;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE P120 (Fragment).  
 GN P120.  
 OS Mycoplasma hominis.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=2098;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=V2785;  
 RA Nyvold C., Birkelund S., Christiansen G.;  
 RT "The Mycoplasma hominis P120 membrane protein gene contains a 659 base

RT pair hypervariable domain.";  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U22025; AA67455.1; -  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 869 MW; 914457605B02C05D CRC64;

Query Match 30.0%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 IPN 10  
 DB 5 IPN 7

## RESULT 3

ID O71066 PRELIMINARY; PRT; 9 AA.  
 AC O71066;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Fusion protein (Fragment).  
 GN F.  
 OS Canine distemper virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
 OX NCBI\_TaxID=11232;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dog #10757/96;  
 RA Liermann H., Harder T., Haas L.;  
 RT "Genetic analysis of the central untranslated genome region and the  
 proximal coding part of the F gene of wild-type and vaccine distemper  
 morbilliviruses.";  
 RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF026234; AAC09164.1; -  
 DR NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;  
 Query Match 30.0%; Score 3; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 IPN 10  
 DB 5 IPN 7

## RESULT 4

ID Q9P229 PRELIMINARY; PRT; 10 AA.  
 AC Q9P229;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE Epidermal growth factor receptor (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=91337091; PubMed=1678600;  
 RA Humphrey P.A., Gangarosa L.M., Wong A.J., Archer G.E.,  
 RA Lund-Johansen M., Bjerkvig R., Laerum O.D., Friedman H.S.,  
 RA Bigner D.D.;  
 RT "Deletion-mutant epidermal growth factor receptor in human gliomas:  
 effects of type II mutation on receptor function.";  
 RT Biochem. Biophys. Res. Commun. 178:1413-1420(1991).  
 DR EMBL; S51343; AAB19486.2; -  
 KW Receptor.  
 FT NON\_TER 1 1

FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1020 MW; 439DEABEB87B1727 CRC64;

Query Match  
Best Local Similarity 30.0%; Score 3; DB 4; Length 10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
DB 8 TGP 10

RESULT 5  
Q9FS93 ID Q9FS93 PRELIMINARY; PRT; 10 AA.  
AC Q9FS93;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene pentelica.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Caryophyllaceae; Silene.  
OX NCBI\_TaxID=49735;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Popp M.; Oxelman B.;  
RT "Inferring the history of the polyploid silene aegaea  
(Caryophyllaceae) using nuclear and chloroplast DNA sequence data."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296133; CAC13025.1; -  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1108 MW; CFIAB6D1B2CAB1A9 CRC64;

Query Match  
Best Local Similarity 30.0%; Score 3; DB 10; Length 10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5  
DB 2 PPT 4

RESULT 6  
Q91W23 ID Q91W23 PRELIMINARY; PRT; 10 AA.  
AC Q91W23;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Luteinizing hormone/chorionic gonadotropin receptor homolog  
(Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=96147985; PubMed=8571710;  
RA Shen Q.X., Liu H.H., Chen W.Y., Bahl O.P.;  
RT "[Cloning and overexpression of rat ovary LH/hCG receptor cDNA in  
insect cells]."  
RL Shih Yen Sheng Wu Heuh Pao 28:283-290(1995).  
DR EMBL; S80660; AAB50710.1; -  
KW Chorion; Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 10 AA; 1129 MW; 09A5F2DC417760 CRC64;

Query Match  
Best Local Similarity 30.0%; Score 3; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIP 9  
DB 2 PIP 4

RESULT 7  
Q9N2B9 ID Q9N2B9 PRELIMINARY; PRT; 12 AA.  
AC Q9N2B9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Indolethylamine N-methyltransferase (Fragment).  
GN INMT.  
OS Gorilla gorilla (gorilla).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
OX NCBI\_TaxID=9593;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=gorilla-UL;  
RA Kitano T., Kobayakawa H., Saitou N.;  
RT "Silver Project."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB041364; BAA94453.1; -  
KW Methyltransferase; Transferase.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 3; DB 6; Length 12;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
DB 5 FTG 7

RESULT 8  
Q9N2B8 ID Q9N2B8 PRELIMINARY; PRT; 12 AA.  
AC Q9N2B8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Indolethylamine N-methyltransferase (Fragment).  
GN INMT.  
OS Pongo pygmaeus (Orangutan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
OX NCBI\_TaxID=9600;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=oran-Pol3;  
RA Kitano T., Kobayakawa H., Saitou N.;  
RT "Silver Project."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB041365; BAA94454.1; -  
KW Methyltransferase; Transferase.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1290 MW; CF079554917861A9 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 3; DB 6; Length 12;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
DB 5 FTG 7

RESULT 9  
Q9N2C0 PRELIMINARY; PRT; 12 AA.  
AC Q9N2C0;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Indolethylamine N-methyltransferase (Fragment).  
GN INMT.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=chimp-220;  
RA Kitano T., Kobayakawa H., Saitou N.;  
RT "Silver Project";  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB041363; BAA94452.1; -;  
KW Methyltransferase; Transferase.  
FT NON TER 12  
SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;  
Query Match 30.0%; Score 3; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 FTG 6  
DB 5 FTG 7  
RESULT 10  
Q9SYT4 PRELIMINARY; PRT; 12 AA.  
AC Q9SYT4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Pathogenesis related protein 1 (Fragment).  
GN PR1.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=99056846; PubMed=9839467;  
RA Lebel E., Heifetz P., Thorne L., Uknes S., Ryals J., Ward E.;  
RT "Functional analysis of regulatory sequences controlling PR-1 gene expression in Arabidopsis";  
RL Plant J. 16:223-233(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Neuenschwander U., Maleck K., Chandler D., Lebel E., Ward E.,  
RA Ryals J.;  
RT "In vivo monitoring of SAR gene expression";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF096294; AAD0988.1; -;  
FT NON TER 12  
SQ SEQUENCE 12 AA; 1448 MW; 2992D580ED15AB58 CRC64;  
Query Match 30.0%; Score 3; DB 10; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 FTG 6  
DB 5 FTG 7

Db 3 FTG 5  
RESULT 11  
Q9FSA9 PRELIMINARY; PRT; 12 AA.  
AC Q9FSA9;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene aegaea.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
OX NCBI\_TaxID=49732;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Popp M., Oxelman B.;  
RT "Inferring the history of the polyploid Silene aegaea  
(Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296130; CAC13014.1; -;  
FT NON TER 12  
SQ SEQUENCE 12 AA; 1304 MW; 83269695B41B2CA CRC64;  
Query Match 30.0%; Score 3; DB 10; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 FTG 5  
DB 2 FTG 4  
RESULT 12  
Q8WEKO PRELIMINARY; PRT; 13 AA.  
AC Q8WEKO;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE NADH dehydrogenase (Fragment).  
GN NAD1.  
OS Cycas circinalis.  
OG Mitochondrion.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Cycadophyta; Cycadales; Cycadaceae; Cycas.  
OX NCBI\_TaxID=3397;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21555473; PubMed=11697913;  
RA Gugerli F., Sperisen C., Buchler U., Brunner I., Brodbeck S.,  
RA Palmer J.D., Qiu Y.L.;  
RT "The evolutionary split of pinaceae from other conifers: evidence from  
an intron loss and a multigene phylogeny";  
RL Mol. Phylogenet. Evol. 21:167-175(2001).  
DR EMBL; AF227465; AAL38909.1; -;  
KW Mitochondrion.  
FT NON TER 13  
SQ SEQUENCE 13 AA; 1393 MW; C00F6BDAB94945BD CRC64;  
Query Match 30.0%; Score 3; DB 8; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GPI 8  
DB 9 GPI 11

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RESULT 13
Q9FSA8      PRELIMINARY;      PRT;      13 AA.
AC Q9FSA8;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene baccifera (Berry catchfly) (Cucubalus baccifer).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=54818;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296139; CAC13015.1; --
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1437 MW; D931E2CFIAB6D1B2 CRC64;

Query Match      30.0%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5
Db 2 PPT 4

RESULT 14
Q9FS94      PRELIMINARY;      PRT;      13 AA.
AC Q9FS94;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene pentelica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49735;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296132; CAC13024.1; --
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1437 MW; D931E2CFIAB6D1B2 CRC64;

Query Match      30.0%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5
Db 2 PPT 4

RESULT 15
P90442      PRELIMINARY;      PRT;      13 AA.
ID P90442
AC P90442;

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DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Polyhedrin (Fragment).
OS Spodoptera littoralis nuclear polyhedrosis virus (SLNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10456;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E15;
RX MEDLINE=97300849; PubMed=9155869;
RA Faktor O., Tolster-Achituv M., Nachum O.;
RT "Enhancer element, repetitive sequences and gene organization in an 8-
RT kbp region containing the polyhedrin gene of the Spodoptera littoralis
RT nucleopolyhedrovirus.";
RL Arch. Virol. 142:11-15 (1997).
DR EMBL; X99711; CAA68046.1; --
DR InterPro; IPR001746; Polyhedrin.
DR Pfam; PF00738; Polyhedrin; 1.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1383 MW; 2B0CD62832655737 CRC64;

Query Match      30.0%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
Db 9 TGP 11

RESULT 16
Q8KSE3      PRELIMINARY;      PRT;      14 AA.
ID Q8KSE3;
AC Q8KSE3;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE Truncated protein kinase.
GN VANS.
OS Enterococcus faecium (Streptococcus faecium).
OG Plasmid pUW786.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1352;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UW786;
RA Werner G., Klare I., Witte W.;
RT "Multi-resistance gene cluster on a plasmid in a clinical isolate of
RT Enterococcus faecium.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516335; AAU77883.1; --
KW Kinase; Plasmid.
SQ SEQUENCE 14 AA; 1628 MW; 0AAE44BCDE720A34 CRC64;

Query Match      30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IPN 10
Db 12 IPN 14

RESULT 17
Q8J1G5      PRELIMINARY;      PRT;      14 AA.
ID Q8J1G5;
AC Q8J1G5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE YLR191 (Fragment).

```

GN YLR191.  
OS Ashbya gossypii (Brethothecium gossypii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Ashbya.  
OX NCBI\_TaxID=33169;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alberti-Segui C., Dietrich F., Philippsen P.;  
RT "Identification of kinesin-related proteins in the filamentous fungus  
RT Ashbya gossypii".  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF378569; AAN87136.1; -  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1205 MW; 36967F5A00467868 CRC64;  
Query Match 30.0%; Score 3; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 TGP 7  
DB 6 TGP 8  
RESULT 18  
Q9FS95 PRELIMINARY; PRT; 14 AA.  
AC Q9FS95;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene pentelica.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
OX NCBI\_TaxID=49735;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Popp M., Oxelman B.;  
RT "Inferring the history of the polyploid Silene aegaea  
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296131; CAC13023.1; -  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1508 MW; 980931E2CF1AB6D1 CRC64;  
Query Match 30.0%; Score 3; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PPT 5  
DB 2 PPT 4  
RESULT 19  
Q9FSB1 PRELIMINARY; PRT; 14 AA.  
AC Q9FSB1;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene aegaea.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
OX NCBI\_TaxID=49732;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Popp M., Oxelman B.;  
RT "Inferring the history of the polyploid Silene aegaea  
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296131; CAC13023.1; -  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1508 MW; 980931E2CF1AB6D1 CRC64;  
Query Match 30.0%; Score 3; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PPT 5  
DB 2 PPT 4  
RESULT 20  
Q9FS91 PRELIMINARY; PRT; 14 AA.  
AC Q9FS91;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene sedoides.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
OX NCBI\_TaxID=39790;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Popp M., Oxelman B.;  
RT "Inferring the history of the polyploid Silene aegaea  
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296105; CAC13028.1; -  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1508 MW; 980931E2CF1AB6D1 CRC64;  
Query Match 30.0%; Score 3; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PPT 5  
DB 2 PPT 4  
RESULT 21  
P83291 PRELIMINARY; PRT; 14 AA.  
AC P83291;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Unknown mitochondrial protein At5g20080 (Fragment).  
OS Arabidopsis thaliana (Mouse-ear cress).  
GN Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE, AND SUBCELLULAR LOCATION.  
RC TISSUE=Leaf, and Stem;  
RX MEDLINE=21608403; PubMed=11743114;  
RA Kruft V., Eubel H., Jaensch L., Werhahn W., Braun H.-P.;  
RT "Proteomic approach to identify novel mitochondrial proteins in

RP SEQUENCE FROM N.A.  
RA Popp M., Oxelman B.;  
RT "Inferring the history of the polyploid Silene aegaea  
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296122; CAC13007.1; -  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1508 MW; 980931E2CF1AB6D1 CRC64;  
Query Match 30.0%; Score 3; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PPT 5  
DB 2 PPT 4  
RESULT 20  
Q9FS91 PRELIMINARY; PRT; 14 AA.  
AC Q9FS91;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene sedoides.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
OX NCBI\_TaxID=39790;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Popp M., Oxelman B.;  
RT "Inferring the history of the polyploid Silene aegaea  
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296105; CAC13028.1; -  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1508 MW; 980931E2CF1AB6D1 CRC64;  
Query Match 30.0%; Score 3; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PPT 5  
DB 2 PPT 4  
RESULT 21  
P83291 PRELIMINARY; PRT; 14 AA.  
AC P83291;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Unknown mitochondrial protein At5g20080 (Fragment).  
OS Arabidopsis thaliana (Mouse-ear cress).  
GN Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE, AND SUBCELLULAR LOCATION.  
RC TISSUE=Leaf, and Stem;  
RX MEDLINE=21608403; PubMed=11743114;  
RA Kruft V., Eubel H., Jaensch L., Werhahn W., Braun H.-P.;  
RT "Proteomic approach to identify novel mitochondrial proteins in

```
RT Arabidopsis.";
RL Plant Physiol. 127:1694-1710(2001).
CC -I- SUBCELLULAR LOCATION: MITOCHONDRIAL INTERMEMBRANE SPACE.
KW Mitochondrion.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1502 MW; 85036436E2263C61 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
DB 7 TGP 9

RESULT 22
Q8JDM3 PRELIMINARY; PRT; 14 AA.
AC Q8JDM3;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Truncated tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=patient Q168;
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandalika K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5 Coreceptor for Entry, Regardless of the Genetic Complexity of the Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR EMBL; AF407149; AAM66202.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
DB 10 TGP 12

RESULT 23
Q8JDM7 PRELIMINARY; PRT; 14 AA.
AC Q8JDM7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Truncated tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=patient Q168;
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandalika K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5 Coreceptor for Entry, Regardless of the Genetic Complexity of the Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR EMBL; AF407148; AAM66198.1; -.
FT NON_TER 1 1
```

```
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
DB 10 TGP 12

RESULT 24
Q8JDM0 PRELIMINARY; PRT; 14 AA.
AC Q8JDM0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Truncated tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=patient Q168;
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandalika K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5 Coreceptor for Entry, Regardless of the Genetic Complexity of the Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR EMBL; AF407150; AAM66205.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
DB 10 TGP 12

RESULT 25
Q9RAM8 PRELIMINARY; PRT; 15 AA.
AC Q9RAM8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Catalase isozyme I (Fragment).
OS Bacillus firmus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1399;
RN [1]_TaxID=1399;
RP SEQUENCE.
RX MEDLINE=95267795; PubMed=7748885;
RA Hicks D.B.;
RT "Purification of three catalase isozymes from facultatively alkaliphilic Bacillus firmus OF4.";
RL Biochim. Biophys. Acta 1229:347-355(1995).
SQ SEQUENCE 15 AA; 1677 MW; 12E47DC8F66876ED CRC64;

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5
DB 13 PPT 15
```

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RESULT 26
Q05463 ID O05463 PRELIMINARY; PRT; 15 AA.
AC O05463;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ammonia monooxygenase subunit AmoC1 (Fragment).
GN AMOC1.
OS Nitrosospirilla multiformis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosospirilla.
OX NCBI_TaxID=1231;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC25196;
RA Norton J.M., Alzerreca J., Klotz M.G.;
RT "The ammonia monooxygenase operon in Nitrosolobus multiformis.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U91603; AAB51758.1; -.
KW Monooxygenase.
FT NON TER 1
SQ SEQUENCE 15 AA; 1774 MW; 030B7989F128A467 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IPN 10
DB 3 IPN 5

RESULT 27
Q09UC2 ID Q09UC2 PRELIMINARY; PRT; 15 AA.
AC Q09UC2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 35 kDa heparin-RELEASABLE protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94059921; PubMed=8241100;
RA Novotny W.F., Maffei T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the
RT cytokines midkine and pleiotrophin, in human postheparin plasma.";
RL Arterioscler. Thromb. 13:1798-1805(1993).
SQ SEQUENCE 15 AA; 1454 MW; 0585FEF4FE8F6265 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIP 9
DB 7 PIP 9

RESULT 28
P81831 ID P81831 PRELIMINARY; PRT; 15 AA.
AC P81831;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Phosphoenolpyruvate carboxylase 2 (EC 4.1.1.31) (PEPCase) (PEPC
(Fragment)).
```

```
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE.
RC STRAIN=cw15;
RX PubMed=9512480;
RA Rivoal J., Plaxton W.C., Turpin D.H.;
RT "Purification and characterization of high- and low-molecular-mass
RT isoforms of phosphoenolpyruvate carboxylase from Chlamydomonas
RT reinhardtii. Kinetic, structural and immunological evidence that the
RT green algal enzyme is distinct from the prokaryotic and higher plant
RT enzymes.";
RL Biochem. J. 331:201-209(1998).
CC -|- FUNCTION: TO FORM OXALOACETATE, A FOUR-CARBON DICARBOXYLIC ACID
CC -|- SOURCE FOR THE TRICARBOXYLIC ACID CYCLE (BY SIMILARITY).
CC -|- CATALYTIC ACTIVITY: PHOSPHATE + OXALOACETATE = H(2)O +
CC PHOSPHOENOLPYRUVATE + CO(2).
CC -|- ENZYME REGULATION: ACTIVATED BY GLUTAMINE AND DIHYDROXYACETONE
CC PHOSPHATE. INHIBITED BY GLUTAMATE, ASPARTATE, 2-OXOGLUTARATE AND
CC MALATE.
CC -|- PATHWAY: TRICARBOXYLIC ACID CYCLE.
CC -|- SUBUNIT: EXISTS AS A HOMOTETRAMER OR HETEROLIGOMER.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -|- MISCELLANEOUS: OPTIMUM PH IS 8.1.
CC -|- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
DR InterPro; IPR001449; PEPCase.
DR PROSITE; PS00781; PEPCASE_1; PARTIAL.
DR PROSITE; PS00393; PEPCASE_2; PARTIAL.
KW Lyase; Carbon dioxide fixation; Allosteric enzyme;
KW Tricarboxylic acid cycle.
FT NON TER 15
SQ SEQUENCE 15 AA; 1660 MW; D760F1F67301D418 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
DB 5 TGP 7

RESULT 29
Q9FSA5 ID Q9FSA5 PRELIMINARY; PRT; 15 AA.
AC Q9FSA5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene cryptoneura.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Caryophyllaceae; Silene.
OX NCBI_TaxID=39877;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296138; CAC13016.1; -.
FT NON TER 1
FT NON TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931B2CFLAB6 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



Query Match 30.0%; Score 3; DB 10; Length 15  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels

Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFT 5  
|||  
Db 2 PFT 4

## RESULT 34

Q9FS99 PRELIMINARY; PRT; 15 AA.  
AC Q9FS99; (Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene integrifolia.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllaceae; Silene.  
OC NCBI\_TaxID=39889;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Popp M., Oxelman B.;  
RT "Inferring the history of the polyploid Silene aegaea  
(Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296112; CAC13035.1; -  
FT NON\_TER 1 15  
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFT 5  
|||  
Db 2 PFT 4

## RESULT 35

Q9FE15 PRELIMINARY; PRT; 15 AA.  
AC Q9FE15;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene sedoides.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllaceae; Silene.  
OC NCBI\_TaxID=39790;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Popp M., Oxelman B.;  
RT "Inferring the history of the polyploid Silene aegaea  
(Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296112; CAC13035.1; -  
DR EMBL; AJ296104; CAC13027.1; -  
DR EMBL; AJ296106; CAC13029.1; -  
DR EMBL; AJ296107; CAC13030.1; -  
DR EMBL; AJ296108; CAC13031.1; -  
DR EMBL; AJ296109; CAC13032.1; -  
DR EMBL; AJ296110; CAC13033.1; -  
DR EMBL; AJ296111; CAC13034.1; -  
FT NON\_TER 1 15  
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFT 5  
|||  
Db 2 PFT 4

## RESULT 36

Q9S929 PRELIMINARY; PRT; 15 AA.  
AC Q9S929;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Pyroline-5-carboxylate reductase, PSOR (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OC NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91378472; PubMed=1898034;  
RA Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;  
RT "Pyroline-5-carboxylate reductase in soybean nodules:  
isolation/partial primary structure/evidence for isozymes.";  
RL Arch. Biochem. Biophys. 288:350-357(1991).  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1715 MW; D9821F773F3DF524 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIP 9  
|||  
Db 5 PIP 7

## RESULT 37

Q9FE14 PRELIMINARY; PRT; 15 AA.  
AC Q9FE14;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene pentelica.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllaceae; Silene.  
OC NCBI\_TaxID=49735;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Popp M., Oxelman B.;  
RT "Inferring the history of the polyploid Silene aegaea  
(Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296134; CAC13026.1; -  
DR EMBL; AJ296129; CAC13022.1; -  
FT NON\_TER 1 15  
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFT 5  
|||  
Db 2 PFT 4

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RESULT 38
Q9FS80 PRELIMINARY; PRT; 15 AA.
AC Q9FS80;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene zawadskii (Zawadskii's campion).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39923;
RN [1]_TaxID=39923;
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
(R Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296141; CAC13039.1; -
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CFIAB6 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFT 5
   |||
DB 2 PFT 4

RESULT 39
Q9FS80 PRELIMINARY; PRT; 15 AA.
AC Q9FS80;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene aegaea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49732;
RN [1]_TaxID=49732;
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
(R Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296124; CAC13009.1; -
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1616 MW; C96B0931E2CFOAF6 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFT 5
   |||
DB 2 PFT 4

RESULT 40
Q9QV00 PRELIMINARY; PRT; 15 AA.
ID Q9QV00

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AC Q9QV00;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Eosinophil cationic protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]_TaxID=10118;
RP SEQUENCE.
RA MEDLINE=95375557; PubMed=7647580;
RA Watanabe M., Nittoh T., Suzuki T., Kitoh A., Mue S., Ohuchi K.;
RT "Isolation and partial characterization of eosinophil granule proteins
in rats-eosinophil cationic protein and major basic protein.";
RL Int. Arch. Allergy Immunol. 108:11-18(1995).
SQ SEQUENCE 15 AA; 1785 MW; 2AF6D99C12BED794 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6
   |||
DB 6 FTG 8

RESULT 41
Q90594 PRELIMINARY; PRT; 15 AA.
ID Q90594;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Globin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RA MEDLINE=81261952; PubMed=6266925;
RA Padavatty J., Cummings I., Manske C.L., Higuchi R., Woo S., Salser W.;
RT "Cloning of chicken globin cDNA in bacterial plasmids.";
RL Gene 13:417-422(1981).
DR EMBL; M10380; AAA48803.1; -
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1881 MW; 23E61DA734PA7962 CRC64;

Query Match 30.0%; Score 3; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYP 3
   |||
DB 6 VYP 8

RESULT 42
Q9F1S7 PRELIMINARY; PRT; 16 AA.
ID Q9F1S7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphoribosyl carboxyamide aminimidazole transformylase (EC 6.3.2.6)
   (Fragment).
GN PURH.
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.

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OX NCBI_TaxID=1307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=205;
RX MEDLINE=20576151; PubMed=11133943;
RA Sekizaki T., Otani Y., Osaki M., Takamatsu D., Shimoji Y.;
RT "Evidence for horizontal transfer of the SsuDATII restriction-
RL modification genes to the Streptococcus suis genome.";
RL J. Bacteriol. 183:500-511(2001).
RW EMBL; AB045610; BAB20834.1; -.
KW Ligase.
FT NON TER
SQ SEQUENCE 16 AA; 1935 MW; 1FC8DB8BAE391D40 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6
DB 8 FTG 10

RESULT 43
Q9F1S4 PRELIMINARY; PRT; 16 AA.
AC Q9F1S4
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Phosphoribosyl carboxyamido aminimidazole transformylase (EC 6.3.2.6)
DE (Fragment).
GN PURH.
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=220;
RX MEDLINE=20576151; PubMed=11133943;
RA Sekizaki T., Otani Y., Osaki M., Takamatsu D., Shimoji Y.;
RT "Evidence for horizontal transfer of the SsuDATII restriction-
RL modification genes to the Streptococcus suis genome.";
RL J. Bacteriol. 183:500-511(2001).
RW EMBL; AB045612; BAB20838.1; -.
KW Ligase.
FT NON TER
SQ SEQUENCE 16 AA; 1949 MW; 6978DB8BAE391D44 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6
DB 8 FTG 10

RESULT 44
Q9TWK1 PRELIMINARY; PRT; 16 AA.
AC Q9TWK1
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE Proximal collagen (Fragment).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.

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RX MEDLINE=95230211; PubMed=7714453;
RA Qin X., Waite J.H.;
RT "Exotic collagen gradients in the byssus of the mussel Mytilus
RT edulis.";
RL J. Exp. Biol. 198:633-644(1995).
SQ SEQUENCE 16 AA; 1418 MW; 72887820BC282660 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
DB 10 TGP 12

RESULT 45
Q8MIB2 PRELIMINARY; PRT; 16 AA.
AC Q8MIB2
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Ribosomal protein S4, X isoform (Fragment).
GN RPS4X.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Cepica S., Masopust M., Rohrer G.A.;
RT "Detailed mapping of porcine chromosome X region harbouring QTL for
RT fatness.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AJ429141; CAD22105.1; -.
FT NON TER
FT NON TER
SQ SEQUENCE 16 AA; 1749 MW; 55CE50FC71A4F4B8 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
DB 9 TGP 11

RESULT 46
Q34699 PRELIMINARY; PRT; 16 AA.
AC Q34699
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cob protein (Fragment).
GN COB.
OS Helianthus annuus (Common sunflower).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Asteroidae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CMSBASO;
RA Koehler R.H.;
RL Submitted (OCT-1991) to the EMBL/GenBank/DBSJ databases.
DR EMBL; X62592; CAA44477.1; -.
KW Mitochondrion.
FT NON TER

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SQ SEQUENCE 16 AA; 1990 MW; A2980BEE7E26E700 CRC64;

Query Match 30.0%; Score 3; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IPN 10

Db |||  
1 IPN 3

RESULT 47

Q8HU42 ID Q8HU42 PRELIMINARY; PRT; 16 AA.

AC Q8HU42;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Feba (Fragment).

OS Passiflora elegans.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC euboids 1; Malpighiales; Passifloraceae; Passiflora.

OX NCBI\_TaxID=159423;

RN [1]

RP SEQUENCE FROM N.A.

RA Muschner V.C., Lorenz A.P., Scherer N.M., Souza-Chies T.T.,

RA Cervi A.C., Salzano F.M., Bonatto S.L., Freitas L.B.;

RT "Comparative Phylogenetic Analysis of Nuclear and Plastid Sequences in

RT Passiflora (Passifloraceae).";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AV032806; AAK69782.1; -.

KW Chloroplast.

FT NON\_TER 1 1

SQ SEQUENCE 16 AA; 1676 MW; 4A810A81DD549D80 CRC64;

Query Match 30.0%; Score 3; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5

Db |||  
12 PPT 14

RESULT 48

Q8HU29 ID Q8HU29 PRELIMINARY; PRT; 16 AA.

AC Q8HU29;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Feba (Fragment).

OS Passiflora haematostigma.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC euboids 1; Malpighiales; Passifloraceae; Passiflora.

OX NCBI\_TaxID=159429;

RN [1]

RP SEQUENCE FROM N.A.

RA Muschner V.C., Lorenz A.P., Scherer N.M., Souza-Chies T.T.,

RA Cervi A.C., Salzano F.M., Bonatto S.L., Freitas L.B.;

RT "Comparative Phylogenetic Analysis of Nuclear and Plastid Sequences in

RT Passiflora (Passifloraceae).";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AV032819; AAK69795.1; -.

KW Chloroplast.

FT NON\_TER 1 1

SQ SEQUENCE 16 AA; 1676 MW; 4A810A81DD549D80 CRC64;

Query Match 30.0%; Score 3; DB 8; Length 16;

Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPT 5

Db |||  
12 PPT 14

RESULT 49

Q55091 ID Q55091 PRELIMINARY; PRT; 17 AA.

AC Q55091;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Beta-lactamase (Fragment).

GN AMPC.

OS Shigella sonnei.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Shigella.

OX NCBI\_TaxID=624;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=OS10;

RX MEDLINE=84170267; PubMed=6369321;

RT "ampC beta-lactamase hyperproduction in Escherichia coli: Natural

RT ampicillin resistance generated by horizontal chromosomal DNA transfer

RL from Shigella.";

RL Proc. Natl. Acad. Sci. U.S.A. 80:7556-7560 (1983).

DR EMBL; K01234; AAA26514.1; -.

DR InterPro; IPR001586; Beta lactamase C.

DR PROSITE; PS00336; BETA\_LACTAMASE\_C; 1.

FT NON\_TER 1 1

FT NON\_TER 17 17

SQ SEQUENCE 17 AA; 1756 MW; 7FAC3A40A4809623 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6

Db |||  
12 FTG 14

RESULT 50

P83488 ID P83488 PRELIMINARY; PRT; 17 AA.

AC P83488;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Exochitosanase (EC 3.2.1.-) (Exo-beta-D-glucosaminidase)

DE (Fragment).

OS Aspergillus flavus.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OX NCBI\_TaxID=5059;

RN [1]

RP SEQUENCE, AND FUNCTION.

RC STRAIN=IAM 2044;

RA Ji J.-H., Hur J.-W.;

RT "Purification and characterization of the exo-beta-D-glucosaminidase

RT from the fungus, A. flavus IAM2044.";

RL Appl. Microbiol. Biotechnol. 0:0-0 (2002).

CC -!- FUNCTION: EXOHYDROLYSIS OF BETA-1,4-LINKAGES BETWEEN N-ACETYL-D-

CC GLUCOSAMINE AND D-GLUCOSAMINE RESIDUES, AND D-GLUCOSAMINE AND D-

CC GLUCOSAMINE RESIDUES IN CHITOSAN.

KW Hydrolase; Glycosidase.

FT NON\_TER 17 17

SQ SEQUENCE 17 AA; 1754 MW; F07B490F070D7C70 CRC64;

Query Match 30.0%; Score 3; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
DB 3 TGP 5

RESULT 51  
Q9UCT3 PRELIMINARY; PRT; 17 AA.  
AC Q9UCT3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE ALZHEIMER'S beta-amyloid precursor protein, kunitz-type protease  
inhibitor, neutrophil elastase inhibitor, P1-VAL-APP-KD  
(Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92041969; PubMed=1939150;  
RA Sinha S., Knops J., Esch F., Moyer E.D., Oltersdorf T.;  
RT "Conversion of the Alzheimer's beta-amyloid precursor protein (APP)  
Kunitz domain into a potent human neutrophil elastase inhibitor.";  
RL J. Biol. Chem. 266:21011-21013(1991).  
FT NON\_TER 1 1  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1778 MW; F0CCDC28D6712BA CRC64;

Query Match 30.0%; Score 3; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
DB 10 TGP 12

RESULT 52  
Q9UM85 PRELIMINARY; PRT; 17 AA.  
AC Q9UM85;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Beta-globin protein (Fragment).  
GN BETA-GLOBIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96352914; PubMed=8718696;  
RA Rahbar S., Nozari G., Forrest G., Gelbart T., Forman S.J., Beutler E.;  
RT "A novel intrachromosomal rearrangement in the beta-globin gene found  
in an African-American family.";  
RL Hemoglobin 19:375-388(1995).  
DR EMBL; S82767; AAD14420.1; -.  
DR HSSP; P02023; 1ABW.  
FT NON\_TER 1 1  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 2104 MW; 419775BE5260504 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYP 3

Db 4 VYP 6

RESULT 53  
Q9TWB9 PRELIMINARY; PRT; 17 AA.  
AC Q9TWB9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE PROFILIN-binding cortical COMPLEX-18 kDa polypeptide (Fragment).  
OS Acanthamoeba castellanii (Amoeba).  
OC Eukaryota; Acanthamoebidae; Acanthamoeba.  
OX NCBI\_TaxID=5755;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95014701; PubMed=7929556;  
RA Machesky L.M., Atkinson S.J., Ampe C., Vandekerckhove J.,  
Pollard T.D.;  
RT "Purification of a cortical complex containing two unconventional  
RT actins from Acanthamoeba by affinity chromatography on profilin-  
agarose.";  
RL J. Cell Biol. 127:107-115(1994).  
FT NON\_TER 1 1  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1875 MW; 7260445CDF5AE78B CRC64;

Query Match 30.0%; Score 3; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
DB 2 TGP 4

RESULT 54  
O46473 PRELIMINARY; PRT; 17 AA.  
ID O46473;  
AC O46473;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Lactase dehydrogenase A (Fragment).  
GN LDHA.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=domesticus;  
RX MEDLINE=97141918; PubMed=8988168;  
RA Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,  
O'Brien S.J.;  
RT "Comparative anchor tagged sequences (CATS) for integrative mapping of  
mammalian genomes.";  
RL Nat. Genet. 15:47-56(1997).  
DR EMBL; AF012095; AAC00072.2; -.  
FT NON\_TER 1 1  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 2018 MW; E47943B2E187C1FC CRC64;

Query Match 30.0%; Score 3; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IDN 10  
DB 14 IDN 16

```
RESULT 55
Q9TRY8 PRELIMINARY; PRT; 17 AA.
AC Q9TRY8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Insulin-like growth factor-binding protein-3, IGFBP-3 (Fragment).
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; PubMed=1719383;
RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1618 MW; 14B17C38D32A400F CRC64;

Query Match 30.0%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
Db 7 TGP 9

RESULT 56
Q9QUW6 PRELIMINARY; PRT; 17 AA.
AC Q9QUW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Collagen-like heparin-binding glycoprotein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96278823; PubMed=8662884;
RA Chernousov M.A., Stahl R.C., Carey D.J.;
RT "Schwann cells secrete a novel collagen-like adhesive protein that
RT binds N-syndecan.";
RL J. Biol. Chem. 271:13844-13853(1996).
SQ SEQUENCE 17 AA; 1485 MW; 49EC70BA9220BEE3 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPI 8
Db 7 GPI 9

RESULT 57
Q9QEY2 PRELIMINARY; PRT; 17 AA.
AC Q9QEY2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21103026; PubMed=1170057;
RA Lin H.J., Siwak E.B., Lauder I.J., Hollinger F.B.;
RT "Long-term culture of human immunodeficiency virus type 1 resulting in
RT loss of glycosylation sites.";
RL J. Med. Virol. 63:197-202(2001).
DR EMBL; AF178659; AAF04364.1; -.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
KW NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1793 MW; 3DF87B6C850AE665 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
Db 4 TGP 6

RESULT 58
Q9QEV1 PRELIMINARY; PRT; 17 AA.
AC Q9QEV1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21103026; PubMed=1170057;
RA Lin H.J., Siwak E.B., Lauder I.J., Hollinger F.B.;
RT "Long-term culture of human immunodeficiency virus type 1 resulting in
RT loss of glycosylation sites.";
RL J. Med. Virol. 63:197-202(2001).
DR EMBL; AF178659; AAF04365.1; -.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
KW NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1793 MW; 3DF87B6C850AE665 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
Db 4 TGP 6

RESULT 59
Q9R4C3 PRELIMINARY; PRT; 18 AA.
AC Q9R4C3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Protocatechuate 3,4-dioxygenase type I beta subunit (EC 1.13.11.3)
DE (Fragment).
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
```

```
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21103026; PubMed=1170057;
RA Lin H.J., Siwak E.B., Lauder I.J., Hollinger F.B.;
RT "Long-term culture of human immunodeficiency virus type 1 resulting in
RT loss of glycosylation sites.";
RL J. Med. Virol. 63:197-202(2001).
DR EMBL; AF178658; AAF04364.1; -.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
KW NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1793 MW; 3DF87B6C850AE665 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
Db 4 TGP 6

RESULT 58
Q9QEV1 PRELIMINARY; PRT; 17 AA.
AC Q9QEV1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21103026; PubMed=1170057;
RA Lin H.J., Siwak E.B., Lauder I.J., Hollinger F.B.;
RT "Long-term culture of human immunodeficiency virus type 1 resulting in
RT loss of glycosylation sites.";
RL J. Med. Virol. 63:197-202(2001).
DR EMBL; AF178659; AAF04365.1; -.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
KW NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1793 MW; 3DF87B6C850AE665 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7
Db 4 TGP 6

RESULT 59
Q9R4C3 PRELIMINARY; PRT; 18 AA.
AC Q9R4C3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Protocatechuate 3,4-dioxygenase type I beta subunit (EC 1.13.11.3)
DE (Fragment).
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
```

OX NCBI\_TaxID=358;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=96337865; PubMed=8772173;  
 RA Hammer A., Stolz A., Knackmuss H.;  
 RT "Purification and characterization of a novel type of protocatechuate  
 RT 3,4-dioxygenase with the ability to oxidize 4-sulfocatechol.";  
 RL Arch. Microbiol. 166:92-100(1996).  
 SQ SEQUENCE 18 AA; 2008 MW; C7EBD971BBE5BBE9 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
 Db |||  
 7 TGP 9

RESULT 60  
 Q9BU72 PRELIMINARY; PRT; 18 AA.  
 ID Q9BU72  
 AC Q9BU72;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002861; AA002861.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 18 AA; 2064 MW; 371B21FD1E289B18 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYP 3  
 Db |||  
 12 VYP 14

RESULT 61  
 Q28069 PRELIMINARY; PRT; 18 AA.  
 ID Q28069  
 AC Q28069;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)  
 DE Alpha-si-casein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Maki M., Nagao M., Hirose M., Chiba H.;  
 RT "Cloning of cDNA sequence coding for bovine alpha-si-casein.";  
 RL Agric. Biol. Chem. 47:441-444(1983).  
 DR EMBL; D00412; BAA00313.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 18 AA; 1880 MW; 8DEDC1740674108C CRC64;

Query Match 30.0%; Score 3; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IPN 10  
 Db |||  
 13 IPN 15

RESULT 62  
 Q9FSB3 PRELIMINARY; PRT; 18 AA.  
 ID Q9FSB3  
 AC Q9FSB3;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2.  
 OS Silene aegaea.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=49732;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296114; CAC12999.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 18 AA; 1969 MW; FA34E03ABD9CCC2A CRC64;

Query Match 30.0%; Score 3; DB 10; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFT 5  
 Db |||  
 2 PFT 4

RESULT 63  
 Q39829 PRELIMINARY; PRT; 18 AA.  
 ID Q39829  
 AC Q39829;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Lipoxigenase (Fragment).  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Ransom;  
 RX MEDLINE=96151505; PubMed=8587989;  
 RA Saravitz D.M., Siedow J.N.;  
 RT "The differential expression of wound-inducible lipoxigenase genes in  
 RT soybean leaves.";  
 RL Plant Physiol. 110:287-299(1996).  
 DR EMBL; U36442; AAC49161.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 18 AA; 1850 MW; F372E98F9F99240F CRC64;

Query Match 30.0%; Score 3; DB 10; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IPN 10



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Db      12 IPN 14
|||
RESULT 64
QBRL70  PRELIMINARY;      PRT;      18 AA.
AC QBRL70;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 2.2 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025130; AAH25130.1;
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2156 MW; 0CA09EB94C27668D CRC64;

Query Match      30.0%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PFT 5
      |||
Db      11 PFT 13

RESULT 65
Q9R4D8  PRELIMINARY;      PRT;      19 AA.
AC Q9R4D8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DEXTRANICIN 24 (Fragment).
OS Leuconostoc mesenteroides.
OC Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
OX NCBI_TaxID=1245;
RN [1]_TaxID=1245;
RP SEQUENCE.
RX MEDLINE=96281532; PubMed=8662187;
RA Revol-Junelles A.M., Lefebvre G.;
RT "Purification and N-terminal amino acid sequence of dextranin 24, a
RT bacteriocin of Leuconostoc sp.".
RL Curr. Microbiol. 33:136-137(1996).
SQ SEQUENCE 19 AA; 1931 MW; BACA1B2DF098B100 CRC64;

Query Match      30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TGP 7
      |||
Db      15 TGP 17

RESULT 66
Q9TWG5  PRELIMINARY;      PRT;      19 AA.
AC Q9TWG5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Alpha-latrotoxin-associated LOW molecular weight protein 2 (Fragment).
OS Latrodectus mactans (Black widow spider).

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OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneioidea; Theridiidae; Latrodectus.
OX NCBI_TaxID=6924;
RN [1]_TaxID=6924;
RP SEQUENCE.
RX MEDLINE=96018131; PubMed=75706333;
RA Volkova T.M., Pluzhnikov K.A., Woll P.G., Grishin E.V.;
RT "Low molecular weight components from black widow spider venom.";
RL Toxicon 33:483-489(1995).
SQ SEQUENCE 19 AA; 2419 MW; E310A821C2ED1A85 CRC64;

Query Match      30.0%; Score 3; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PFT 5
      |||
Db      3 PFT 5

RESULT 67
Q9TWJ8  PRELIMINARY;      PRT;      19 AA.
AC Q9TWJ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Proximal collagen (Fragment).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]_TaxID=6550;
RP SEQUENCE.
RX MEDLINE=952320211; PubMed=7714453;
RA Qin X., Waite J.H.;
RT "Exotic collagen gradients in the byssus of the mussel Mytilus
RT edulis.".
RL J. Exp. Biol. 198:633-644(1995).
SQ SEQUENCE 19 AA; 1605 MW; 8DC1622B63973220 CRC64;

Query Match      30.0%; Score 3; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GPI 8
      |||
Db      1 GPI 3

RESULT 68
Q9S8G6  PRELIMINARY;      PRT;      19 AA.
AC Q9S8G6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Type 2 lectin (Fragment).
OS Colocasia esculenta (Elephant's ear) (Taro).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Colocasia.
OX NCBI_TaxID=4460;
RN [1]_TaxID=4460;
RP SEQUENCE.
RX MEDLINE=95288362; PubMed=7770523;
RA Van Damme E.J., Goossens K., Smeets K., van Leuven F., Verhaert P.,
RA Peumans W.J.;
RT "The major tuber storage protein of araceae species is a lectin.
RT Characterization and molecular cloning of the lectin from Arum
RT maculatum L.";
RL Plant Physiol. 107:1147-1158(1995).
SQ SEQUENCE 19 AA; 2066 MW; F9C18865CA58608A CRC64;

```

Query Match 30.0%; Score 3; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFT 5  
 |||  
 Db 3 PFT 5

## RESULT 69

Q64977 Q64977 PRELIMINARY; PRT; 19 AA.  
 AC Q64977;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
 DE (Strain ALMV-S) 5' end of RNA-1 (fragment).  
 OS Alfalfa mosaic virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
 OC Alfamovirus.  
 OX NCBI\_TaxID=12321;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ALMV-S;  
 RX MEDLINE=83220821; PubMed=6856476;  
 RA Ravelonandro M., Godefroy-Colburn T., Pinck L.;  
 RT "Structure of the 5'-terminal untranslated region of the genomic RNAs  
 from two strains of alfalfa mosaic virus.";  
 RL Nucleic Acids Res. 11:2815-2826(1983).  
 DR EMBL; M35975; AAA66594.1; -;  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2163 MW; A1D2EFEC7C1E409A CRC64;

Query Match 30.0%; Score 3; DB 12; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PIP 9  
 |||  
 Db 7 PIP 9

## RESULT 70

Q905J2 Q905J2 PRELIMINARY; PRT; 19 AA.  
 AC Q905J2;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
 DE Tat protein (fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=96CG24;  
 RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 Republic of Congo-Brazzaville.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF410441; AAL10230.1; -;  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2174 MW; 2A837680D1068D66 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PIP 9  
 |||

Db 16 PIP 18

## RESULT 71

Q905E0 Q905E0 PRELIMINARY; PRT; 19 AA.  
 AC Q905E0;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
 DE Tat protein (fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97CG316;  
 RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 Republic of Congo-Brazzaville.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF410454; AAL10282.1; -;  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2289 MW; 3661AD2BA069237 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PIP 9  
 |||  
 Db 16 PIP 18

## RESULT 72

Q905I8 Q905I8 PRELIMINARY; PRT; 19 AA.  
 AC Q905I8;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
 DE Tat protein (fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=96CG27;  
 RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 Republic of Congo-Brazzaville.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF410442; AAL10234.1; -;  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2359 MW; 3E59E860D0069237 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PIP 9  
 |||  
 Db 16 PIP 18

## RESULT 73

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Q90RF4
ID Q90RF4 PRELIMINARY; PRT; 19 AA.
AC Q90RF4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG282;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127551; AAK84917.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2163 MW; 2A83630189068236 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIP 9
DB 16 PIP 18

RESULT 74
Q90RE9
ID Q90RE9 PRELIMINARY; PRT; 19 AA.
AC Q90RE9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG307;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127552; AAK84921.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2183 MW; 2A91D034D10685A8 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIP 9
DB 16 PIP 18

RESULT 75
Q90RG9
ID Q90RG9 PRELIMINARY; PRT; 19 AA.
AC Q90RG9;

```

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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG21;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127547; AAK84904.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2281 MW; 367E76D6D66068236 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIP 9
DB 16 PIP 18

Search completed: November 25, 2003, 18:25:43
Job time : 27.1457 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 32.3936 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-18

Perfect score: 10

Sequence: 1 VYFPTGPIPN 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2004.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	22	Colostrinin derive
2	10	100.0	10	22	Colostrinin peptid
3	10	100.0	10	22	Colostrinin peptid
4	10	100.0	10	22	Ewe colostrinin
5	10	100.0	10	23	Colostrinin consti
6	10	100.0	10	23	Colostrinin consti
7	10	100.0	10	23	Colostrinin consti
8	10	100.0	16	23	Neural cell regula
9	5	50.0	9	15	Sheep colostrinin
					Opioid peptide #6.

10	5	50.0	10	15	AAR53610	Opioid peptide #4.
11	5	50.0	11	13	AAR27170	Sequence of peptid
12	5	50.0	12	18	AAW31290	Bovine beta casein
13	5	50.0	13	17	AAW03286	CNS-inhibiting pep
14	5	50.0	14	21	AAV69542	Bioactive peptide
15	4	40.0	4	18	AAW31294	Bovine beta casein
16	4	40.0	5	18	AAW31288	Bovine beta casein
17	4	40.0	5	22	AAW70110	N-terminal sequenc
18	4	40.0	6	13	AAR25087	BGRF prodtrug analo
19	4	40.0	7	9	APR0636	Synthetic hydropho
20	4	40.0	8	13	AAR25088	BGRF prodtrug analo
21	4	40.0	8	14	AAR35969	Hepatitis C virus
22	4	40.0	8	14	AAR35970	Hepatitis C virus
23	4	40.0	8	14	AAR35971	Hepatitis C virus
24	4	40.0	8	14	AAR35972	Hepatitis C virus
25	4	40.0	8	14	AAR35973	Hepatitis C virus
26	4	40.0	8	15	AAR53626	Opioid peptide #20
27	4	40.0	8	22	ABP16676	HIV B07 super moti
28	4	40.0	8	22	ABP18797	HIV B62 super moti
29	4	40.0	8	22	ABP67361	Human peptide #3.
30	4	40.0	8	23	ABG32117	Mannan-binding lec
31	4	40.0	8	23	AAE14567	Human MASP-2 pepti
32	4	40.0	9	7	APR60121	Sequence of pharma
33	4	40.0	9	7	APR60122	Sequence of pharma
34	4	40.0	9	13	AAR26793	Prolyl endopeptida
35	4	40.0	9	13	AAR26798	Prolyl endopeptida
36	4	40.0	9	13	AAR26794	Prolyl endopeptida
37	4	40.0	9	13	AAR26795	Prolyl endopeptida
38	4	40.0	9	14	AAR30450	C242:11 MAB kappa
39	4	40.0	9	17	AAR98490	Anti-human interle
40	4	40.0	9	17	AAR98491	Mouse PAF receptor
41	4	40.0	9	19	AAW59175	Anti-human interle
42	4	40.0	9	19	AAW42469	Mouse PAF receptor
43	4	40.0	9	19	AAW42470	Fab2 light chain c
44	4	40.0	9	19	AAW42470	Fab15 light chain
45	4	40.0	9	19	AAW39877	Light chain CDR3 o
46	4	40.0	9	19	AAW39817	Light chain CDR3 o
47	4	40.0	9	19	AAW39823	Light chain CDR3 o
48	4	40.0	9	19	AAW39826	Light chain CDR3 o
49	4	40.0	9	21	AAV97234	Complementary dete
50	4	40.0	9	21	AAV92171	Murine 1JH10 light
51	4	40.0	9	21	AAV32256	Light chain CDR L3
52	4	40.0	9	22	AAE13142	Humanised antibody
53	4	40.0	9	22	AAE10479	Humanised Ab light
54	4	40.0	9	22	AAE10495	Humanised Ab clone
55	4	40.0	9	22	AAE2708	VEGF antagonist an
56	4	40.0	9	22	AAE63246	Complementarity de
57	4	40.0	9	22	AAE63255	Complementarity de
58	4	40.0	9	22	AAE63256	Complementarity de
59	4	40.0	9	22	AAE63257	Complementarity de
60	4	40.0	9	22	AAE47113	Mutant scFv 508F 1
61	4	40.0	9	22	AAE62867	Anti-SAF-1 antibod
62	4	40.0	9	22	AAE62896	Anti-human Cbl54 a
63	4	40.0	9	22	AAE63993	Complementarity de
64	4	40.0	9	23	ABP55880	B15 class I sHLA m
65	4	40.0	9	23	ABJ15164	Immunogenic HIV pe
66	4	40.0	9	23	ABG97127	Human leukocyte an
67	4	40.0	9	23	AAE28015	Human modified ant
68	4	40.0	9	23	AAE28025	Human modified ant
69	4	40.0	9	23	AAE28070	Human RSV antibody
70	4	40.0	9	23	ABP66360	Human RSV antibody
71	4	40.0	9	23	ABP66370	Human RSV antibody
72	4	40.0	9	23	ABP66415	Human RSV antibody
73	4	40.0	9	23	AAE25954	Mouse anti-KOR p1c
74	4	40.0	9	23	AAO14751	H16-67 variant bet
75	4	40.0	9	23	AAO14752	Beta-casein protei
76	4	40.0	9	23	AAU74411	Light chain comple
77	4	40.0	9	24	ABU69223	Respiratory syncyt
78	4	40.0	9	24	ABU69233	Respiratory syncyt
79	4	40.0	9	24	ABU69278	Respiratory syncyt
80	4	40.0	9	24	ABG75671	Synagis light chai
81	4	40.0	9	24	ABR05943	Human cancer-relat
82	4	40.0	9	24	ABJ26723	VEGF binding relat

83 Neurological/CNS d  
 84 Neurological/CNS d  
 85 Arg134>Phe hGH. H  
 86 Opioid peptide #12  
 87 Opioid peptide #13  
 88 Opioid peptide #14  
 89 Opioid peptide #15  
 90 Opioid peptide #16  
 91 Opioid peptide #2.  
 92 Opioid peptide #3.  
 93 Mycobacterium tube  
 94 Mycobacterium tube  
 95 M. tuberculosis po  
 96 M. tuberculosis po  
 97 M. tuberculosis an  
 98 M. tuberculosis re  
 99 N-terminus #3 of p  
 100 HIV A02 super moti

## ALIGNMENTS

RESULT 1  
 AAB72263  
 ID AAB72263 standard; peptide; 10 AA.  
 XX  
 AC AAB72263;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 18.  
 XX  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22818.  
 XX  
 PR 17-AUG-1999; 99US-0149311.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 DR WPI; 2001-202804/20.  
 XX  
 DR Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0;  
 QY 1 VYPFTGPIPN 10  
 |||||  
 DB 1 VYPFTGPIPN 10  
 |||||  
 RESULT 2  
 AAB72516  
 ID AAB72516 standard; Peptide; 10 AA.  
 XX  
 AC AAB72516;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #17.  
 XX  
 KW Dermatological; oxidative stress regulator; colostrinin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22665.  
 XX  
 PR 17-AUG-1999; 99US-0149310.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2001-218342/22.  
 XX  
 DR Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0;  
 QY 1 VYPFTGPIPN 10  
 |||||  
 DB 1 VYPFTGPIPN 10  
 |||||  
 RESULT 3  
 AAB72548  
 ID AAB72548 standard; Peptide; 10 AA.  
 XX  
 AC AAB72548;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX

DE Colostrinin peptide #17.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 PI  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 XX Sequence 10 AA;  
 SQ

Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6e-05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VVPFTGPIPN 10  
 Db 1 VVPFTGPIPN 10  
 |||||

RESULT 4  
 AAB59326  
 ID AAB59326 standard; Peptide; 10 AA.  
 XX  
 AC AAB59326;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment C-1.  
 XX  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 XX Ovis sp.  
 OS  
 XX WO200075173-A2.  
 PN  
 XX 14-DEC-2000.  
 PD  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REG- ) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI  
 XX WPI; 2001-071058/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 PS Claim 7; Page 27; 63pp; English.  
 XX  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 XX Sequence 10 AA;  
 SQ

Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6e-05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VVPFTGPIPN 10  
 Db 1 VVPFTGPIPN 10  
 |||||

RESULT 5  
 AAE20245  
 ID AAE20245 standard; peptide; 10 AA.  
 XX  
 AC AAE20245;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide #17.  
 XX  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnery.  
 XX  
 OS Unidentified.  
 XX  
 PH Key Location/Qualifiers  
 FT Modified-site 7 /note= "Optionally C-terminal amide"  
 FT  
 XX WO200213850-A1.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2000; 2000WO-US22776.  
 PF  
 XX 17-AUG-2000; 2000WO-US22776.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 PI  
 XX WPI; 2002-269151/31.  
 DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 PS Claim 6; Page 25; 51pp; English.  
 XX  
 XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 10 AA;  
 Query Match 100.0%; Score 10; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6e-05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPFTGPIPN 10  
 |||||  
 Db 1 VYPFTGPIPN 10

## RESULT 6

AA014594  
 ID AA014594 standard; Peptide; 10 AA.

AC AA014594;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide (casein amino acids 74-83).

KW Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Modified-site 10 /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. It is  
 CC classified as having a beta-casein homologue precursor, and  
 CC corresponds to casein amino acids 74-83. Methods are claimed for:  
 CC inducing a cytokine in a cell by contact with an immunological  
 CC regulator, where the cell is present in a cell culture, a tissue,  
 CC an organ or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide. Cytokines  
 CC induced by this peptide in human leucocyte cultures include  
 CC tumour necrosis factor-alpha and interleukin-10.

SQ Sequence 10 AA;

Query Match 100.0%; Score 10; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 6e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPFTGPIPN 10  
 |||||  
 Db 1 VYPFTGPIPN 10

## RESULT 7

AA014594

ID AA014594 standard; peptide; 10 AA.

XX AC AA014594;

XX DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 17.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 10 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for



CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 10; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6e-05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VVPFTGPIPN 10  
 Db 1 VVPFTGPIPN 10  
 RESULT 8  
 ID ABG32207 standard; peptide; 16 AA.  
 XX AC ABG32207;  
 DT 05-NOV-2002 (first entry)  
 DE Sheep colostrinin derived peptide #1.  
 KW Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia;  
 KW central nervous system disorder; neurological disorder; neurosis;  
 KW mental disorder; psychosis; neurodegenerative disorder;  
 KW Alzheimer's disease; motor neuron disease; immune system disorder;  
 KW acquired immunological deficiency; bacterial infection; viral infection;  
 KW amyloid plaque; dietary supplement; cachexia; weight loss;  
 KW senile dementia; Parkinson's disease; emotional disturbance; depression;  
 KW drug addiction; drug withdrawal.  
 XX Ovis aries.  
 OS  
 XX WO200246211-A2.  
 PN 13-JUN-2002.  
 PD 05-DEC-2001; 2001WO-GB03376.  
 PF 06-DEC-2000; 2000GB-002977.  
 PR (REG-) REGEN THERAPEUTICS PLC.  
 PA Georgiades JA;  
 PI  
 XX WPI; 2002-619016/66.  
 DR Novel peptides isolated from colostrinin polypeptide, useful for  
 PT treating viral and bacterial infections, disorders of immune system and  
 PT central nervous system e.g., Alzheimer's disease, dementia, and as food  
 PT additive  
 PS Claim 1; Page 8; 16pp; English.  
 XX The invention relates to a peptide derived from colostrinin (a colostrum  
 CC protein known to be a cytokine inducer) substantially entirely consists  
 CC of the peptide sequences appearing as ABG32207-ABG32223. Also included  
 CC are a composition comprising two or more of the peptides in combination  
 CC with a carrier, a dietary supplement comprising an orally ingestible  
 CC combination of the peptide in combination with a carrier and an antibody  
 CC which binds to the peptide, and which is obtainable by using peptide as  
 CC an antigen. The peptide is useful as a medicament for treating chronic  
 CC disorders of central nervous system e.g., neurological disorders and/or  
 CC mental disorders such as psychosis and/or neurosis, dementia,  
 CC neurodegenerative disorders such as Alzheimer's disease, motor  
 CC neuron disease, chronic disorders of immune system, diseases  
 CC with bacterial and viral etiology, acquired immunological deficiencies,  
 CC chronic bacterial, viral infections. The peptide is also useful for  
 CC treating diseases characterised by presence of amyloid plaque. The  
 CC peptide is also useful as a dietary supplement for babies, small

CC children, adults who have been subjected to chemotherapy and/or  
 CC adults who have suffered from cachexia or weight loss due to chronic  
 CC disease. The peptide is also useful for treating senile dementia,  
 CC Parkinson's disease, emotional disturbances and depression. The peptides  
 CC may also be used as an auxiliary withdrawal treatment for drug addicts,  
 CC after a period of detoxification, and in persons dependent on stimulants.  
 CC The present sequence is a colostrinin derived peptide of the invention.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 100.0%; Score 10; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VVPFTGPIPN 10  
 Db 2 VVPFTGPIPN 11  
 RESULT 9  
 ID AAR53612 standard; peptide; 9 AA.  
 XX AC AAR53612;  
 DT 25-JAN-1995 (first entry)  
 DE Opioid peptide #6.  
 KW Opioid; activity; hydrolysis; lactoprotein; neutral protease;  
 KW alkali protease; gastrointestinal hormone stimulating agents;  
 KW analgesics; hypnotics; electrolyte adsorption stimulating agents;  
 KW diarrhoea treating agents; drug.  
 XX Mammalian.  
 OS  
 XX JP06128287-A.  
 PN 10-MAY-1994.  
 PD 02-NOV-1992; 92JP-0315515.  
 PF 07-NOV-1991; 91JP-0318569.  
 PR 25-DEC-1991; 91JP-0356633.  
 PR 01-SEP-1992; 92JP-0255403.  
 XX (NISS) NISSHIN FLOUR MILLING CO.  
 PA  
 XX WPI; 1994-188987/23.  
 DR New opioid peptide(s) and their salts - are used as analgesic,  
 PT for stimulating e.g. electrolyte absorption and treating  
 PT diarrhoea  
 XX Claim 8; Page 12; 15pp; Japanese.  
 PS The sequences given in AAR53607-26 are peptides which have opioid  
 CC activity. These peptides are produced by hydrolysing lactoprotein  
 CC with neutral protease derived from alkali protease. The peptides and  
 CC their salts are useful as analgesics, hypnotics, gastrointestinal  
 CC hormone stimulating agents, electrolyte adsorption stimulating agents,  
 CC diarrhoea treating agents, etc. The peptide given in AAR53608 shows  
 CC lower opioid activity and is therefore expected to be used as processed  
 CC drug.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 50.0%; Score 5; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 GPIPN 10  
 |||||

DB 5 GPIPN 9

## RESULT 10

AAR53610  
ID AAR53610 standard; peptide; 10 AA.

AC AAR53610;

DT 25-JAN-1995 (first entry)

XX Opioid peptide #4.

XX Opioid; activity; hydrolysis; lactoprotein; neutral protease;

KW alkali protease; gastrointestinal hormone stimulating agents;

KW analgesics; hypnotics; electrolyte adsorption stimulating agents;

KW diarrhoea treating agents; drug.

OS Mammalian.

PN JP06128287-A.

XX 10-MAY-1994.

XX 02-NOV-1992; 92JP-0315515.

XX 07-NOV-1991; 91JP-0318569.

PR 25-DEC-1991; 91JP-0356633.

PR 01-SEP-1992; 92JP-0255403.

XX (NISS ) NISSHIN FLOUR MILLING CO.

XX WPI; 1994-188987/23.

XX New opioid peptide(s) and their salts - are used as analgesic,  
PT for stimulating e.g. electrolyte absorption and treating  
PT diarrhoea

XX Claim 6; Page 12; 15pp; Japanese.

XX The sequences given in AAR53607-26 are peptides which have opioid  
CC activity. These peptides are produced by hydrolysing lactoprotein  
CC with neutral protease derived from alkali protease. The peptides and  
CC their salts are useful as analgesics, hypnotics, gastrointestinal  
CC hormone stimulating agents, electrolyte adsorption stimulating agents,  
CC diarrhoea treating agents, etc. The peptide given in AAR53608 shows  
CC lower opioid activity and is therefore expected to be used as processed  
CC drug.

XX Sequence 10 AA;

Query Match 50.0%; Score 5; DB 15; Length 10;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIPN 10

DB 6 GPIPN 10

## RESULT 11

AAR27170

ID AAR27170 standard; Protein; 11 AA.

AC AAR27170;

XX 25-MAR-2003 (updated)

DT 03-FEB-1993 (first entry)

XX Sequence of peptide derived from milk casein with opioid activity.

XX Milk casein; opioid; sunburn; ageing; therapy.

KW

XX

OS Synthetic.

XX WO9215279-A1.

XX 17-SEP-1992.

XX 02-MAR-1992; 92WO-FR00191.

XX 01-MAR-1991; 91FR-0002510.

XX (OREA ) L'OREAL SA.

XX Barey M, Bitri L, Darmanton P;

XX WPI; 1992-331438/40.

XX Cosmetic compsn. contg. peptide as active principle - obtd. by  
PT hydrolysis of casein, with opioid activity, used for improving  
PT appearance of skin sunburn or other irritation

XX Claim 1; Page 13; 16pp; French.

XX The inventors claim a cosmetic compsn. contg. the peptide as an  
CC active ingredient. The peptide is derived from milk casein and has  
CC opioid activity. Compsn. contg. it are used to improve the  
CC appearance of sunburned skin or skin irritated by other agents or to  
CC counteract the effects of ageing on the skin. The amt. of peptide in  
CC the compsn. is 0.1-10 (pref. 0.1-5) a wt. %. The peptide is free of  
CC other peptides of mol. wt. > 3000.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 11 AA;

Query Match 50.0%; Score 5; DB 13; Length 11;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIPN 10

DB 5 GPIPN 9

## RESULT 12

AAW31290

ID AAW31290 standard; peptide; 12 AA.

XX AAW31290;

XX 25-MAR-2003 (updated)

DT 05-MAR-1998 (first entry)

XX Bovine beta casein variant A2 immunogenic peptide.

DE A2 variant beta-casein; immunogenic; molecular mimicry; cow;

KW milk product; insulin-dependent diabetes; GLUT2; diet.

XX Bos taurus.

XX Bos indicus.

XX WO9724371-A1.

XX 10-JUL-1997.

XX 27-DEC-1996; 96WO-EP05846.

XX 27-DEC-1995; 95IT-RM00850.

XX (BIOS-) BIOSISTEMA DI SARAPANI &amp; C SAS PIER LUIG.

XX (MIDI-) MIDIA LTD.

XX Pozzilli P;

XX WPI; 1997-363622/33.

XX Beta-casein or fragments not showing mimicry with GLUT2 - used in  
PT food or pharmaceutical products for prevention of insulin dependent  
PT diabetes, particularly in early infancy  
XX Claim 5; Page 4; 34pp; English.  
XX This sequence represents an immunogenic peptide from the A2 variant of  
CC beta-casein found in both Bos taurus and Bos indicus. The peptide  
CC contains a motif (see AAW31288) corresponding to amino acids 63-68 of  
CC the A2 beta casein protein and is found to be capable of mimicking a  
CC fragment of the GLUT2 protein found in insulin producing cells of the  
CC pancreas. There is a known correlation between exposure to cow's milk and  
CC the development of insulin-dependent diabetes which could possibly be  
CC linked to this molecular mimicry. Dietary or pharmaceutical products  
CC derived from milk substantially free of non-human beta casein or  
CC containing modified beta-casein without this motif could be used in diets  
CC for the prevention of insulin dependent diabetes particularly during  
CC early infancy.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX Sequence 12 AA;  
SQ  
Query Match 50.0%; Score 5; DB 18; Length 12;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GPIPN 10  
DB 8 GPIPN 12  
RESULT 13  
AAW03286  
ID AAW03286 standard; peptide; 13 AA.  
XX  
AC AAW03286;  
XX  
DT 23-MAR-1997 (first entry)  
XX  
DE CNS-inhibiting peptide from casein.  
XX  
KW casein; central nervous system; CNS inhibiting; antitussive;  
KW analgesic; sedative.  
XX  
OS Synthetic.  
XX  
PN JP08269090-A.  
XX  
PD 15-OCT-1996.  
XX  
PF 28-MAR-1995; 95JP-0094516.  
XX  
PR 28-MAR-1995; 95JP-0094516.  
XX  
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
XX  
DR WPI; 1996-515013/51.  
XX  
XX New peptide(s) obtd. by digestion of casein - useful as drugs  
PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative  
PT activities  
XX  
PS Claim 1; Page 2; 11pp; Japanese.  
XX  
XX Acid casein was prepared from raw milk by acid precipitation, and  
CC beta casein was formed by the product by the method of Hipp et al.  
CC This material was digested with porcine pepsin. The digested protein  
CC was neutralised with NaOH, then heated to inactivate the enzyme. The  
CC product was further digested with bovine pancreatin, trypsin and porcine  
CC kidney-derived LAP and then subjected to reverse phase chromatography  
CC to provide the present peptide.  
CC The peptide is useful as a drug having CNS inhibiting, antitussive,

CC analgesic and sedative activities  
XX  
SQ Sequence 13 AA;  
Query Match 50.0%; Score 5; DB 17; Length 13;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GPIPN 10  
DB 5 GPIPN 9  
RESULT 14  
AAV69542  
ID AAV69542 standard; peptide; 19 AA.  
XX  
AC AAV69542;  
XX  
DT 19-APR-2000 (first entry)  
XX  
DE Bioactive peptide #8 from whey protein hydrolysate.  
XX  
KW Whey protein hydrolysate; bioactive peptide; non bitter flavour;  
KW food product; digestible; hypotensive.  
XX  
OS Unidentified.  
XX  
PN WO9965326-A1.  
XX  
PD 23-DEC-1999.  
XX  
PF 14-JUN-1999; 99WO-NZ000084.  
XX  
PR 17-JUN-1998; 98NZ-0330710.  
XX  
PA (NZDA-) NEW ZEALAND DAIRY BOARD.  
XX  
PI Schlothauer R, Schollum LM, Singh AM, Reid JR;  
XX  
DR WPI; 2000-116705/10.  
XX  
PT Preparation of whey protein hydrolysate containing bioactive peptides  
PT but does not have bitter flavor -  
XX  
PS Claim 19; Page 21; 32pp; English.  
XX  
XX Sequences AAV69535-Y69536 represent bioactive peptides which are  
CC components of whey protein hydrolysate. The invention relates to the  
CC preparation of whey protein hydrolysate containing such bioactive  
CC peptides by treating a whey protein containing substrate with one or more  
CC enzymes capable of hydrolysing whey proteins to produce the whey protein  
CC hydrolysate containing bioactive peptides, and terminating the hydrolysis  
CC before substantial production of unacceptable bitter flavours. The  
CC invention also encompasses a non bitter product produced by partial  
CC hydrolysis of a substrate containing whey proteins, where the product  
CC comprises bioactive peptides and has a degree of hydrolysis of the whey  
CC proteins of below 10%, a food product containing the non bitter product,  
CC any one or a combination of two or more of the bioactive peptides of the  
CC invention, and a method for reducing systolic blood pressure in a patient  
CC which comprises administering the non bitter product to the patient. The  
CC peptides, products and food products are useful in a method for the  
CC reduction of systolic blood pressure. The whey protein products are free  
CC from bitter flavours and contain bioactive peptides. The products of the  
CC process have high digestibility and good organoleptic properties. The  
CC products may have bland or slightly sweet taste and are free of soapy  
CC and/or brothy flavours.  
XX  
SQ Sequence 19 AA;  
Query Match 50.0%; Score 5; DB 21; Length 19;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIN 10  
 DB 7 GPIN 11

RESULT 15  
 AAW31294  
 ID AAW31294 standard; peptide; 4 AA.  
 XX  
 AC AAW31294;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 05-MAR-1998 (first entry)  
 XX  
 DE Bovine beta casein immunogenic peptide motif 2.  
 XX  
 KW Beta-casein; immunogenic; molecular mimicry; cow;  
 KW milk product; insulin-dependent diabetes; GLUT2; diet.  
 XX  
 OS Bos taurus.  
 XX  
 PN WO9724371-A1.  
 XX  
 PD 10-JUL-1997.  
 XX  
 PF 27-DEC-1996; 96WO-EP05846.  
 XX  
 PR 27-DEC-1995; 95IT-RM00850.  
 XX  
 PA (BIOS-) BIOSISTEMA DI SARAPANI & C SAS PIER LUIG.  
 PA (MIDI-) MIDIA LTD.  
 XX  
 PI Pozzilli P;  
 XX  
 DR WPI; 1997-363622/33.  
 XX  
 PT Beta-casein or fragments not showing mimicry with GLUT2 - used in  
 PT food or pharmaceutical products for prevention of insulin dependent  
 PT diabetes, particularly in early infancy  
 XX  
 PS Claim 10; Page 6; 34pp; English.  
 XX  
 CC This sequence represents an immunogenic peptide motif found in bovine  
 CC beta casein. This motif is capable of mimicking a fragment of the  
 CC GLUT2 protein found in insulin producing cells of the pancreas. There is  
 CC a known correlation between exposure to cow's milk and the development of  
 CC insulin-dependent diabetes which could possibly be linked to this  
 CC molecular mimicry. Dietary or pharmaceutical products derived from milk  
 CC substantially free of non-human beta casein or containing modified  
 CC beta-casein without this motif could be used in diets for the prevention  
 CC of insulin dependent diabetes particularly during early infancy.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 4 AA;

Query Match 40.0%; Score 4; DB 18; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIN 9  
 DB 1 GPIN 4

RESULT 16  
 AAW31288  
 ID AAW31288 standard; peptide; 5 AA.  
 XX  
 AC AAW31288;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 05-MAR-1998 (first entry)

XX Bovine beta casein variant A2 immunogenic peptide motif.  
 DE  
 XX  
 KW A2 variant beta-casein; immunogenic; molecular mimicry; cow;  
 KW milk product; insulin-dependent diabetes; GLUT2; diet.  
 XX  
 OS Bos taurus.  
 OS Bos indicus.  
 XX  
 PN WO9724371-A1.  
 XX  
 PD 10-JUL-1997.  
 XX  
 PF 27-DEC-1996; 96WO-EP05846.  
 XX  
 PR 27-DEC-1995; 95IT-RM00850.  
 XX  
 PA (BIOS-) BIOSISTEMA DI SARAPANI & C SAS PIER LUIG.  
 PA (MIDI-) MIDIA LTD.  
 XX  
 PI Pozzilli P;  
 XX  
 DR WPI; 1997-363622/33.  
 XX  
 PT Beta-casein or fragments not showing mimicry with GLUT2 - used in  
 PT food or pharmaceutical products for prevention of insulin dependent  
 PT diabetes, particularly in early infancy  
 XX  
 PS Claim 5; Page 4; 34pp; English.  
 XX  
 CC This sequence represents an immunogenic peptide motif from the A2 variant  
 CC beta-casein found in both Bos taurus and Bos indicus (amino acid  
 CC position 63-68). This motif is capable of mimicking a fragment of the  
 CC GLUT2 protein found in insulin producing cells of the pancreas. There is  
 CC a known correlation between exposure to cow's milk and the development of  
 CC insulin-dependent diabetes which could possibly be linked to this  
 CC molecular mimicry. Dietary or pharmaceutical products derived from milk  
 CC substantially free of non-human beta casein or containing modified  
 CC beta-casein without this motif could be used in diets for the prevention  
 CC of insulin dependent diabetes particularly during early infancy.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 5 AA;

Query Match 40.0%; Score 4; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIN 9  
 DB 2 GPIN 5

RESULT 17  
 AAB70110  
 ID AAB70110 standard; peptide; 5 AA.  
 XX  
 AC AAB70110;  
 XX  
 DT 18-MAY-2001 (first entry)  
 XX  
 DE N-terminal sequence of peptide cleaved by novel protease enzyme.  
 XX  
 KW Gelatin; protease; jelly production; gelatin capsule synthesis;  
 KW drug synthesis.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2000325095-A.  
 XX  
 PD 28-NOV-2000.  
 XX  
 PF 18-MAY-1999; 99JP-0137528.





XX WO9300365-A2.  
 XX 07-JAN-1993.  
 XX 24-JUN-1992; 92WO-US05388.  
 XX 24-JUN-1991; 91US-0722489.  
 XX (CHIR ) CHIRON CORP.  
 XX Chien DY, Rutter W;  
 XX WPI; 1993-036334/04.  
 XX Polypeptide(s) comprising truncated hepatitis C virus sequences -  
 PT for detection, prevention and treatment of hepatitis C infection  
 XX  
 XX Example A; Page 36; 80pp; English.  
 XX This octamer was found to be immunoreactive with anti-HCV anti-sera.  
 CC In the epitope mapping experiment three different samples of anti-sera  
 CC were reacted with the peptide octamer, and then incubated with  
 CC HRP-labelled goat anti-human Ig antiser, to enable detection of  
 CC binding. This epitope starts from amino acid 1617 of the HCV  
 CC polyprotein.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 8 AA;  
 PI Chien DY, Rutter W;  
 XX WPI; 1993-036334/04.  
 XX Polypeptide(s) comprising truncated hepatitis C virus sequences -  
 PT for detection, prevention and treatment of hepatitis C infection  
 XX  
 XX Example A; Page 36; 80pp; English.  
 XX This octamer was found to be immunoreactive with anti-HCV anti-sera.  
 CC In the epitope mapping experiment three different samples of anti-sera  
 CC were reacted with the peptide octamer, and then incubated with  
 CC HRP-labelled goat anti-human Ig antiser, to enable detection of  
 CC binding. This epitope starts from amino acid 1617 of the HCV  
 CC polyprotein.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 8 AA;  
 PI Chien DY, Rutter W;  
 XX WPI; 1993-036334/04.  
 XX Polypeptide(s) comprising truncated hepatitis C virus sequences -  
 PT for detection, prevention and treatment of hepatitis C infection  
 XX

Query Match 40.0%; Score 4; DB 14; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GPIP 9  
 DB 4 GPIP 7

RESULT 23  
 AAR35971  
 ID AAR35971 standard; protein; 8 AA.  
 AC AAR35971;  
 XX 25-MAR-2003 (updated)  
 DT 24-MAY-1993 (first entry)  
 XX Hepatitis C virus (HCV) epitope.  
 XX Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;  
 KW immobilised reagent; immunoassay; diagnosis; detection; treatment;  
 KW infection.  
 XX Hepatitis C virus type 1.  
 OS WO9300365-A2.  
 PN 07-JAN-1993.  
 XX 24-JUN-1992; 92WO-US05388.  
 XX 24-JUN-1991; 91US-0722489.  
 XX (CHIR ) CHIRON CORP.  
 XX Chien DY, Rutter W;  
 XX WPI; 1993-036334/04.  
 XX Polypeptide(s) comprising truncated hepatitis C virus sequences -  
 PT for detection, prevention and treatment of hepatitis C infection  
 XX

Query Match 40.0%; Score 4; DB 14; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GPIP 9  
 DB 4 GPIP 7

PS Example A; Page 36; 80pp; English.  
 XX This octamer was found to be immunoreactive with anti-HCV anti-sera.  
 CC In the epitope mapping experiment three different samples of anti-sera  
 CC were reacted with the peptide octamer, and then incubated with  
 CC HRP-labelled goat anti-human Ig antiser, to enable detection of  
 CC binding. This epitope starts from amino acid 1618 of the HCV  
 CC polyprotein.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 40.0%; Score 4; DB 14; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GPIP 9  
 DB 3 GPIP 6

RESULT 24  
 AAR35972  
 ID AAR35972 standard; protein; 8 AA.  
 AC AAR35972;  
 XX 25-MAR-2003 (updated)  
 DT 24-MAY-1993 (first entry)  
 XX Hepatitis C virus (HCV) epitope.  
 XX Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;  
 KW immobilised reagent; immunoassay; diagnosis; detection; treatment;  
 KW infection.  
 XX Hepatitis C virus type 1.  
 OS WO9300365-A2.  
 PN 07-JAN-1993.  
 XX 24-JUN-1992; 92WO-US05388.  
 XX 24-JUN-1991; 91US-0722489.  
 XX (CHIR ) CHIRON CORP.  
 XX Chien DY, Rutter W;  
 XX WPI; 1993-036334/04.  
 XX Polypeptide(s) comprising truncated hepatitis C virus sequences -  
 PT for detection, prevention and treatment of hepatitis C infection  
 XX  
 XX Example A; Page 36; 80pp; English.  
 XX This octamer was found to be immunoreactive with anti-HCV anti-sera.  
 CC In the epitope mapping experiment three different samples of anti-sera  
 CC were reacted with the peptide octamer, and then incubated with  
 CC HRP-labelled goat anti-human Ig antiser, to enable detection of  
 CC binding. This epitope starts from amino acid 1619 of the HCV  
 CC polyprotein.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 40.0%; Score 4; DB 14; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GPIP 9  
 DB 3 GPIP 6

```

Db          2 GPIP 5

RESULT 25
AAR35973
ID AAR35973 standard; protein; 8 AA.
XX
AC AAR35973;
XX
XX 25-MAR-2003 (updated)
DT 24-MAY-1993 (first entry)
XX
XX Hepatitis C virus (HCV) epitope.
DE
XX Hepatitis; liver disease; HCV; monoclonal antibody; epitope;
KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
KW infection.
XX
OS Hepatitis C virus type 1.
XX
PN WO9300365-A2.
XX
PD 07-JAN-1993.
XX
PF 24-JUN-1992; 92WO-0505388.
XX
PR 24-JUN-1991; 91US-0722489.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Chien DY, Rutter W;
XX
DR WPI; 1993-036334/04.
XX
PT Polypeptide(s) comprising truncated hepatitis C virus sequences -
PT for detection, prevention and treatment of hepatitis C infection
XX
PS Example A; Page 36; 80pp; English.
XX
CC This octamer was found to be immunoreactive with anti-HCV anti-sera.
CC In the epitope mapping experiment three different samples of anti-sera
CC were reacted with the peptide octamer, and then incubated with
CC HRP-labelled goat anti-human Ig antiserum, to enable detection of
CC binding. This epitope starts from amino acid 1620 of the HCV
CC polyprotein.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIP 9
Db 1 GPIP 4

RESULT 26
AAR35626
ID AAR35626 standard; peptide; 8 AA.
XX
AC AAR35626;
XX
XX 25-JAN-1995 (first entry)
DT
DE Opioid peptide #20.
XX
XX Opioid; activity; hydrolysis; lactoprotein; neutral protease;
KW alkali protease; gastrointestinal hormone stimulating agents;
KW analgesics; hypnotics; electrolyte adsorption stimulating agents;
KW diarrhoea treating agents; drug.
XX
XX

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OS Mammalian.
XX
PN JP06128287-A.
XX
PD 10-MAY-1994.
XX
PF 02-NOV-1992; 92JP-0315515.
XX
PR 07-NOV-1991; 91JP-0318569.
PR 25-DEC-1991; 91JP-0358633.
PR 01-SEP-1992; 92JP-0255403.
XX
XX (NISS ) NISSHIN FLOUR MILLING CO.
PA
XX
XX WPI; 1994-188987/23.
DR
XX New opioid peptide(s) and their salts - are used as analgesic,
PT for stimulating e.g. electrolyte absorption and treating
PT diarrhoea
XX
PS Disclosure; Page 13; 15pp; Japanese.
XX
CC The sequences given in AAR53607-26 are peptides which have opioid
CC activity. These peptides are produced by hydrolysing lactoprotein
CC with neutral protease derived from alkali protease. The peptides and
CC their salts are useful as analgesics, hypnotics, gastrointestinal
CC hormone stimulating agents, electrolyte adsorption stimulating agents,
CC diarrhoea treating agents, etc. The peptide given in AAR53608 shows
CC lower opioid activity and is therefore expected to be used as processed
CC drug.
XX
XX
SQ Sequence 8 AA;

Query Match 40.0%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPP 4
Db 1 VYPP 4

RESULT 27
ABP16676
ID ABP16676 standard; Peptide; 8 AA.
XX
AC ABP16676;
XX
XX 15-JUL-2002 (first entry)
DT
DE HIV B07 super motif gag peptide #9.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
OS
XX
XX WO200124810-A1.
PN
XX
XX 12-APR-2001.
PD
XX
XX 05-OCT-2000; 2000WO-US27766.
PF
XX
XX 05-OCT-1999; 99US-0412863.
PR
XX (EPIM-) EPIMUNE INC.
PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HW;
XX WPI; 2001-354887/37.
XX
XX

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CC The invention is useful in medicine, in the manufacture of a  
CC medicament for treating obesity and for treating and preventing  
CC obesity in a patient.

XX SQ Sequence 8 AA;  
Query Match 40.0%; Score 4; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GP1P 9  
Db 1 GP1P 4

RESULT 30  
ABG32117  
ID ABG32117 standard; Peptide; 8 AA.  
XX AC ABG32117;  
XX DT 15-NOV-2002 (first entry)  
XX DE Mannan-binding lectin associated serine protease-2 related peptide #2.  
XX KW Mannan-binding lectin associated serine protease-2; MASP-2;  
XX antinflammatory; gene therapy; complement fixation inhibitor;  
KW MBLectin response; infectious disease; inflammatory disease;  
KW anti-idiotypic antibody production.  
XX OS Homo sapiens.  
XX US2002082209-A1.  
XX PD 27-JUN-2002.  
XX PF 04-JUN-2001; 2001US-0874238.  
XX PR 03-APR-1997; 97US-042678P.  
XX PR 02-APR-1998; 98US-0054218.  
XX PA (JENS/) JENSENIUS J C.  
XX PA (THIE/) THIEL S.  
XX PI Jensenius JC, Thiel S;  
XX WPI; 2002-635487/68.  
XX Novel mannin-binding lectin associated serine protease-2, MASP-2  
XX polypeptide, useful for treating patients deficient in MASP-2 such as  
XX inflammatory and infectious diseases -

XX Example 4; Page 13; 22pp; English.  
XX The invention describes a Mannan-binding lectin associated serine  
XX protease-2 (MASP-2) polypeptides (I) with a molecular mass of 52K or 20K.  
XX (I) and the encoding polynucleotide (III) are useful for treating  
XX patients deficient in MASP-2. A compound (II) able to specifically  
XX inhibit MASP-2 (especially MASP-2 antisense nucleic acid sequence which  
XX inhibits complexing of MBL and MASP-2), is useful for inhibiting the  
XX activity of MASP-2. (I) is useful for evaluating MASP-2 function, and for  
XX identifying other cellular gene products or compounds that can modulate  
XX the MBLectin response. (I) and (II) are useful as diagnostic or  
XX therapeutic agents for treating infectious or inflammatory diseases, for  
XX identifying compounds that modulate the expression or activity of MASP-2,  
XX and for producing antibodies which are useful in screening assays to  
XX measure the effect of a candidate compound on expression or localisation  
XX of MASP-2, and for inhibiting abnormal MASP-2 activity. (III) is useful  
XX as primers for the identification of gene mutations, allelic variations  
XX and regulatory defects in MASP-2 gene, and for generating anti-idiotypic  
XX antibodies. This is the amino acid sequence of a human mannin-binding  
XX lectin associated serine protease-2 (MASP-2) related peptide used in the  
XX design of primers for isolating DNA encoding MASP-2.

XX SQ Sequence 8 AA;  
Query Match 40.0%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PFTG 6  
Db 2 PFTG 5

RESULT 31  
AAE14567  
ID AAE14567 standard; peptide; 8 AA.  
XX AC AAE14567;  
XX DT 17-MAY-2002 (first entry)  
XX DE Human MASP-2 peptide #2.  
XX KW Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL;  
XX complement fixation; infection; microbe; retrovirus; HIV; abortion;  
KW human immunodeficiency virus; pathogenic bacteria; inflammatory disorder.  
XX OS Homo sapiens.  
XX WO200206460-A2.  
XX PD 24-JAN-2002.  
XX PF 13-JUL-2001; 2001WO-DK00499.  
XX PR 13-JUL-2000; 2000DK-0001089.  
XX PR 01-JUN-2001; 2001DK-0000870.  
XX PA (JENS/) JENSENIUS J C.  
XX PA (THIE/) THIEL S.  
XX PI Jensenius JC, Thiel S;  
XX WPI; 2002-179791/23.  
XX Use of a polypeptide comprising amino acid sequence derived from  
XX mannin-binding lectin associated serine protease-2 (MASP-2) for  
XX producing pharmaceutical composition, to treat bacterial, fungal, viral  
XX infections -

XX Example 4; Page 44; 76pp; English.  
XX The invention relates to use of a polypeptide derived from  
XX mannin-binding lectin (MBL) associated serine protease-2 (MASP-2) for  
XX producing a pharmaceutical composition. MASP-2 is a complement-  
XX fixing enzyme and involved in lectin pathway of complement activation.  
XX The pharmaceutical composition comprising MASP-2 is useful for  
XX treating infections caused by microbes such as fungus, Yeast,  
XX retrovirus (e.g. human immunodeficiency virus (HIV)), or pathogenic  
XX bacteria which are resistant to at least one antibiotic medicament or  
XX multiresistant. The polynucleotide encoding MASP-2 is useful for  
XX treating patients deficient in MASP-2. The invention also discloses  
XX MASP-2 assays which are useful for determination of MASP-2 activity or  
XX levels in patients suffering from e.g. infections, inflammatory disorders  
XX and spontaneous recurrent abortion. The pharmaceutical composition  
XX comprising MASP-2 inhibitor is useful for treating inflammatory  
XX disorders. The present sequence is human MASP-2 peptide used for  
XX producing PCR primer.

XX SQ Sequence 8 AA;  
Query Match 40.0%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
 DB 2 PFTG 5

RESULT 32  
 AAP60121  
 ID AAP60121 standard; peptide; 9 AA.

XX  
 AC AAP60121;

XX 25-MAR-2003 (updated)  
 DT 31-OCT-2002 (updated)

XX 26-JUN-1991 (first entry)

DE Sequence of pharmacologically active peptides.

XX Analgesic; endocrine activity; immunomodulatory.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 5..9  
 FT Misc-difference 9

FT /label= a chain of 0-5 AA units in D or L form  
 FT /notes= "attached to OH, OR, NH<sub>2</sub>, NHR, N(R)2, or NHNH<sup>+</sup>;  
 R= substd. 1-10C alkyl, adamantyl, 3-10C  
 cycloalkyl, phenyl or 7-8C aralkyl; R' = H,  
 1-10C alkyl, cycloalkyl, phenyl, 7-8C  
 aralkyl, 1-16C aliphatic or cycloaliphatic  
 acyl, opt. substd. by OH, NH<sub>2</sub>, 1-14C alkoxy  
 or halogen, aryl opt. substd. by OH, NH<sub>2</sub>,  
 halogen or 1-4C alkoxy, or a linear,  
 branched or cyclic 3-11C aliphatic urethane  
 gp."

XX EP199331-A.

XX 29-OCT-1986.

XX 21-APR-1986; 86EP-0105507.

XX 23-APR-1985; 85DE-3514587.

XX (BRAN/) BRANTL V.

XX Brantl V;

XX WPI; 1986-286087/44.

XX New pharmacologically active peptide cpds. - with N-terminal  
 PT sequence of tyrosine, proline, phenyl-alanine and threonine, used  
 PT as analgesic, anti-psychotic etc.

XX Claim 1; Page 12; 18pp; German.

XX The peptides of the invention may have opiate-like analgesic  
 CC activity, endocrine activity, immunomodulatory activity, and  
 CC stimulatory activity on mammalian cellular metabolism. They may be  
 CC used as antitussive, antidiarrhoeal, immunomodulatory, analgesic,  
 CC antipsychotic, tranquilising, circulation-promoting and wound-  
 CC healing-promoting medicaments.  
 CC (Updated on 31-OCT-2002 to add missing OS field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 9 AA;

Query Match 40.0%; Score 4; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

DB 1 YPFT 4

RESULT 33  
 AAP60122  
 ID AAP60122 standard; peptide; 9 AA.

XX  
 AC AAP60122;

XX 25-MAR-2003 (updated)  
 DT 31-OCT-2002 (updated)

XX 26-JUN-1991 (first entry)

DE Sequence of pharmacologically active peptides.

XX Analgesic; endocrine activity; immunomodulatory.

XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 5..9  
 FT /label= 1,II,IIG,IIGO,IIGOV

FT /note= "attached to OH at C-terminal"

FT Misc-difference 4  
 FT /notes= "when AA(4) is at C-terminal, it may be  
 attached to -OH or -NH<sub>2</sub>"

XX EP199331-A.

XX 29-OCT-1986.

XX 21-APR-1986; 86EP-0105507.

XX 23-APR-1985; 85DE-3514587.

XX (BRAN/) BRANTL V.

XX Brantl V;

XX WPI; 1986-286087/44.

XX New pharmacologically active peptide cpds. - with N-terminal  
 PT sequence of tyrosine, proline, phenyl-alanine and threonine, used  
 PT as analgesic, anti-psychotic etc.

XX Claim 8; Page 15; 18pp; German.

XX The peptides of the invention may have opiate-like analgesic  
 CC activity, endocrine activity, immunomodulatory activity, and  
 CC stimulatory activity on mammalian cellular metabolism. They may be  
 CC used as antitussive, antidiarrhoeal, immunomodulatory, analgesic,  
 CC antipsychotic, tranquilising, circulation-promoting and wound-  
 CC healing-promoting medicaments.  
 CC (Updated on 31-OCT-2002 to add missing OS field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 9 AA;

Query Match 40.0%; Score 4; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

DB 1 YPFT 4

RESULT 34  
 AAR26793  
 ID AAR26793 standard; peptide; 9 AA.

XX  
 AC AAR26793;

XX 11-FEB-1993 (first entry)  
 XX Prolyl endopeptidase inhibitor (1).  
 DE Amnesia; endopeptidase.  
 KW Synthetic.  
 OS JP04208299-A.  
 XX 29-JUL-1992.  
 XX 30-NOV-1990; 90JP-0337219.  
 XX 30-NOV-1990; 90JP-0337219.  
 XX (AJIN ) AJINOMOTO KK.  
 XX WPI; 1992-303600/37.  
 XX Prolyl endopeptidase inhibitors - for treating and preventing  
 PT amnesia  
 XX Claim 1; Page 1; 11pp; Japanese.  
 XX The peptides given in AAR26793-801 inhibit prolyl endopeptidase and  
 CC are used in prevention and treatment of amnesia. They may be  
 CC administered orally as powder, granules, tablets, capsules or liq.  
 CC prepn. or parenterally as suspension, liq. prepn., emulsion or  
 CC injection. E.g. they may be included as a component of a nutrient.  
 CC The peptides may be prepd. by condensation of two suitable fragments,  
 CC i.e. one having a reactive carboxy gp. and the other having  
 CC a reactive amino gp., by a method using DCC, and subsequent  
 CC deprotection. The condensation may be made by the liq.-phase or  
 CC solid-phase method.  
 XX Sequence 9 AA;  
 XX Query Match 40.0%; Score 4; DB 13; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 VYPF 4  
 DB 1 VYPF 4

RESULT 35  
 AAR26798  
 ID AAR26798 standard; peptide; 9 AA.  
 AC AAR26798;  
 XX 11-FEB-1993 (first entry)  
 DE Prolyl endopeptidase inhibitor (6).  
 XX Amnesia; endopeptidase.  
 XX Synthetic.  
 XX JP04208299-A.  
 XX 29-JUL-1992.  
 XX 30-NOV-1990; 90JP-0337219.  
 XX 30-NOV-1990; 90JP-0337219.  
 XX (AJIN ) AJINOMOTO KK.  
 XX WPI; 1992-303600/37.

XX Prolyl endopeptidase inhibitors - for treating and preventing  
 PT amnesia  
 XX Claim 1; Page 1; 11pp; Japanese.  
 XX The peptides given in AAR26793-801 inhibit prolyl endopeptidase and  
 CC are used in prevention and treatment of amnesia. They may be  
 CC administered orally as powder, granules, tablets, capsules or liq.  
 CC prepn. or parenterally as suspension, liq. prepn., emulsion or liq.  
 CC injection. E.g. they may be included as a component of a nutrient.  
 CC The peptides may be prepd. by condensation of two suitable fragments,  
 CC i.e. one having a reactive carboxy gp. and the other having  
 CC a reactive amino gp., by a method using DCC, and subsequent  
 CC deprotection. The condensation may be made by the liq.-phase or  
 CC solid-phase method.  
 XX Sequence 9 AA;  
 XX Query Match 40.0%; Score 4; DB 13; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 GPIIP 9  
 DB 6 GPIIP 9

RESULT 36  
 AAR26794  
 ID AAR26794 standard; peptide; 9 AA.  
 AC AAR26794;  
 XX 11-FEB-1993 (first entry)  
 DE Prolyl endopeptidase inhibitor (2).  
 XX Amnesia; endopeptidase.  
 XX Synthetic.  
 XX JP04208299-A.  
 XX 29-JUL-1992.  
 XX 30-NOV-1990; 90JP-0337219.  
 XX 30-NOV-1990; 90JP-0337219.  
 XX (AJIN ) AJINOMOTO KK.  
 XX WPI; 1992-303600/37.  
 XX Prolyl endopeptidase inhibitors - for treating and preventing  
 PT amnesia  
 XX Claim 1; Page 1; 11pp; Japanese.  
 XX The peptides given in AAR26793-801 inhibit prolyl endopeptidase and  
 CC are used in prevention and treatment of amnesia. They may be  
 CC administered orally as powder, granules, tablets, capsules or liq.  
 CC prepn. or parenterally as suspension, liq. prepn., emulsion or  
 CC injection. E.g. they may be included as a component of a nutrient.  
 CC The peptides may be prepd. by condensation of two suitable fragments,  
 CC i.e. one having a reactive carboxy gp. and the other having  
 CC a reactive amino gp., by a method using DCC, and subsequent  
 CC deprotection. The condensation may be made by the liq.-phase or  
 CC solid-phase method.  
 XX Sequence 9 AA;  
 XX Query Match 40.0%; Score 4; DB 13; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 GPIIP 9  
 DB 6 GPIIP 9

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPF 4  
|||  
Db 1 VYPF 4

## RESULT 37

AAR26795  
ID AAR26795 standard; peptide; 9 AA.

XX  
AC AAR26795;

XX 11-FEB-1993 (first entry)

DE Prolyl endopeptidase inhibitor (3).

XX Annesia; endopeptidase.

XX Synthetic.

XX JP04208299-A.

XX 29-JUL-1992.

XX 30-NOV-1990; 90JP-0337219.

XX 30-NOV-1990; 90JP-0337219.

PA (AJIN ) AJINOMOTO KK.

DR WPI; 1992-303600/37.

XX Prolyl endo-peptidase inhibitors - for treating and preventing  
PT amnesia

XX Claim 1; Page 1; 11pp; Japanese.

XX The peptides given in AAR26793-801 inhibit prolyl endopeptidase and  
CC are used in prevention and treatment of amnesia. They may be  
CC administered orally as powder, granules, tablets, capsules or liq.  
CC prepn. or parenterally as suspension, liq. prepn., emulsion or  
CC injection. E.g. they may be included as a component of a nutrient.  
CC The peptides may be prepd. by condensation of two suitable fragments,  
CC i.e. one having a reactive carboxy gp. and the other having  
CC a reactive amino gp., by a method using DCC, and subsequent  
CC deprotection. The condensation may be made by the liq.-phase or  
CC solid-phase method.

XX Sequence 9 AA;

Query Match 40.0%; Score 4; DB 13; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPF 4  
|||  
Db 1 VYPF 4

## RESULT 38

AAR30450  
ID AAR30450 standard; peptide; 9 AA.

XX  
AC AAR30450;

XX 25-MAR-2003 (updated)

DT 06-MAY-1993 (first entry)

XX C242:11 MAB kappa chain CDR3.

XX Kappa; chain; heavy; complementarity determining region; CDR; MAb;

KW monoclonal antibody; C242:II; murine; IGG; hybridoma; cell line;  
KW spleen; human; colonic; adenocarcinoma; myeloma; Sp2/0; antigen;  
endocytosis.

XX Synthetic.

XX EP521842-A2.

XX 07-JAN-1993.

XX 03-JUL-1992; 92EP-0850166.

XX 03-JUL-1991; 91SE-0002074.

PA (KABI ) KABI PHARMACIA AB.

PA (PHAA ) PHARMACIA & UPJOHN AB.

PI Holmgren J, Lind P, Lindholm L;

XX WPI; 1993-002345/01.

XX Monoclonal antibody reacting with CA-242 antigen - obt'd. by  
PT culturing hybridoma cell line C242:11 or mutants, useful for  
PT diagnosis and therapy of pancreatic or colorectal cancers

XX Claim 5; Page 11; 15pp; English.

XX The sequences given in AAR30448-50 represent the kappa chain and  
CC AAR30451-53 the heavy chain complementarity determining regions (CDR)  
CC of a monoclonal antibody (MAB), C242:II. C242:II is a monoclonal  
CC murine Ab of IGG class produced when culturing in an appropriate  
CC medium a hybridoma cell line obtained by fusing spleen cells from a  
CC mouse, which has been immunised with a human colonic adenocarcinoma  
CC cell line, with the murine myeloma cell line Sp2/0. C242:II when  
CC bound to a cell surface antigen is capable of being endocytosed or  
CC internalised into cells.

XX (Updated on 25-MAR-2003 to correct PN field.)  
XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 9 AA;

Query Match 40.0%; Score 4; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
|||  
Db 6 YPFT 9

## RESULT 39

AAR98490  
ID AAR98490 standard; Peptide; 9 AA.

XX  
AC AAR98490;

XX 12-OCT-1996 (first entry)

XX Anti-human interleukin-5 MAb 286 Fab2 CDR3.

XX Antibody engineering; humanised antibody; chimeric antibody; Fab;  
KW interleukin-5; IL-5; eosinophil; asthma; therapy; diagnosis;  
KW complementarity determining region; CDR; monoclonal antibody; MAB.

XX Mus sp.

XX WO9621000-A2.

XX 11-JUL-1996.

XX 22-DEC-1995; 95WO-US17082.

XX 06-JUN-1995; 95US-0470110.

```

PR 23-DEC-1994; 94US-0363131.
PR 06-JUN-1995; 95US-0467420.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;
PI Holmes SD, McWilliam LJ, Theisen TW;
XX WPI; 1996-333976/33.
XX
XX New monoclonal antibody to human interleukin-5 - used to produce
PT products for the treatment and diagnosis of conditions associated
PT with excess eosinophil prodn., e.g asthma etc.
XX
XX Claim 16; Page 69; 120pp; English.
XX
XX Fab2 and Fab15 were constructed from the anti-human interleukin-5
CC (IL-5) murine monoclonal antibody 2B6 by construction of a
CC chain-shuffled library and biopanning vs. immobilised IL-5.
CC The sequences of these 2 Vks were similar to that of 2B6 Vκ. For
CC Fab2 and Fab15, CDRs 1 and 2 have the sequences given in AAR98484-85,
CC respectively. For Fab2, CDR3 has the sequence given in AAR98490.
CC For Fab15, CDR3 has the sequence given in AAR98491. Anti-IL-5 Fabs
CC can be useful in the treatment of IL-5-mediated conditions, e.g.
CC asthma, allergic rhinitis and atopic dermatitis.
XX
XX Sequence 9 AA;
SQ
Query Match 40.0%; Score 4; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YPFT 5
DB 6 YPFT 9
|||||
RESULT 40
AAR98491
ID AAR98491 standard; Peptide; 9 AA.
XX
XX AAR98491;
XX
XX 12-OCT-1996 (first entry)
XX
XX Anti-human interleukin-5 Mab 2B6 Fab15 CDR3.
XX
XX Antibody engineering; humanised antibody; chimeric antibody; Fab;
KW interleukin-5; IL-5; eosinophil; asthma; therapy; diagnosis;
KW complementarity determining region; CDR; monoclonal antibody; Mab.
XX
XX Mus sp.
XX
XX WO9621000-A2.
XX
XX 11-JUL-1996.
XX
XX 22-DEC-1995; 95WO-US17082.
XX
XX 06-JUN-1995; 95US-0470110.
XX
XX 23-DEC-1994; 94US-0363131.
XX
XX 06-JUN-1995; 95US-0467420.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;
PI Holmes SD, McWilliam LJ, Theisen TW;
XX WPI; 1996-333976/33.
XX
XX New monoclonal antibody to human interleukin-5 - used to produce
PT products for the treatment and diagnosis of conditions associated
PT with excess eosinophil prodn., e.g asthma etc.
XX
XX Claim 16; Page 69; 120pp; English.
XX
XX Fab2 and Fab15 were constructed from the anti-human interleukin-5
CC (IL-5) murine monoclonal antibody 2B6 by construction of a
CC chain-shuffled library and biopanning vs. immobilised IL-5.
CC The sequences of these 2 Vks were similar to that of 2B6 Vκ. For
CC Fab2 and Fab15, CDRs 1 and 2 have the sequences given in AAR98484-85,
CC respectively. For Fab2, CDR3 has the sequence given in AAR98490.
CC For Fab15, CDR3 has the sequence given in AAR98491. Anti-IL-5 Fabs
CC can be useful in the treatment of IL-5-mediated conditions, e.g.
CC asthma, allergic rhinitis and atopic dermatitis.
XX
XX Sequence 9 AA;
SQ
Query Match 40.0%; Score 4; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YPFT 5
DB 6 YPFT 9
|||||
RESULT 40
AAR98491
ID AAR98491 standard; Peptide; 9 AA.
XX
XX AAR98491;
XX
XX 12-OCT-1996 (first entry)
XX
XX Anti-human interleukin-5 Mab 2B6 Fab15 CDR3.
XX
XX Antibody engineering; humanised antibody; chimeric antibody; Fab;
KW interleukin-5; IL-5; eosinophil; asthma; therapy; diagnosis;
KW complementarity determining region; CDR; monoclonal antibody; Mab.
XX
XX Mus sp.
XX
XX WO9621000-A2.
XX
XX 11-JUL-1996.
XX
XX 22-DEC-1995; 95WO-US17082.
XX
XX 06-JUN-1995; 95US-0470110.
XX
XX 23-DEC-1994; 94US-0363131.
XX
XX 06-JUN-1995; 95US-0467420.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;
PI Holmes SD, McWilliam LJ, Theisen TW;
XX WPI; 1996-333976/33.
XX
XX New monoclonal antibody to human interleukin-5 - used to produce
PT products for the treatment and diagnosis of conditions associated
PT with excess eosinophil prodn., e.g asthma etc.
XX
XX Claim 16; Page 69; 120pp; English.
XX
XX Fab2 and Fab15 were constructed from the anti-human interleukin-5
CC (IL-5) murine monoclonal antibody 2B6 by construction of a
CC chain-shuffled library and biopanning vs. immobilised IL-5.
CC The sequences of these 2 Vks were similar to that of 2B6 Vκ. For
CC Fab2 and Fab15, CDRs 1 and 2 have the sequences given in AAR98484-85,
CC respectively. For Fab2, CDR3 has the sequence given in AAR98490.
CC For Fab15, CDR3 has the sequence given in AAR98491. Anti-IL-5 Fabs
CC can be useful in the treatment of IL-5-mediated conditions, e.g.
CC asthma, allergic rhinitis and atopic dermatitis.
XX
XX Sequence 9 AA;
SQ
Query Match 40.0%; Score 4; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YPFT 5
DB 6 YPFT 9
|||||
RESULT 40
AAR98491
ID AAR98491 standard; Protein; 9 AA.
XX
XX AAR98491;
XX
XX 13-AUG-1998 (first entry)
XX
XX Mouse PAF receptor antibody light chain hypervariable region CDR3.
XX
XX Immunoglobulin light chain; hypervariable region; PAF; CDR; antibody;
KW platelet activating factor receptor; murine; chimeric; anti-PAF;
KW complementarity determining region.
XX
XX Mus sp.
XX
XX JP10136981-A.
XX
XX 26-MAY-1998.
XX
XX 12-NOV-1996; 96JP-0317047.
XX
XX 12-NOV-1996; 96JP-0317047.
XX
XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX
XX WPI; 1998-355043/31.
XX
XX Polypeptide comprising variable region of antibody recognising PAF
PT receptor - useful for the preparation of chimeric antibody
XX
XX Claim 2; Page 10; 14pp; Japanese.
XX
XX This sequence represents the complementarity determining region (CDR)
CC 3 of the light chain hypervariable region of an antibody recognising
CC the platelet activating factor (PAF) receptor. The variable region of
CC mouse anti-PAF receptor monoclonal antibody is useful for the
CC preparation of chimeric antibodies.
XX
XX Sequence 9 AA;
SQ
Query Match 40.0%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YPFT 5
|||||

```

Db 6 YPFT 9

## RESULT 42

AAW42469  
ID AAW42469 standard; Peptide; 9 AA.XX  
AC AAW42469;XX  
DT 22-JUN-1998 (first entry)XX  
DE Fab2 light chain complementarity determining region 3.XX  
KW Neutralising antibody; monoclonal antibody; MAB; 2B6; Fab; mouse;  
interleukin-5; IL-5; human; eosinophil; asthma; allergic rhinitis;  
atopic dermatitis; therapy; diagnosis; chain shuffling;  
complementarity determining region; CDR.XX  
OS Mus musculus.XX  
PN WO9748418-A1.XX  
PD 24-DEC-1997.XX  
PF 20-JUN-1997; 97WO-US10769.XX  
PR 21-JUN-1996; 96US-0667769.XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.XX  
PI Appelbaum ER, Cook RM;XX  
DR WPI; 1998-062853/06.XX  
PT Use of neutralising antibody to human interleukin-5 - that does not  
block binding to receptor alpha chain, to treat e.g. asthma,  
allergic rhinitis or atopic dermatitisXX  
PS Example 3; Page 71; 116pp; English.XX  
CC This peptide comprises complementarity determining region 3 (CDR3)  
of the light chain sequence of Fab2 (see AAW42467), an anti-human  
interleukin-5 (hIL-5) Fab obtained by chain shuffling; CDR1 and  
CDR2 of Fab2 are derived from the light chain variable region  
(see AAW42452) of anti-hIL-5 murine monoclonal antibody 2B6. The  
invention provides antibodies, especially altered, chimeric and  
humanised antibodies which are characterised by hIL-5 specificity,  
neutralising activity and affinity for hIL-5. The antibodies are  
useful for treating hIL-5-mediated disorders such as asthma,  
allergic rhinitis and atopic dermatitis, and can also be used in  
the diagnosis of such conditions by measurement (e.g. by ELISA) of  
endogenous hIL-5 levels. Also provided are vectors and transformed  
host cells for expression of the novel antibodies.XX  
SQ Sequence 9 AA;

## Query Match

Best Local Similarity 40.0%; Score 4; DB 19; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

Db 6 YPFT 9

## RESULT 43

AAW42470  
ID AAW42470 standard; Peptide; 9 AA.XX  
AC AAW42470;XX  
DT 22-JUN-1998 (first entry)

XX

DE Fab15 light chain complementarity determining region 3.

XX  
KW Neutralising antibody; monoclonal antibody; MAB; 2B6; Fab; mouse;  
interleukin-5; IL-5; human; eosinophil; asthma; allergic rhinitis;  
atopic dermatitis; therapy; diagnosis; chain shuffling;  
complementarity determining region; CDR.XX  
OS Mus musculus.XX  
PN WO9748418-A1.XX  
PD 24-DEC-1997.XX  
PF 20-JUN-1997; 97WO-US10769.XX  
PR 21-JUN-1996; 96US-0667769.XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.XX  
PI Appelbaum ER, Cook RM;XX  
DR WPI; 1998-062853/06.XX  
PT Use of neutralising antibody to human interleukin-5 - that does not  
block binding to receptor alpha chain, to treat e.g. asthma,  
allergic rhinitis or atopic dermatitisXX  
PS Example 3; Page 71; 116pp; English.XX  
CC This peptide comprises complementarity determining region 3 (CDR3)  
of the light chain sequence of Fab15 (see AAW42468), an anti-human  
interleukin-5 (hIL-5) Fab obtained by chain shuffling; CDR1 and  
CDR2 of Fab15 are derived from the light chain variable region  
(see AAW42452) of anti-hIL-5 murine monoclonal antibody 2B6. The  
invention provides antibodies, especially altered, chimeric and  
humanised antibodies which are characterised by hIL-5 specificity,  
neutralising activity and affinity for hIL-5. The antibodies are  
useful for treating hIL-5-mediated disorders such as asthma,  
allergic rhinitis and atopic dermatitis, and can also be used in  
the diagnosis of such conditions by measurement (e.g. by ELISA) of  
endogenous hIL-5 levels. Also provided are vectors and transformed  
host cells for expression of the novel antibodies.XX  
SQ Sequence 9 AA;

## Query Match

Best Local Similarity 40.0%; Score 4; DB 19; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

Db 6 YPFT 9

## RESULT 44

AAW39877

ID AAW39877 standard; peptide; 9 AA.

XX  
AC AAW39877;XX  
DT 16-JUN-1998 (first entry)XX  
DE Light chain CDR3 of a catalytic antibody capable of degrading cocaine.XX  
KW Variable domain; lambda light chain; catalytic antibody; degradation;  
cocaine; cocaine transition state analogue; TSA; benzoic acid;  
phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
overdose; addiction.XX  
OS Mus sp.XX  
FH KeyXX  
FT Misc-difference 2 Location/Qualifiers

FT Misc-difference 4 /note= "not specified"  
 FT FT /note= "not specified"  
 FT Misc-difference 5 /note= "not specified"  
 FT FT

PN WO9749800-A1.  
 XX  
 XX 31-DEC-1997.  
 XX  
 XX 25-JUN-1997; 97WO-US10965.  
 XX  
 XX 25-JUN-1996; 96US-0672345.  
 XX  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX

PI Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required  
 PT in far smaller doses than antibodies that antagonise cocaine by  
 PT simply binding

XX Claim 10; Page 5; 147pp; English.

XX AAW39875-77 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of a catalytic antibody which is capable of  
 CC degrading cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release  
 CC 3H-benzoic acid from 3H-phenyl cocaine. These antibodies were found  
 CC to have CDRs of the present sequence. The antibodies reduce the  
 CC concentration of cocaine in a subject, and are used particularly for the  
 CC treatment of an overdose. They are also used for treating addiction (by  
 CC reducing the in vivo concentration that can be achieved).

XX Sequence 9 AA;

Query Match 40.0%; Score 4; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
 DB ||||  
 6 YPFT 9

RESULT 45

AAW39817  
 ID AAW39817 standard; peptide; 9 AA.

AC AAW39817;

XX 16-JUN-1998 (first entry)

DE Light chain CDR3 of catalytic antibody 3B9.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

OS Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US10965.

XX 25-JUN-1996; 96US-0672345.

XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required  
 PT in far smaller doses than antibodies that antagonise cocaine by  
 PT simply binding

XX Claim 11; Page 81; 147pp; English.

XX AAW39815-17 represent the sequences of the light chain complementarity  
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues  
 CC (TSAs) were prepared and used to immunise mice for production of  
 CC hybridomas. Catalytic antibodies were identified by their capacity to  
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was  
 CC identified using TSA1, which is an immunogenic conjugate of a phosphate  
 CC monoster transition state analogue. Antibody 3B9 has a per minute Kcat  
 CC of 0.11. The antibodies reduce the concentration of cocaine in a subject,  
 CC and are used particularly for the treatment of an overdose. They are also  
 CC used for treating addiction (by reducing the in vivo concentration that  
 CC can be achieved).

XX Sequence 9 AA;

Query Match 40.0%; Score 4; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
 DB ||||  
 6 YPFT 9

RESULT 46

AAW39820  
 ID AAW39820 standard; peptide; 9 AA.

AC AAW39820;

XX 16-JUN-1998 (first entry)

DE Light chain CDR3 of catalytic antibody 6A12.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

OS Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US10965.

XX 25-JUN-1996; 96US-0672345.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required  
 PT in far smaller doses than antibodies that antagonise cocaine by  
 PT simply binding



XX Claim 13; Page 82; 147pp; English.

PS AAW39818-20 represent the sequences of the light chain complementarity

CC determining regions (CDRs) of the catalytic antibody 6A12, which is able

CC to degrade cocaine. A series of cocaine transition state analogues

CC (TSAs) were prepared and used to immunise mice for production of

CC hybridomas. Catalytic antibodies were identified by their capacity to

CC release 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was

CC identified using TSA1, which is an immunogenic conjugate of a phosphate

CC monoester transition state analogue. Antibody 6A12 has a per minute Kcat

CC of 0.072. The antibodies reduce the concentration of cocaine in a

CC subject, and are used particularly for the treatment of an overdose. They

CC are also used for treating addiction (by reducing the in vivo

CC concentration that can be achieved).

XX Sequence 9 AA;

QY Query Match 40.0%; Score 4; DB 19; Length 9;

DB Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

DB |||||

6 YPFT 9

RESULT 47

AAW39823

ID AAW39823 standard; peptide; 9 AA.

AC AAW39823;

XX

XX 16-JUN-1998 (first entry)

XX

DE Light chain CDR3 of catalytic antibody 2A10.

XX

XX Variable domain; lambda light chain; catalytic antibody; degradation;

KW cocaine; cocaine transition state analogue; TSA; benzoic acid;

KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

KW overdose; addiction.

XX

OS Mus sp.

XX

PN WO9749800-A1.

XX

XX 31-DEC-1997.

XX

XX 25-JUN-1997; 97WO-US10965.

XX

XX 25-JUN-1996; 96US-0672345.

XX

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX

XX Landry DW;

XX

XX WPI; 1998-077166/07.

XX

XX New catalytic antibodies able to decompose cocaine, single-chain

PT analogues - used to treat cocaine overdose and addiction, required

PT in far smaller doses than antibodies that antagonise cocaine by

PT simply binding

XX

PS Claim 15; Page 82; 147pp; English.

XX

XX AAW39821-23 represent the sequences of the light chain complementarity

CC determining regions (CDRs) of the catalytic antibody 2A10, which is able

CC to degrade cocaine. A series of cocaine transition state analogues

CC (TSAs) were prepared and used to immunise mice for production of

CC hybridomas. Catalytic antibodies were identified by their capacity to

CC release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was

CC identified using TSA1, which is an immunogenic conjugate of a phosphate

CC monoester transition state analogue. Antibody 2A10 has a per minute Kcat

CC of 0.011. The antibodies reduce the concentration of cocaine in a

CC subject, and are used particularly for the treatment of an overdose. They

CC are also used for treating addiction (by reducing the in vivo

CC concentration that can be achieved).

XX Sequence 9 AA;

QY Query Match 40.0%; Score 4; DB 19; Length 9;

DB Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

DB |||||

6 YPFT 9

RESULT 48

AAW39826

ID AAW39826 standard; peptide; 9 AA.

XX

XX AAW39826;

XX

XX 16-JUN-1998 (first entry)

XX

DE Light chain CDR3 of catalytic antibody 12H1.

XX

XX Variable domain; lambda light chain; catalytic antibody; degradation;

KW cocaine; cocaine transition state analogue; TSA; benzoic acid;

KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

KW overdose; addiction.

XX

OS Mus sp.

XX

PN WO9749800-A1.

XX

XX 31-DEC-1997.

XX

XX 25-JUN-1997; 97WO-US10965.

XX

XX 25-JUN-1996; 96US-0672345.

XX

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX

XX Landry DW;

XX

XX WPI; 1998-077166/07.

XX

XX New catalytic antibodies able to decompose cocaine, single-chain

PT analogues - used to treat cocaine overdose and addiction, required

PT in far smaller doses than antibodies that antagonise cocaine by

PT simply binding

XX

PS Claim 17; Page 83; 147pp; English.

XX

XX AAW39824-26 represent the sequences of the light chain complementarity

CC determining regions (CDRs) of the catalytic antibody 12H1, which is able

CC to degrade cocaine. A series of cocaine transition state analogues

CC (TSAs) were prepared and used to immunise mice for production of

CC hybridomas. Catalytic antibodies were identified by their capacity to

CC release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was

CC identified using TSA2, and has a per minute Kcat of 0.16. The antibodies

CC reduce the concentration of cocaine in a subject, and are used

CC particularly for the treatment of an overdose. They are also used for

CC treating addiction (by reducing the in vivo concentration that can be

CC achieved).

XX Sequence 9 AA;

QY Query Match 40.0%; Score 4; DB 19; Length 9;

DB Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

Db 6 YPFT 9

||||

## RESULT 49

AA97234  
ID AAY97234 standard; Protein; 9 AA.XX  
AC AAY97234;XX  
DT 19-DEC-2000 (first entry)XX  
DE Complementary determining region (CDRL3) of anti-SI (KDR) antibody.XX  
KW Immunoglobulin; antibody; complementary determining region; CDR;  
KW VEGF; vascular endothelial growth factor; KDR;  
KW kinase insert domain containing receptor; multivalent; monovalent;  
KW humanised antibody; chimeric antibody; tumour; diabody; triabody;  
KW glioblastoma multiforme; hemangioblastoma; AIDS;  
KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;  
KW acquired immune deficiency syndrome; AIDS; human.XX  
OS Homo sapiens.  
OS Synthetic.XX  
PN WO200044777-A1.XX  
PD 03-AUG-2000.XX  
PF 28-JAN-2000; 2000WO-US02180.XX  
PR 29-JAN-1999; 99US-0117726.XX  
PR 29-JAN-1999; 99US-0240736.XX  
PA (IMCL-) IMCLONE SYSTEMS INC.XX  
PI Zhu Z, Witte L;XX  
DR WPI; 2000-505966/45.XX  
DR N-PSDB; AAA53766.XX  
PT Novel immunoglobulin molecules binding kinase insert domain-containing  
PT receptor with the same affinity as vascular endothelial growth factor,  
PT used to reduce tumour growthXX  
PS Claim 3; Page 50; 55pp; English.XX  
CC New immunoglobulin molecules are described that bind kinase insert  
CC domain-containing receptor (KDR) with a comparable affinity to human  
CC vascular endothelial growth factor (VEGF). The antibodies neutralise  
CC KDR activation. The immunoglobulin may be a multivalent single  
CC chain antibody, a monovalent single chain antibody, a diabody, a  
CC triabody, a humanised antibody or a chimerised antibody.  
CC The immunoglobulin molecules bind specifically to an  
CC extracellular domain of the KDR receptor with the same affinity as  
CC VEGF. Overexpression of VEGF has been implicated in a number of  
CC human tumour cell lines including glioblastoma multiforme,  
CC hemangioblastoma, central nervous system neoplasms and AIDS  
CC associated Kaposi's sarcoma. The antibodies therefore have  
CC applications in treating these conditions. This sequence encodes a  
CC preferred heavy chain complementary determining region of the  
CC immunoglobulins of the invention.XX  
SQ Sequence 9 AA;

Query Match 40.0%; Score 4; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

||||

Db 6 YPFT 9

## RESULT 50

AAY92171

ID AAY92171 standard; Peptide; 9 AA.

XX  
AC AAY92171;XX  
DT 01-AUG-2000 (first entry)XX  
DE Murine 13H10 light chain variable region CDR 3.XX  
KW Light chain; variable region; complementarity determining region; CDR 3;  
KW anti-Tie2 kinase receptor; monoclonal antibody; 1588; angiogenetic;  
KW vascular-general; proliferative; antischismic; cerebroprotective;  
KW cardiant; agonist; antibody inhibition.XX  
OS Mus musculus.XX  
PN WO200018804-A1.XX  
PD 06-APR-2000.XX  
PF 28-SEP-1999; 99WO-US22428.XX  
PR 28-SEP-1998; 98US-0102098.XX  
PA (SMIK) SMITHKLINE BEECHAM CORP.XX  
PA (SMIK) SMITHKLINE BEECHAM PLC.XX  
PI Holmes SD, Erickson-miller CL, Winkler JD;XX  
DR WPI; 2000-293114/25.XX  
PT Tie2 receptor agonist antibodies useful for promoting angiogenesis in  
PT patients suffering from strokes and myocardial infarctionsXX  
PS Claim 20; Page 46; 50pp; English.XX  
CC AAY92169-71 are light chain CDR (complementarity determining regions)  
CC from a novel murine anti-Tie2 kinase receptor agonist monoclonal  
CC antibody 13H10. Tie2 is a single-transmembrane, tyrosine kinase receptor  
CC ('Tie' stands for tyrosine kinase receptor with immunoglobulin and  
CC endothelial growth factor (EGF) homology domain(s)). Anti-Tie2  
CC antibodies may be administered to enhance angiogenesis in mammals  
CC suffering from ischemic disease, myocardial infarction or cerebral stroke  
CC or other vascular diseases such as diabetes. It may also be used to  
CC enhance endothelial cell survival and to promote haematopoietic or  
CC megakaryocyte cell proliferation (claimed).XX  
SQ Sequence 9 AA;

Query Match 40.0%; Score 4; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

||||

Db 6 YPFT 9

## RESULT 51

AAY32256

ID AAY32256 standard; Peptide; 9 AA.

XX  
AC AAY32256;XX  
DT 15-FEB-2000 (first entry)XX  
DE Light chain CDR L3 of mouse anti-CD23 Mab C11.XX  
KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;  
KW monoclonal antibody; chimeric antibody; humanised antibody;  
KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.

OS Mus musculus.

XX WO9958679-A1.

PN 18-NOV-1999.

PD 07-MAY-1999; 99WO-GB01434.

XX 09-MAY-1998; 98GB-0009839.

XX (GLAXO) GLAXO GROUP LTD.

PA Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J; WPI: 2000-053101/04.

DR N-PSDB; AAZ34741.

XX Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis -

PT Claim 1; Page 40; 81pp; English.

PS This sequence represents complementarity determining region 3 (CDR L3) of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11 (see also AAY32262). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation for treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type 1 diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents.

XX Query Match 40.0%; Score 4; DB 21; Length 9;

SQ Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
|  
|  
|  
|  
6 YPFT 9

Db

RESULT 52  
AAE13142

ID AAE13142 standard; peptide; 9 AA.

XX AAE13142;

XX 28-JAN-2002 (first entry)

DT Humanised antibody murine light chain hypervariable region (VL) CDR3.

DE Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour; cytostatic; light chain hypervariable region; VL; myelocytic leukaemia; lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;

KW Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.

XX Mus sp.

XX WO200174296-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10504.

XX 31-MAR-2000; 2000US-0540770.

XX (IMCL-) IMCLONE SYSTEMS INC.

PA (CORR) CORNELL RES FOUND INC.

XX Witte L, Rafii S;

XX WPI: 2001-662942/76.

DR N-PSDB; AAD21668.

XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow tumors such as leukemias or multiple myeloma comprises treatment with an antagonist of a vascular endothelial growth factor receptor -

PT Claim 8; Page 15; 68pp; English.

PS The invention relates to a method for inhibiting the growth of non-solid tumour cells that are stimulated by a ligand of vascular endothelial growth factor receptor (VEGFR) in mammals particularly humans. The method involves treating the mammals with humanised VEGFR monoclonal antibodies (antagonists). Humanised monoclonal antibody comprises humanised mouse variable region joined to human constant region, where the humanised mouse variable region contains mouse complementarity determining region (CDR) grafted into human variable region. The method is useful for treating leukaemias such as acute or chronic myelocytic leukaemia, acute or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia, multiple myelomas and lymphoid cells, particularly those related to non-Hodgkin's and Hodgkin's disease. The present sequence is humanised antibody murine light chain hypervariable region (VL) CDR-3 used in the exemplification of the invention.

XX Query Match 40.0%; Score 4; DB 22; Length 9;

SQ Best Local Similarity 100.0%; Pred. No. 9.3e+05; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
|  
|  
|  
|  
6 YPFT 9

Db

RESULT 53  
AAE10479

ID AAE10479 standard; peptide; 9 AA.

XX AAE10479;

XX 10-DEC-2001 (first entry)

DT Humanised Ab light chain complementarity determining region, CDR-L3.

DE Human; light chain; respiratory syncytial virus infection; virucide; parainfluenza virus; therapy; high potency antibody; drug; cocaine; cancer cell; toxic substance; complementarity determining region; CDR-L3.

XX Homo sapiens.

OS Synthetic.

XX WO200164751-A2.

PN 07-SEP-2001.

XX

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PF 01-MAR-2001; 2001WO-US06815.
XX
PR 01-MAR-2000; 2000US-0186252.
XX
XX (MEDI-) MEDIMMUNE INC.
XX
PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
XX
DR WPI; 2001-582150/65.
XX
PT High potency recombinant antibody, useful for preventing and treating
PT diseases induced or caused by viruses, especially respiratory syncytial
PT virus and parainfluenza virus, has high kinetic association rate
PT constant -
XX
PS Example 1; Page 30; 98pp; English.
XX
CC The invention relates to a high potency antibody including its
CC immunologically active portions, fragments and segments other than
CC vitaxin. The antibody has increased potency, high rate constant for
CC antibody-antigen complex formation and high affinity for any desired
CC antigen. The high potency antibody is also useful for nullifying or
CC ameliorating the effects of addictive drugs, such as cocaine. The high
CC potency has specificity for antigenic determinants found on microbes
CC such as viruses, bacteria or fungi, antigens found on cancer cells and
CC toxic substances or product of toxic substances. The high potency
CC antibody is useful for preventing or treating a disease caused by a
CC virus such as respiratory syncytial virus (RSV) and parainfluenza
CC virus (PIV). The present sequence is humanised antibody light chain
CC variable region complementarity determining region (CDR) which is used
CC for producing high potency antibody.
XX
SQ Sequence 9 AA;
Query Match 40.0%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YPFT 5
DB 6 YPFT 9
RESULT 54
AAE10495
ID AAE10495 standard; peptide; 9 AA.
XX
XX AAE10495;
AC
DT 10-DEC-2001 (first entry)
XX
DE Humanised Ab clone 6 high potency modified light chain CDR, CDR-L3.
XX
KW Human; light chain; respiratory syncytial virus infection; virucide;
KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
KW cancer cell; toxic substance; complementarity determining region; CDR-L3.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 5 /note= "wild type Gly substituted with Phe"
FT
XX WO200164751-A2.
XX
PD 07-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US06815.
XX
PR 01-MAR-2000; 2000US-0186252.
XX
XX (MEDI-) MEDIMMUNE INC.
XX

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XX Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
XX
XX WPI; 2001-582150/65.
XX
XX High potency recombinant antibody, useful for preventing and treating
XX diseases induced or caused by viruses, especially respiratory syncytial
XX virus and parainfluenza virus, has high kinetic association rate
XX constant -
XX
XX Claim 22; Page 35; 98pp; English.
XX
XX The invention relates to a high potency antibody including its
XX immunologically active portions, fragments and segments other than
XX vitaxin. The antibody has increased potency, high rate constant for
XX antibody-antigen complex formation and high affinity for any desired
XX antigen. The high potency antibody is also useful for nullifying or
XX ameliorating the effects of addictive drugs, such as cocaine. The high
XX potency has specificity for antigenic determinants found on microbes
XX such as viruses, bacteria or fungi, antigens found on cancer cells and
XX toxic substances or product of toxic substances. The high potency
XX antibody is useful for preventing or treating a disease caused by a
XX virus such as respiratory syncytial virus (RSV) and parainfluenza
XX virus (PIV). The present sequence is humanised high potency modified
XX antibody light chain variable region complementarity determining region
XX (CDR).
XX
XX Sequence 9 AA;
SQ
Query Match 40.0%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YPFT 5
DB 6 YPFT 9
RESULT 55
AAB82708
ID AAB82708 standard; Peptide; 9 AA.
XX
XX AAB82708;
AC
DT 15-OCT-2001 (first entry)
XX
DE VEGF antagonist antibody IMC-1C11 VL CDR-3.
XX
KW IMC-1C11; Chimeric antibody; mouse; human; antagonist; VEGF;
KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
KW colon carcinoma; ovarian carcinoma; neuroblastoma;
KW glioblastoma multiforme; melanoma; therapy; light chain; CDR;
KW complementarity determining region.
XX
XX Chimeric - Mus sp.
XX Chimeric - Homo sapiens.
XX
XX WO200154723-A1.
XX
XX 02-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US02839.
XX
XX 28-JAN-2000; 2000US-0178791.
XX
XX 31-MAR-2000; 2000US-0539692.
XX
XX (SUNN-) SUNNVERBROOK HEALTH SCI CENT.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX
XX Kerbel R;
XX

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DR WPI; 2001-514531/56.  
 XX Treating or controlling an angiogenic dependent condition (e.g. a  
 PT neoplasm, collagen-vascular or autoimmune disease) in mammal by  
 PT administering a combination of an antiangiogenic molecule and a  
 PT chemotherapeutic agent -  
 XX  
 PS Disclosure; Page 37; 42pp; English.  
 XX  
 CC The present sequence is that of complementarity determining region  
 CC 3 of the light chain variable region (see also AAB82702) of  
 CC IMC-1C11, a mouse-human chimeric antibody that has vascular  
 CC endothelial growth factor (VEGF) antagonist activity. The antibody,  
 CC or a fragment of it, can be used as an anti-angiogenic molecule,  
 CC together with a chemotherapeutic acid, for the treatment of an  
 CC angiogenic dependent condition in a mammal, especially a human.  
 CC The invention relates generally to a method of treating or  
 CC controlling an angiogenic dependent condition by administering an  
 CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a  
 CC regression or arrest of the condition while minimising or  
 CC preventing significant toxicity of the chemotherapeutic agent.  
 CC The anti-angiogenic molecule inhibits or blocks the action of a  
 CC vascular endothelium survival factor such as VEGF or its receptor,  
 CC and is especially IMC-1C11. Conditions that can be treated include  
 CC a neoplasm, a collagen-vascular disease or an autoimmune disease,  
 CC especially a solid tumour, including breast carcinoma, lung  
 CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,  
 CC ovarian carcinoma, neuroblastoma, central nervous system tumour,  
 CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).  
 XX  
 SQ Sequence 9 AA;  
 Query Match 40.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YPFT 5  
 Db ||||  
 6 YPFT 9  
 RESULT 56  
 AAG63246  
 ID AAG63246 standard; peptide; 9 AA.  
 AC AAG63246;  
 XX  
 DT 01-OCT-2001 (first entry)  
 XX  
 DE Complementarity determining region 3 of light chain of RSV-antibody.  
 XX  
 KW Light chain; heavy chain; chimeric antibody; respiratory syncytial virus;  
 KW RSV.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200155217-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 26-JAN-2001; 2001WO-US02618.  
 XX  
 PR 27-JAN-2000; 2000US-0178426.  
 XX  
 PA (MEDI-) MEDIMUNE INC.  
 XX  
 PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;  
 XX WPI; 2001-476194/51.  
 XX  
 PT High affinity neutralizing immunoglobulin, used to prevent and treat  
 PT RSV infection, comprises at least 3 high affinity complementarity  
 PT determining regions -  
 XX  
 SQ Sequence 9 AA;  
 Query Match 40.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

XX  
 PS Example 1; Page 25; 80pp; English.  
 XX  
 CC AAG63244-49 represent the complementarity determining regions (CDRs)  
 CC of the light chain and heavy chain variable regions of a murine  
 CC antibody which targets respiratory syncytial virus (RSV). This reference  
 CC antibody is used to create high affinity neutralising antibodies with  
 CC binding affinities in the range of 10 to the power 10/M. The antibodies  
 CC comprise at least 3 high affinity CDRs, especially those with frame-work  
 CC and constant regions derived from either humans and mice. The antibodies  
 CC are used to prevent and/or treat a virus-induced disease, such as RSV  
 CC disease.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 40.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YPFT 5  
 Db ||||  
 6 YPFT 9  
 RESULT 57  
 AAG63255  
 ID AAG63255 standard; peptide; 9 AA.  
 XX  
 AC AAG63255;  
 XX  
 DT 01-OCT-2001 (first entry)  
 XX  
 DE Complementarity determining region of heavy chain of antiRSV-antibody.  
 XX  
 KW Light chain; heavy chain; chimeric antibody; respiratory syncytial virus;  
 KW RSV.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200155217-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 26-JAN-2001; 2001WO-US02618.  
 XX  
 PR 27-JAN-2000; 2000US-0178426.  
 XX  
 PA (MEDI-) MEDIMUNE INC.  
 XX  
 PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;  
 XX WPI; 2001-476194/51.  
 XX  
 PT High affinity neutralizing immunoglobulin, used to prevent and treat  
 PT RSV infection, comprises at least 3 high affinity complementarity  
 PT determining regions -  
 XX  
 PS Claim 17; Page 32; 80pp; English.  
 XX  
 CC AAG63250-57 represent high affinity complementarity determining regions  
 CC (CDRs) of the light chain and heavy chain variable regions of an  
 CC antibody which targets respiratory syncytial virus (RSV). This reference  
 CC antibody is used to create high affinity neutralising antibodies with  
 CC binding affinities in the range of 10 to the power 10/M. The antibodies  
 CC comprise at least 3 high affinity CDRs, especially those with frame-work  
 CC and constant regions derived from either humans and mice. The antibodies  
 CC are used to prevent and/or treat a virus-induced disease, such as RSV  
 CC disease.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 40.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YPFT 5  
 |||||  
 Db 6 YPFT 9

RESULT 58  
 AAG63256  
 ID AAG63256 standard; peptide; 9 AA.  
 XX AC  
 XX AAG63256;  
 XX DT 01-OCT-2001 (first entry)  
 XX DE Complementarity determining region of heavy chain of antiRSV-antibody.  
 XX KW Light chain; heavy chain; chimeric antibody; respiratory syncytial virus;  
 XX KW RSV.  
 XX OS Synthetic.  
 XX PN WO200155217-A1.  
 XX PD 02-AUG-2001.  
 XX PF 26-JAN-2001; 2001WO-US02618.  
 XX PR 27-JAN-2000; 2000US-0178426.  
 XX PA (MEDI-) MEDIMMUNE INC.  
 XX PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;  
 XX WPI; 2001-476194/51.  
 XX PS Claim 17; Page 32; 80pp; English.  
 XX CC AAG63250-57 represent high affinity complementarity determining regions  
 CC (CDRs) of the light chain and heavy chain variable regions of an  
 CC antibody which targets respiratory syncytial virus (RSV). This reference  
 CC antibody is used to create high affinity neutralising antibodies with  
 CC binding affinities in the range of 10 to the power 10/M. The antibodies  
 CC comprise at least 3 high affinity CDRs, especially those with frame-work  
 CC and constant regions derived from either humans and mice. The antibodies  
 CC are used to prevent and/or treat a virus-induced disease, such as RSV  
 CC disease.  
 XX Sequence 9 AA;  
 Query Match 40.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YPFT 5  
 |||||  
 Db 6 YPFT 9

RESULT 59  
 AAG63257  
 ID AAG63257 standard; peptide; 9 AA.  
 XX AC  
 XX AAG63257;  
 XX DT 01-OCT-2001 (first entry)  
 XX DE Complementarity determining region of heavy chain of antiRSV-antibody.  
 XX KW Light chain; heavy chain; chimeric antibody; respiratory syncytial virus;  
 XX KW RSV.  
 XX OS Synthetic.  
 XX PN WO200155217-A1.  
 XX PD 02-AUG-2001.  
 XX PF 26-JAN-2001; 2001WO-US02618.  
 XX PR 27-JAN-2000; 2000US-0178426.  
 XX PA (MEDI-) MEDIMMUNE INC.  
 XX PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;  
 XX WPI; 2001-476194/51.  
 XX PS Claim 17; Page 32; 80pp; English.  
 XX CC AAG63250-57 represent high affinity complementarity determining regions  
 CC (CDRs) of the light chain and heavy chain variable regions of an  
 CC antibody which targets respiratory syncytial virus (RSV). This reference  
 CC antibody is used to create high affinity neutralising antibodies with  
 CC binding affinities in the range of 10 to the power 10/M. The antibodies  
 CC comprise at least 3 high affinity CDRs, especially those with frame-work  
 CC and constant regions derived from either humans and mice. The antibodies  
 CC are used to prevent and/or treat a virus-induced disease, such as RSV  
 CC disease.  
 XX Sequence 9 AA;  
 Query Match 40.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW Light chain; heavy chain; chimeric antibody; respiratory syncytial virus;  
 KW RSV.  
 XX Synthetic.  
 XX OS  
 XX PN WO200155217-A1.  
 XX PD 02-AUG-2001.  
 XX PF 26-JAN-2001; 2001WO-US02618.  
 XX PR 27-JAN-2000; 2000US-0178426.  
 XX PA (MEDI-) MEDIMMUNE INC.  
 XX PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;  
 XX WPI; 2001-476194/51.  
 XX PS High affinity neutralizing immunoglobulin, used to prevent and treat  
 PT RSV infection, comprises at least 3 high affinity complementarity  
 PT determining regions -  
 XX Claim 17; Page 32; 80pp; English.  
 XX CC AAG63250-57 represent high affinity complementarity determining regions  
 CC (CDRs) of the light chain and heavy chain variable regions of an  
 CC antibody which targets respiratory syncytial virus (RSV). This reference  
 CC antibody is used to create high affinity neutralising antibodies with  
 CC binding affinities in the range of 10 to the power 10/M. The antibodies  
 CC comprise at least 3 high affinity CDRs, especially those with frame-work  
 CC and constant regions derived from either humans and mice. The antibodies  
 CC are used to prevent and/or treat a virus-induced disease, such as RSV  
 CC disease.  
 XX Sequence 9 AA;  
 Query Match 40.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YPFT 5  
 |||||  
 Db 6 YPFT 9

RESULT 60  
 AAB47113  
 ID AAB47113 standard; Peptide; 9 AA.  
 XX AC AAB47113;  
 XX DT 04-JUN-2001 (first entry)  
 XX DE Mutant scFv 508F light chain CDR3, Phe96.  
 XX KW Human; prion protein; plaque forming disease; display vehicle; kuru;  
 KW aggregating protein; amyloid plaque; brain; early onset; senility;  
 KW Alzheimer's disease; late onset; pre-symptomatic; SAA amyloidosis;  
 KW hereditary Icelandic syndrome; multiple myeloma; scrapie; BSE; CJD;  
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob Disease; FFI;  
 KW Gerstmann-Strausler-Sheinker Disease; GSS; fatal familial insomnia;  
 KW antibody.  
 XX Synthetic.  
 XX OS  
 XX PN WO200118169-A2.  
 XX PD 15-MAR-2001.  
 XX PF 31-AUG-2000; 2000WO-IL00518.  
 XX PR 03-SEP-1999; 99US-0152417.



DR WPI; 2001-590062/66.

XX CD154 binding molecule, in particular antibody to human CD154 for use

PT in treatment, prevention of autoimmune, inflammatory diseases,

PT atherosclerosis, Alzheimer's disease and prevention of transplant

PT rejection

XX Claim 2; Page 23; 37pp; English.

XX The present sequence is that of complementarity determining region

CC 3 (CDR3) of the light chain variable region (VL, see also AAB82890)

CC of mouse anti-human CD154 monoclonal antibody ABR1793. The invention

CC provides a CD154 binding molecule, in particular an antibody to

CC human CD154, in which the VH region has the CDR1, CDR2 and CDR3 of

CC ABR1793 VH and the VL region has the CDR1, CDR2 and CDR3 of ABR1793

CC VL. The CD154 binding molecule is especially a human antibody in

CC which the VH and VL domains are essentially those of ABR1793, with

CC constant regions from human heavy and light chains. The antibodies

CC are used to inhibit an immune response mediated by CD154-positive

CC cell interactions with CD40-positive cells, in the treatment and/or

CC prevention of diseases, disorders or conditions where CD154

CC modulation and/or interference with or inhibition of the CD154:CD40

CC interactions is therapeutically beneficial, prevention of

CC macrophage-associated inflammatory processes and in the treatment of

CC diseases where suppression of antibody responses to antigens is

CC desirable (claimed). The CD154 binding molecules are useful for

CC prevention of cell, tissue or organ graft rejection, in the prevention

CC and treatment of autoimmune or inflammatory diseases, atherosclerosis

CC or Alzheimer's disease, and also for inhibiting B cell proliferation

CC and differentiation, T cell responses, induction or modulation of T

CC or B cell tolerance or inhibition of the growth of tumour cells

CC expressing CD154 antigen. Such conditions include autoimmune and

CC non-autoimmune disorders, in particular, Addison's disease, Celiac

CC sprue, glomerulonephritis, Grave's disease, Hashimoto's thyroiditis,

CC haemolytic disease of the newborn, keratitis, multiple sclerosis,

CC polymyositis, psoriasis, rheumatic fever, rheumatoid arthritis,

CC sarcoidosis, syphilis, tuberculosis, ulcerative colitis,

CC HIV infection, leukaemia or lymphoma.

XX SQ Sequence 9 AA;

Query Match 40.0%; Score 4; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 YPFT 5

Db ||||

6 YPFT 9

RESULT 63

AAG63993

ID AAG63993 standard; peptide; 9 AA.

XX AC AAG63993;

XX DT 26-NOV-2001 (first entry)

XX DE Complementarity determining region of light chain of antibody 2C4.

XX KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;

XX KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;

XX KW leukemia; eosinophil.

XX OS Mus sp.

XX PN WO200166126-A1.

XX PD 13-SEP-2001.

XX PF 05-MAR-2001; 2001WO-US07193.

XX PR 07-MAR-2000; 2000US-0187595.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PA (UYJO ) UNIV JOHNS HOPKINS.

XX Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;

PI Schleimer R;

XX WPI; 2001-570749/64.

XX Novel monoclonal antibody specific for human sialoadhesin factor-2 for

PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases

PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal

XX Claim 10; Page 34; 35pp; English.

XX AAG63991-93 represent the complementarity determining regions (CDRs)

CC of the light chain variable region of murine monoclonal antibody 2C4.

CC This antibody binds to human sialoadhesin factor-2 (SAF-2). The

CC antibody is useful for treating or preventing allergic rhinitis,

CC allergies, asthma, anemia, eczema or diseases such as lymphoma,

CC leukemia or systemic mastocytosis in a mammal. It is also useful for

CC detecting the presence of a cell, especially eosinophil in a sample,

CC by detecting binding of the antibody to SAF-2. The antibody can be

CC coupled to toxins, antiproliferative drugs or radionuclides to

CC kill cells in areas of excessive SAF-2 expression.

XX SQ Sequence 9 AA;

Query Match 40.0%; Score 4; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 YPFT 5

Db ||||

6 YPFT 9

RESULT 64

ABP55880

ID ABP55880 standard; Peptide; 9 AA.

XX AC ABP55880;

XX DT 25-FEB-2003 (first entry)

XX DE B15 class I sHLA molecule ligand related peptide #174.

XX KW HLA ligand; human leukocyte antigen; predictive algorithm; database;

XX KW MHC ligand; major histocompatibility complex; viral; bacterial; tumour.

XX OS Synthetic.

XX PN WO200269198-A2.

XX PD 06-SEP-2002.

XX PF 21-FEB-2002; 2002WO-US05298.

XX PR 21-FEB-2001; 2001US-270357P.

XX PR 10-OCT-2001; 2001US-0974366.

XX PR 18-DEC-2001; 2001US-0022066.

XX PA (HILD/) HILDEBRAND W H.

XX PA (PRIL/) PRILLMAN K R.

XX PA (HICK/) HICKMAN H D.

XX PI Hildebrand WH, Prillman KR, Hickman HD;

XX WPI; 2002-732755/79.

XX Human leukocyte antigen ligand database assembled by producing HLA

PT having loaded ligands, isolating and sequencing loaded ligands to



PT obtain HLA ligand data and populating database in computer system with  
 XX ligand data -  
 PS Disclosure; Fig 5; 118pp; English.  
 XX  
 XX The present invention describes a human leukocyte antigen (HLA)  
 CC (e.g. soluble HLA) ligand database assembled by a process which involves  
 CC providing a computer system capable of storing HLA data as a database,  
 CC producing HLA having ligands loaded on it, isolating the loaded ligands  
 CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and  
 CC populating the database with HLA ligand data. Also described:  
 CC (1) accessing HLA (e.g. sHLA) data stored in a database; and (2) a  
 CC computer system for HLA (e.g. sHLA) ligand database. The database is  
 CC populated with HLA ligand sequences, motifs, extended motifs, submotifs,  
 CC ligands unique to infected cells, tumour specific ligands, as well as a  
 CC collection of current and future developed HLA ligand sequences. The  
 CC database which contains endogenously bound and loaded ligands facilitates  
 CC searching of viral, bacterial, tumour or human protein sequences for  
 CC ligands likely to bind a particular HLA class I or class II protein. The  
 CC database allows the user to screen an unknown peptide sequence for  
 CC potential matches with sHLA ligand discrete sequences or sHLA ligand  
 CC motifs of sequences. Due to the completeness and concentration of sHLA  
 CC HLA ligands is found in the sHLA ligand database, and by comparison of  
 CC such ligands to each other and to the genomic sequence, better motifs are  
 CC also found in the sHLA ligand database. ABP55692 to ABP55912 represent  
 CC amino acid sequences used in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 40.0%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPTG 6  
 DB 2 PPTG 5

RESULT 65  
 ABJ15164  
 ID ABJ15164 standard; Peptide; 9 AA.  
 XX  
 AC ABJ15164;  
 XX  
 XX 02-JAN-2003 (first entry)  
 XX  
 DE Immunogenic HIV peptide #24.  
 KW HIV; gene therapy; vaccine; immunogenic HIV peptide;  
 KW cytotoxic T lymphocyte; HIV infection.  
 XX Human immunodeficiency virus.  
 OS  
 XX WO200269691-A2.  
 PN  
 XX 12-SEP-2002.  
 PD  
 XX 01-MAR-2002; 2002WO-US06314.  
 PF  
 XX 01-MAR-2001; 2001US-272565P.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (UYBR-) UNIV BROWN RES FOUND.  
 XX  
 XX Mcnicholl JM, Bond K, Sriwanthana B, Pau C, Degroot A;  
 XX WPI; 2002-750429/81.  
 DR  
 XX New immunogenic HIV peptide having one or more epitopes immunoreactive  
 PT with cytotoxic T lymphocytes, useful for diagnosing, treating and  
 PT monitoring HIV infection in humans -

XX Claim 6; Page 42; 65pp; English.  
 PS  
 XX The invention comprises immunogenic HIV peptides which contain one or  
 CC more epitopes that are immunoreactive with cytotoxic T lymphocytes from  
 CC an HIV-positive individual. The immunogenic HIV peptides of the invention  
 CC are useful for diagnosing, treating and monitoring HIV infection. The  
 CC present amino acid sequence represents an immunogenic HIV peptide of the  
 CC invention.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 40.0%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GPPI 9  
 DB 1 GPPI 4

RESULT 66  
 ABG97127  
 ID ABG97127 standard; Peptide; 9 AA.  
 XX  
 AC ABG97127;  
 XX  
 DT 16-DEC-2002 (first entry)  
 XX  
 XX Human leukocyte antigen (HLA) B15 ligand #456.  
 XX  
 KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;  
 KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;  
 KW viral infection; cancer; autoimmune disease; vaccine development; MHC;  
 KW major histocompatibility complex; diagnostic development;  
 KW HLA class I polymorphism; HLA-B15 allotype; ligand.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200262846-A2.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 18-DEC-2001; 2001WO-US49744.  
 XX  
 PR 18-DEC-2000; 2000US-256409P.  
 PR 18-DEC-2000; 2000US-256410P.  
 PR 10-OCT-2001; 2001US-0974366.  
 XX  
 PA (HILD/) HILDEBRAND W H.  
 PA (PRIL/) PRILLIMAN K R.  
 XX  
 XX Hildebrand WH, Prilliman KR;  
 PI  
 XX WPI; 2002-698563/75.  
 DR  
 XX Producing soluble human leukocyte antigen (HLA) in cell pharm useful  
 PT for studies of peptide loading for characterizing human immune  
 PT responses involves using HLA allelic cDNA or genomic DNA as starting  
 PT material -  
 XX  
 XX Disclosure; Page 185; 300pp; English.  
 PS  
 XX The invention describes a method of producing soluble human leukocyte  
 CC antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA  
 CC allelic DNA by PCR using a locus specific primer to produce truncated a  
 CC PCR product (PI), inserting PI into mammalian expression vector;  
 CC electroporating the plasmid into a host cell; inoculating the cell pharm  
 CC with the host cell such that cell pharm produces sHLA. A multimeric HLA  
 CC complex (I) is useful for testing functionality of peptide ligands bound  
 CC by at least two soluble HLA molecules. (I) can be tested for its ability  
 CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune  
 CC responses in humans. (I) is useful for studying T cell responses to

pathological conditions such as viral infections and cancer, and for modulating the human immune system to induce tolerance in autoimmune diseases. The individual secreted major histocompatibility complex (MHC) molecules produced are useful for studies of peptide loading (i.e., in vaccine development) and to the development of diagnostics. With the secreted MHC molecules, naturally loaded peptides can be eluted from the MHC molecule and characterised. The secreted MHC molecules allow the assessment of structural and functional impact of HLA class I polymorphism. The molecules are also useful to generate ligands and hence ligand maps from the peptide pools extracted from series of distinct yet related class I HLA-B\*57 alleles; compare the different ligand maps to identify potentially shared elements; and characterise the elements identified to positively or negatively validate the occurrence of overlapping ligands. The truncated version of (MHC) can be produced in mammalian or insect/bacterial cells such that milligram or greater quantities of an individual class I or class II molecule can be obtained. This sequence represents a HLA (human leukocyte antigen) peptide ligand.

Sequence 9 AA;  
Query Match 40.0%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
| | | |  
DB 2 PFTG 5

RESULT 67  
AAE28015  
ID AAE28015 standard; peptide; 9 AA.

AC AAE28015;  
XX  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Human modified anti-RSV SYNGIS antibody VL domain CDR3.  
XX  
KW Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia; vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;  
KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;  
KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;  
KW complementarity determining region; CDR; virucide; mutant; mutein.

XX Homo sapiens.  
OS Synthetic.

PN WO200260919-A2.

PD 08-AUG-2002.

PF 12-DEC-2001; 2001WO-US48432.

PR 12-DEC-2000; 2000US-254884P.

PR 09-MAY-2001; 2001US-289760P.

XX (MEDI-) MEDIMUNE INC.

XX Dall'Acqua W, Johnson LS, Ward ES;

XX WPI; 2002-666925/71.

XX Modified immunoglobulins useful in the treatment of autoimmune diseases, comprises at least one amino acid modification relative to a wild-type immunoglobulin constant domain -

PS Disclosure; Page 115; 147pp; English.

XX The invention relates to a modified immunoglobulin (IgG1) which comprises an IgG constant domain having at least one amino acid modification. The immunoglobulins are used in the treatment or prevention of a disease or

CC disorder by passive immunotherapy for vaccinating a subject and for in vivo diagnosis of a subject. The disease and disorders include a gamma globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-host, lymphoid malignancies and passive immunotherapies and also for the treatment of various systemic infections. The present sequence is human modified anti-RSV (respiratory syncytial virus) antibody VL domain (light chain variable region) complementarity determining region (CDR).

SQ Sequence 9 AA;

Query Match 40.0%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
| | | |  
DB 6 YPFT 9

RESULT 68

AAE28025  
ID AAE28025 standard; peptide; 9 AA.

AC AAE28025;

XX 13-DEC-2002 (first entry)

XX Human modified anti-RSV AFFF antibody VL domain CDR3.

XX Human; immunoglobulin; IgG1; passive immunotherapy; gamma globulinaemia; vaccination; hypogammaglobulinaemia; autoimmune disease; antibacterial;  
KW immunosuppressive; lymphoid malignancy; respiratory syncytial virus;  
KW anti-RSV; systemic infection; graft-versus-host disease; cytostatic;  
KW complementarity determining region; CDR; virucide; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

PN WO200260919-A2.

PD 08-AUG-2002.

PF 12-DEC-2001; 2001WO-US48432.

PR 12-DEC-2000; 2000US-254884P.

PR 09-MAY-2001; 2001US-289760P.

XX (MEDI-) MEDIMUNE INC.

XX Dall'Acqua W, Johnson LS, Ward ES;

XX WPI; 2002-666925/71.

XX Modified immunoglobulins useful in the treatment of autoimmune diseases, comprises at least one amino acid modification relative to a wild-type immunoglobulin constant domain -

PS Disclosure; Page 118; 147pp; English.

XX The invention relates to a modified immunoglobulin (IgG1) which comprises an IgG constant domain having at least one amino acid modification. The immunoglobulins are used in the treatment or prevention of a disease or disorder by passive immunotherapy for vaccinating a subject and for in vivo diagnosis of a subject. The disease and disorders include a gamma globulinaemia, hypogammaglobulinaemia, autoimmune diseases, graft-versus-host, lymphoid malignancies and passive immunotherapies and also for the treatment of various systemic infections. The present sequence is human modified anti-RSV (respiratory syncytial virus) antibody VL domain (light chain variable region) complementarity determining region (CDR).

SQ Sequence 9 AA;

Query Match 40.0%; Score 4; DB 23; Length 9;



DE Human RSV antibody VL CDR3 fragment.  
 XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;  
 KW complementarity determining region; respiratory syncytial virus;  
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;  
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;  
 KW bronchopulmonary dysplasia; congenital heart disease;  
 KW congenital immunodeficiency; acquired immunodeficiency.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200243660-A2.  
 XX  
 PD 06-JUN-2002.  
 XX  
 PF 28-NOV-2001; 2001WO-US44807.  
 XX  
 PR 28-NOV-2000; 2000US-0724396.  
 XX  
 PR 28-NOV-2000; 2000US-0724531.  
 XX  
 PA (MEDI-) MEDIUMMUNE INC.  
 XX  
 PI Young JF, Koenig S, Johnson LS;  
 XX  
 DR WPI; 2002-706803/76.  
 XX  
 XX Antibody for treating respiratory syncytial virus (RSV) infection,  
 PT comprises a variable heavy/light domain or complementarity determining  
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically  
 PT binds to RSV antigen -  
 XX  
 PS Claim 9; Page 49; 298pp; English.  
 XX  
 XX The invention relates to a novel antibody comprising a variable heavy  
 CC (VH) domain, variable light (VL) domain, VH complementarity determining  
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the  
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)  
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the  
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,  
 CC and immunostimulant activity. The polynucleotides of the invention may  
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for  
 CC treating or ameliorating a RSV infection in a human. The antibody is also  
 CC useful for preventing, treating or ameliorating one or more symptoms  
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis.  
 CC bronchopulmonary dysplasia, congenital heart disease, congenital  
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow  
 CC transplant. The sequence represents a complementary determining region  
 CC peptide from a human RSV antibody of the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 40.0%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YPFT 5  
 Db |||||  
 6 YPFT 9  
 RESULT 72  
 ABP66415  
 ID ABP66415 standard; Peptide; 9 AA.  
 XX  
 AC ABP66415;  
 XX  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Human RSV antibody VL CDR3 fragment.  
 XX  
 KW Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;  
 KW complementarity determining region; respiratory syncytial virus;  
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;

KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;  
 KW bronchopulmonary dysplasia; congenital heart disease;  
 XX congenital immunodeficiency; acquired immunodeficiency.  
 OS Homo sapiens.  
 XX  
 PN WO200243660-A2.  
 XX  
 PD 06-JUN-2002.  
 XX  
 PF 28-NOV-2001; 2001WO-US44807.  
 XX  
 PR 28-NOV-2000; 2000US-0724396.  
 XX  
 PR 28-NOV-2000; 2000US-0724531.  
 XX  
 PA (MEDI-) MEDIUMMUNE INC.  
 XX  
 PI Young JF, Koenig S, Johnson LS;  
 XX  
 DR WPI; 2002-706803/76.  
 XX  
 XX Antibody for treating respiratory syncytial virus (RSV) infection,  
 PT comprises a variable heavy/light domain or complementarity determining  
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically  
 PT binds to RSV antigen -  
 XX  
 PS Claim 9; Page 51; 298pp; English.  
 XX  
 XX The invention relates to a novel antibody comprising a variable heavy  
 CC (VH) domain, variable light (VL) domain, VH complementarity determining  
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the  
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)  
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the  
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,  
 CC and immunostimulant activity. The polynucleotides of the invention may  
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for  
 CC treating or ameliorating a RSV infection in a human. The antibody is also  
 CC useful for preventing, treating or ameliorating one or more symptoms  
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis.  
 CC bronchopulmonary dysplasia, congenital heart disease, congenital  
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow  
 CC transplant. The sequence represents a complementary determining region  
 CC peptide from a human RSV antibody of the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 40.0%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YPFT 5  
 Db |||||  
 6 YPFT 9  
 RESULT 73  
 AAE25954  
 ID AAE25954 standard; peptide; 9 AA.  
 XX  
 AC AAE25954;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Mouse anti-KDR p1c11 scFv antibody CDRL3 peptide.  
 XX  
 KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
 KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
 KW VEGF; tumour growth; light chain complementarity determining region 3;  
 KW CDRL3; angiogenesis; p1c11; scFv antibody.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2002064528-A1.

XX 30-MAY-2002.  
 XX  
 XX 12-OCT-2001; 2001US-0976787.  
 XX  
 XX 28-JAN-2000; 2000US-0493539.  
 XX  
 XX (ZHUZ/) ZHU Z.  
 XX (WITT/) WITTE L.  
 XX  
 XX Zhu Z, Witte L;  
 XX  
 XX WPI; 2002-589175/63.  
 XX N-PSDB; AAD42819.  
 XX  
 XX Novel immunoglobulin molecule for reducing tumor growth, binds to  
 PT kinase insert domain-containing receptor with an affinity comparable to  
 PT human vascular endothelial growth factor, and neutralizes activation of  
 PT KDR  
 XX  
 XX Claim 3; Page 11; 34pp; English.  
 XX  
 XX The present invention relates to novel immunoglobulin molecules that bind  
 CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
 CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
 CC to human vascular endothelial growth factor (VEGF) and that neutralises  
 CC activation of KDR. Sequences of the invention are useful for neutralising  
 CC the activation of KDR, for reducing tumour growth and for inhibiting  
 CC angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody  
 CC light chain complementarity determining region 3 (CDRL3) protein.  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 40.0%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YPFT 5  
 DB 6 YPFT 9  
 RESULT 74  
 AAO14751  
 ID AAO14751 standard; peptide; 9 AA.  
 XX  
 XX AAO14751;  
 AC  
 XX 28-JUN-2002 (first entry)  
 DT  
 DE His-67 variant beta-casein protein (amino acids 59-67).  
 XX  
 XX Beta-casomorphin-7; beta-casein; milk; neurological disorder;  
 KW mental disorder; beta-casein His-67 variant; BCM-7;  
 KW autism spectral disorder; autism; pervasive developmental disorder;  
 KW Asperger's syndrome.  
 XX  
 XX Unidentified.  
 OS  
 XX Key Location/Qualifiers  
 FH Cleavage-site 1..2  
 FT Cleavage-site 8..9  
 FT /note= "The His residue at position 9 of this sequence  
 FT allows the protein to be cleaved at this point, and  
 FT facilitates the formation of beta-casomorphin-7"  
 XX  
 XX WO200219832-A1.  
 PN  
 XX 14-MAR-2002.  
 PD  
 XX 10-SEP-2001; 2001WO-NZ00186.  
 PF  
 XX 08-SEP-2000; 2000NZ-0506827.  
 PR

XX (NZDA-) NEW ZEALAND DAIRY BOARD.  
 XX  
 XX Crawford RA, Boland MJ, Norris CS, Hill JP, Fenwick RM;  
 PI  
 XX WPI; 2002-315618/35.  
 DR  
 XX  
 XX New method of providing nutrition to a susceptible individual while  
 PT avoiding the induction or aggravation of a neurological/mental disorder  
 PT comprising supplying milk which does not contain any histidine variant  
 PT  
 XX  
 XX Disclosure; Fig 1; 32pp; English.  
 PS  
 XX The invention comprises a novel method for providing nutrition (in the  
 CC form of milk) to a susceptible individual, while avoiding the induction  
 CC or aggravation of a neurological/mental disorder. The method of the  
 CC invention comprises supplying milk which does not contain beta-casein  
 CC His-67 variants (e.g. beta-casein proteins which possess a histidine  
 CC residue at position 67 instead of proline). The presence of histidine at  
 CC position 67 of the beta-casein protein allows the production of  
 CC beta-casomorphin-7 (BCM-7), which may induce or aggravate a neurological/  
 CC mental disorder. The method of the invention is useful for preventing an  
 CC autism spectral disorder, such as: autism; pervasive developmental  
 CC disorder; or Asperger's syndrome. The present peptide sequence represents  
 CC amino acids 59-67 of the His-67 variant beta-casein protein.  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 40.0%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VYPP 4  
 DB 1 VYPP 4  
 RESULT 75  
 AAO14752  
 ID AAO14752 standard; peptide; 9 AA.  
 XX  
 XX AAO14752;  
 AC  
 XX 28-JUN-2002 (first entry)  
 DT  
 DE Beta-casein protein (amino acids 59-67).  
 XX  
 XX Beta-casomorphin-7; beta-casein; milk; neurological disorder;  
 KW mental disorder; beta-casein His-67 variant; BCM-7;  
 KW autism spectral disorder; autism; pervasive developmental disorder;  
 KW Asperger's syndrome.  
 XX  
 XX Unidentified.  
 OS  
 XX Key Location/Qualifiers  
 FH Cleavage-site 1..2  
 FT WO200219832-A1.  
 PN  
 XX 14-MAR-2002.  
 PD  
 XX 10-SEP-2001; 2001WO-NZ00186.  
 PF  
 XX 08-SEP-2000; 2000NZ-0506827.  
 PR  
 XX (NZDA-) NEW ZEALAND DAIRY BOARD.  
 XX  
 XX Crawford RA, Boland MJ, Norris CS, Hill JP, Fenwick RM;  
 PI  
 XX WPI; 2002-315618/35.  
 DR  
 XX New method of providing nutrition to a susceptible individual while

PT avoiding the induction or aggravation of a neurological/mental disorder  
 PT comprising supplying milk which does not contain any histidine variant

XX Disclosure; Fig 2; 32pp; English.

XX The invention comprises a novel method for providing nutrition (in the  
 CC form of milk) to a susceptible individual, while avoiding the induction  
 CC or aggravation of a neurological/mental disorder. The method of the  
 CC invention comprises supplying milk which does not contain beta-casein  
 CC His-67 variants (e.g. beta-casein proteins which possess a histidine  
 CC residue at position 67 instead of proline). The presence of histidine at  
 CC position 67 of the beta-casein protein allows the production of  
 CC beta-casomorphin-7 (BCM-7), which may induce or aggravate a neurological/  
 CC mental disorder. The method of the invention is useful for preventing an  
 CC autism spectral disorder, such as: autism; pervasive developmental  
 CC disorder; or Asperger's syndrome. The present peptide sequence represents  
 CC amino acids 59-67 of the beta-casein protein.

XX Sequence 9 AA;

Query Match 40.0%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred.No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPF 4

Db 1 VYPF 4

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 Job time : 34.3936 secs

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OM protein - protein search, using sw model

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Title: US-09-641-801-18  
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Searched: 673684 seqs, 184443283 residues

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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pcp.\*
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- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pcp.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pcp.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	15	US-10-281-652-18
2	5	50.0	6	12	US-10-280-833-1
3	5	50.0	12	15	US-10-284-252-7
4	5	50.0	12	15	US-10-284-252-8
5	4	40.0	4	11	US-09-994-078-2
6	4	40.0	8	9	US-09-874-198-5
7	4	40.0	8	9	US-09-874-238-5
8	4	40.0	8	12	US-10-050-200-17
9	4	40.0	9	9	US-09-808-037-17
10	4	40.0	9	9	US-09-808-037-19
11	4	40.0	9	9	US-09-976-787-6
12	4	40.0	9	9	US-09-796-848A-7
13	4	40.0	9	9	US-09-796-848A-23
14	4	40.0	9	10	US-09-865-198-6
15	4	40.0	9	10	US-09-771-415-5

16	4	40.0	9	10	US-09-771-415-14	Sequence 14, Appl
17	4	40.0	9	10	US-09-771-415-15	Sequence 15, Appl
18	4	40.0	9	10	US-09-771-415-16	Sequence 16, Appl
19	4	40.0	9	10	US-09-996-288-6	Sequence 6, Appl
20	4	40.0	9	10	US-09-996-288-16	Sequence 16, Appl
21	4	40.0	9	10	US-09-996-288-61	Sequence 61, Appl
22	4	40.0	9	11	US-09-940-727B-21	Sequence 21, Appl
23	4	40.0	9	11	US-09-940-727B-24	Sequence 24, Appl
24	4	40.0	9	11	US-09-940-727B-27	Sequence 27, Appl
25	4	40.0	9	11	US-09-940-727B-30	Sequence 30, Appl
26	4	40.0	9	11	US-09-940-727B-81	Sequence 81, Appl
27	4	40.0	9	11	US-09-996-285-6	Sequence 6, Appl
28	4	40.0	9	11	US-09-996-285-16	Sequence 16, Appl
29	4	40.0	9	11	US-09-996-285-61	Sequence 61, Appl
30	4	40.0	9	11	US-09-996-285-61	Sequence 6, Appl
31	4	40.0	9	12	US-10-022-066-543	Sequence 543, App
32	4	40.0	9	12	US-10-020-354-6	Sequence 6, Appl
33	4	40.0	9	12	US-10-020-354-16	Sequence 16, Appl
34	4	40.0	9	12	US-10-020-354-61	Sequence 61, Appl
35	4	40.0	9	15	US-10-144-644-47	Sequence 47, Appl
36	4	40.0	9	15	US-10-144-644-48	Sequence 48, Appl
37	4	40.0	9	15	US-10-162-889-17	Sequence 17, Appl
38	4	40.0	9	15	US-10-162-889-19	Sequence 19, Appl
39	4	40.0	9	15	US-10-232-187-10	Sequence 10, Appl
40	4	40.0	9	15	US-10-135-636-10	Sequence 10, Appl
41	4	40.0	10	12	US-10-084-843-131	Sequence 131, App
42	4	40.0	10	12	US-10-193-002-126	Sequence 126, App
43	4	40.0	10	12	US-09-572-270A-1079	Sequence 1079, Ap
44	4	40.0	10	12	US-10-189-437-624	Sequence 624, App
45	4	40.0	10	15	US-10-057-789-123	Sequence 123, App
46	4	40.0	10	15	US-10-212-628-123	Sequence 123, App
47	4	40.0	11	12	US-09-933-767-830	Sequence 830, App
48	4	40.0	11	12	US-10-189-437-623	Sequence 623, App
49	4	40.0	11	15	US-10-057-789-190	Sequence 190, App
50	4	40.0	11	15	US-10-212-628-190	Sequence 190, App
51	4	40.0	11	15	US-10-023-282-830	Sequence 830, App
52	4	40.0	12	9	US-09-045-020-2	Sequence 2, Appl
53	4	40.0	12	11	US-09-954-385-375	Sequence 375, App
54	4	40.0	12	12	US-10-155-883B-31	Sequence 31, Appl
55	4	40.0	12	15	US-10-158-596A-31	Sequence 31, Appl
56	4	40.0	12	15	US-10-094-401-141	Sequence 141, App
57	4	40.0	12	15	US-10-157-775B-31	Sequence 31, Appl
58	4	40.0	12	15	US-10-254-446A-31	Sequence 31, Appl
59	4	40.0	14	9	US-09-815-156-6	Sequence 6, Appl
60	4	40.0	14	10	US-09-887-280-11	Sequence 11, Appl
61	4	40.0	14	11	US-09-791-393-44	Sequence 44, Appl
62	4	40.0	14	11	US-09-791-389-44	Sequence 44, Appl
63	4	40.0	14	12	US-10-076-047A-29	Sequence 29, Appl
64	4	40.0	14	12	US-10-306-903-16	Sequence 16, Appl
65	4	40.0	14	12	US-10-437-208-67	Sequence 67, Appl
66	4	40.0	14	15	US-10-262-538-33	Sequence 33, Appl
67	4	40.0	15	10	US-09-785-770A-21	Sequence 21, Appl
68	4	40.0	15	10	US-09-785-770A-23	Sequence 23, Appl
69	4	40.0	15	11	US-09-733-179A-2	Sequence 2, Appl
70	4	40.0	15	12	US-09-933-767-829	Sequence 829, App
71	4	40.0	15	15	US-10-273-541-47	Sequence 47, Appl
72	4	40.0	15	15	US-10-273-541-48	Sequence 48, Appl
73	4	40.0	15	15	US-10-023-282-829	Sequence 829, App
74	4	40.0	16	8	US-08-424-550B-247	Sequence 247, App
75	4	40.0	16	12	US-10-161-791-174	Sequence 174, App
76	4	40.0	17	12	US-10-189-437-622	Sequence 622, App
77	4	40.0	18	12	US-10-094-401-189	Sequence 189, App
78	4	40.0	19	12	US-09-933-767-831	Sequence 831, App
79	4	40.0	19	14	US-10-010-114-10	Sequence 10, Appl
80	4	40.0	19	15	US-10-023-282-831	Sequence 831, App
81	4	40.0	20	12	US-10-169-710-7	Sequence 7, Appl
82	4	40.0	20	12	US-10-169-710-39	Sequence 39, Appl
83	4	40.0	20	12	US-10-161-791-136	Sequence 136, App
84	4	40.0	20	12	US-10-189-437-621	Sequence 621, App
85	3	30.0	4	9	US-09-804-733A-3	Sequence 3, Appl
86	3	30.0	4	11	US-09-994-078-1	Sequence 1, Appl
87	3	30.0	4	12	US-10-237-160-1	Sequence 1, Appl
88	3	30.0	4	12	US-10-313-338A-1	Sequence 1, Appl

89 3 30.0 4 12 US-10-313-790A-1 Sequence 1, Appli  
90 3 30.0 4 15 US-10-197-954-50 Sequence 50, Appl  
91 3 30.0 5 8 US-08-891-525-7 Sequence 7, Appli  
92 3 30.0 5 10 US-09-826-290-485 Sequence 485, App  
93 3 30.0 5 10 US-09-826-290-488 Sequence 488, App  
94 3 30.0 5 11 US-09-788-006-9 Sequence 9, Appli  
95 3 30.0 5 11 US-09-788-006-10 Sequence 10, Appl  
96 3 30.0 5 11 US-09-788-006-11 Sequence 11, Appl  
97 3 30.0 5 12 US-10-029-065-22 Sequence 22, Appl  
98 3 30.0 5 12 US-10-197-927-16 Sequence 16, Appl  
99 3 30.0 5 12 US-10-226-629A-7 Sequence 7, Appli  
100 3 30.0 5 15 US-10-198-590-7

## ALIGNMENTS

RESULT 1  
US-10-281-652-18  
; Sequence 18, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-18  
Query Match 100.0%; Score 10; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VYPFTGPIPN 10  
Db 1 VYPFTGPIPN 10  
RESULT 2  
US-10-280-833-1  
; Sequence 1, Application US/10280833  
; Publication No. US20030195150A1  
; GENERAL INFORMATION:  
; APPLICANT: Reynolds, Charles Eric  
; APPLICANT: Daehper, Stuart Geoffrey  
; APPLICANT: O'Brien-Simpson, Neil Martin  
; APPLICANT: Talbo, Gert Hoy  
; APPLICANT: Malkoski, Marina  
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES  
; FILE REFERENCE: BDWP-001CON  
; CURRENT APPLICATION NUMBER: US/10/280,833  
; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: 09/554,997  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: PP 0514  
; PRIOR FILING DATE: 1997-11-24  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-284-252-7  
Query Match 50.0%; Score 5; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 FTGPI 8  
Db 4 FTGPI 8  
RESULT 4  
US-10-284-252-8  
; Sequence 8, Application US/10284252  
; Publication No. US20030109675A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, C. Hal  
; APPLICANT: Dexter, Paul L.  
; APPLICANT: Evans, Amy K.  
; APPLICANT: Hruby, Dennis E.  
; TITLE OF INVENTION: DSGP Protease: Cleavage Site  
; TITLE OF INVENTION: Identification and Proteolysis of a Natural Target in E.  
; FILE REFERENCE: 016921-169  
; CURRENT APPLICATION NUMBER: US/10/284,252  
; CURRENT FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: US 60/330,855  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-284-252-7  
Query Match 50.0%; Score 5; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 FTGPI 8  
Db 4 FTGPI 8  
RESULT 3  
US-10-284-252-7  
; Sequence 7, Application US/10284252  
; Publication No. US20030109675A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, C. Hal  
; APPLICANT: Dexter, Paul L.  
; APPLICANT: Evans, Amy K.  
; APPLICANT: Hruby, Dennis E.  
; TITLE OF INVENTION: DSGP Protease: Cleavage Site  
; TITLE OF INVENTION: Identification and Proteolysis of a Natural Target in E.  
; FILE REFERENCE: 016921-169  
; CURRENT APPLICATION NUMBER: US/10/284,252  
; CURRENT FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: US 60/330,855  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-284-252-7  
Query Match 50.0%; Score 5; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 FTGPI 8  
Db 4 FTGPI 8  
RESULT 4  
US-10-284-252-8  
; Sequence 8, Application US/10284252  
; Publication No. US20030109675A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, C. Hal  
; APPLICANT: Dexter, Paul L.  
; APPLICANT: Evans, Amy K.  
; APPLICANT: Hruby, Dennis E.  
; TITLE OF INVENTION: DSGP Protease: Cleavage Site  
; TITLE OF INVENTION: Identification and Proteolysis of a Natural Target in E.  
; FILE REFERENCE: 016921-169  
; CURRENT APPLICATION NUMBER: US/10/284,252  
; CURRENT FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: US 60/330,855  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-284-252-7



; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-284-252-8

Query Match 50.0%; Score 5; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTGPI 8  
Db 1 FTGPI 5

## RESULT 5

US-09-994-078-2  
; Sequence 2, Application US/09994078  
; Publication No. US2003032774A1  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, WILLIAM  
; APPLICANT: DIMAIO, JOHN  
; APPLICANT: SCHILLER, PETER  
; APPLICANT: MARTEL, RENE  
; APPLICANT: MARTEL, FRANCIS  
; APPLICANT: MARTEL, DIANE  
; APPLICANT: MARTEL, PIERRE  
; TITLE OF INVENTION: NOVEL OPIOID PEPTIDES FOR THE TREATMENT OF PAIN  
; FILE REFERENCE: MAS/81823/282437  
; CURRENT APPLICATION NUMBER: US/09/994,078  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 09/159,518  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 08/392,918  
; PRIOR FILING DATE: 1995-03-03  
; PRIOR APPLICATION NUMBER: 08/718,585  
; PRIOR FILING DATE: 1996-10-02  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-994-078-2

Query Match 40.0%; Score 4; DB 11; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 1 YPFT 4

## RESULT 6

US-09-874-198-5  
; Sequence 5, Application US/09874198  
; Patent No. US20020082208A1  
; GENERAL INFORMATION:  
; APPLICANT: Jensenius, Jens Chr.  
; APPLICANT: Thiel, Steffen  
; TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND  
; FILE REFERENCE: 09011-002002  
; CURRENT APPLICATION NUMBER: US/09/874,198  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 09/054,218  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 60/042,678  
; PRIOR FILING DATE: 1997-04-03

; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-874-198-5

Query Match 40.0%; Score 4; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
Db 2 PFTG 5

## RESULT 7

US-09-874-238-5  
; Sequence 5, Application US/09874238  
; Patent No. US20020082209A1  
; GENERAL INFORMATION:  
; APPLICANT: Jensenius, Jens Chr.  
; APPLICANT: Thiel, Steffen  
; TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND  
; FILE REFERENCE: 09011-002003  
; CURRENT APPLICATION NUMBER: US/09/874,238  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 09/054,218  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 60/042,678  
; PRIOR FILING DATE: 1997-04-03  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-874-238-5

Query Match 40.0%; Score 4; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
Db 2 PFTG 5

## RESULT 8

US-10-050-200-17  
; Sequence 17, Application US/10050200  
; Publication No. US2003016037A1  
; GENERAL INFORMATION:  
; APPLICANT: Fourie, Anne  
; APPLICANT: Coles, Fawn  
; APPLICANT: Karlsson, Lars  
; TITLE OF INVENTION: Aggracanase-1 and -2 Peptide Substrates and Methods  
; FILE REFERENCE: ORT-1417  
; CURRENT APPLICATION NUMBER: US/10/050,200  
; CURRENT FILING DATE: 2002-01-16  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide substrate  
US-10-050-200-17

Query Match 40.0%; Score 4; DB 12; Length 8;

Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GPIP 9  
Db 5 GPIP 8

RESULT 9  
US-09-808-037-17  
; Sequence 17, Application US/09808037  
; Patent No. US20020052311A1  
; GENERAL INFORMATION:  
; APPLICANT: SOLOMON, Beka  
; APPLICANT: HANAN, Eliat  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF  
; FILE REFERENCE: NEUROLOGICAL DISEASES AND DISORDERS  
; CURRENT APPLICATION NUMBER: US/09/808,037  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/629,971  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 09/473,653  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: US 60/152,417  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-808-037-17

Query Match 40.0%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YPFT 5  
Db 6 YPFT 9

RESULT 10  
US-09-808-037-19  
; Sequence 19, Application US/09808037  
; Patent No. US20020052311A1  
; GENERAL INFORMATION:  
; APPLICANT: SOLOMON, Beka  
; APPLICANT: HANAN, Eliat  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF  
; FILE REFERENCE: NEUROLOGICAL DISEASES AND DISORDERS  
; CURRENT APPLICATION NUMBER: US/09/808,037  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/629,971  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 09/473,653  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: US 60/152,417  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 19  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-808-037-19

Query Match 40.0%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YPFT 5  
Db 6 YPFT 9

RESULT 11  
US-09-976-787-6  
; Sequence 6, Application US/09976787  
; Patent No. US20020064528A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Zhenping  
; APPLICANT: Witte, Larry  
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
; FILE REFERENCE: 11245/46505  
; CURRENT APPLICATION NUMBER: US/09/976,787  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/493,539  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/117,726  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-976-787-6

Query Match 40.0%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YPFT 5  
Db 6 YPFT 9

RESULT 12  
US-09-796-848A-7  
; Sequence 7, Application US/09796848A  
; Patent No. US20020098189A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James F.  
; APPLICANT: Johnson, Leslie S.  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of  
; FILE REFERENCE: Producing Them  
; CURRENT APPLICATION NUMBER: US/09/796,848A  
; CURRENT FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: U.S. 60/186,252  
; PRIOR FILING DATE: 2000-03-01  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Light chain  
; OTHER INFORMATION: CDR reference sequence.  
US-09-796-848A-7

Query Match 40.0%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
 ||||  
 Db 6 YPFT 9

## RESULT 13

US-09-796-848A-23  
 ; Sequence 23, Application US/09796848A  
 ; Patent No. US20020098189A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, James F.  
 ; APPLICANT: Johnson, Leslie S.  
 ; APPLICANT: Huse, William D.  
 ; APPLICANT: Wu, Herren  
 ; APPLICANT: Watkins, Jeffrey D.  
 ; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of  
 ; FILE REFERENCE: 469201-526  
 ; CURRENT APPLICATION NUMBER: US/09/796,848A  
 ; CURRENT FILING DATE: 2001-10-30  
 ; PRIOR APPLICATION NUMBER: U.S. 60/186,252  
 ; PRIOR FILING DATE: 2000-03-01  
 ; NUMBER OF SEQ ID NOS: 59  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 23  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:High potency  
 ; OTHER INFORMATION: CDR sequence.  
 US-09-796-848A-23

Query Match 40.0%; Score 4; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
 ||||  
 Db 6 YPFT 9

## RESULT 14

US-09-865-198-6  
 ; Sequence 6, Application US/09865198  
 ; Patent No. US20020103345A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhu, Zhenping  
 ; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods  
 ; FILE REFERENCE: 11245/47102  
 ; CURRENT APPLICATION NUMBER: US/09/865,198  
 ; CURRENT FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: US 60/206,749  
 ; PRIOR FILING DATE: 2000-05-24  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: WordPerfect 8.0 for Windows  
 ; SEQ ID NO 6  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 US-09-865-198-6

Query Match 40.0%; Score 4; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
 ||||  
 Db 6 YPFT 9

## RESULT 15

US-09-771-415-5  
 ; Sequence 5, Application US/09771415  
 ; Patent No. US20020164326A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, James F.  
 ; APPLICANT: Koenig, Scott  
 ; APPLICANT: Johnson, Leslie S.  
 ; APPLICANT: Huse, William D.  
 ; APPLICANT: Wu, Herren  
 ; APPLICANT: Watkins, Jeffrey D.  
 ; TITLE OF INVENTION: Ultra High Affinity Neutralizing Antibodies  
 ; FILE REFERENCE: 469201-520  
 ; CURRENT APPLICATION NUMBER: US/09/771,415  
 ; CURRENT FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: 60/178,426  
 ; PRIOR FILING DATE: 2000-01-27  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Amino acid  
 ; OTHER INFORMATION: sequence of complementarity determining region L3  
 ; OTHER INFORMATION: of reference anti-RSV antibody  
 US-09-771-415-5

Query Match 40.0%; Score 4; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
 ||||  
 Db 6 YPFT 9

## RESULT 16

US-09-771-415-14  
 ; Sequence 14, Application US/09771415  
 ; Patent No. US20020164326A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, James F.  
 ; APPLICANT: Koenig, Scott  
 ; APPLICANT: Johnson, Leslie S.  
 ; APPLICANT: Huse, William D.  
 ; APPLICANT: Wu, Herren  
 ; APPLICANT: Watkins, Jeffrey D.  
 ; TITLE OF INVENTION: Ultra High Affinity Neutralizing Antibodies  
 ; FILE REFERENCE: 469201-520  
 ; CURRENT APPLICATION NUMBER: US/09/771,415  
 ; CURRENT FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: 60/178,426  
 ; PRIOR FILING DATE: 2000-01-27  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 14  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:Amino acid  
 ; OTHER INFORMATION: sequence present in high affinity complementarity  
 ; OTHER INFORMATION: determining regions of antibodies of the invention  
 US-09-771-415-14

Query Match 40.0%; Score 4; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
 ||||  
 Db 6 YPFT 9

## RESULT 17

US-09-771-415-15

; Sequence 15, Application US/09771415  
; Patent No. US20020164326A1

; GENERAL INFORMATION:

; APPLICANT: Young, James F.

; APPLICANT: Koenig, Scott

; APPLICANT: Johnson, Leslie S.

; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren

; APPLICANT: Watkins, Jeffrey D.

; TITLE OF INVENTION: Ultra High Affinity Neutralizing Antibodies

; FILE REFERENCE: 469201-520

; CURRENT APPLICATION NUMBER: US/09/771,415

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 60/178,426

; PRIOR FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Amino acid

; OTHER INFORMATION: sequence present in high affinity complementarity

; OTHER INFORMATION: determining regions of antibodies of the invention

US-09-771-415-15

Query Match

Best Local Similarity 40.0%; Score 4; DB 10; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 YPFT 5

||||

6 YPFT 9

## RESULT 18

US-09-771-415-16

; Sequence 16, Application US/09771415

; Patent No. US20020164326A1

; GENERAL INFORMATION:

; APPLICANT: Young, James F.

; APPLICANT: Koenig, Scott

; APPLICANT: Johnson, Leslie S.

; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren

; APPLICANT: Watkins, Jeffrey D.

; TITLE OF INVENTION: Ultra High Affinity Neutralizing Antibodies

; FILE REFERENCE: 469201-520

; CURRENT APPLICATION NUMBER: US/09/771,415

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 60/178,426

; PRIOR FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Amino acid

; OTHER INFORMATION: sequence present in high affinity complementarity

; OTHER INFORMATION: determining regions of antibodies of the invention

US-09-771-415-16

Query Match

Best Local Similarity 40.0%; Score 4; DB 10; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 YPFT 5

||||

6 YPFT 9

Db

## RESULT 19

US-09-996-288-6

; Sequence 6, Application US/09996288

; Patent No. US20020177126A1

; GENERAL INFORMATION:

; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxi

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996,288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-288-6

Query Match

Best Local Similarity 40.0%; Score 4; DB 10; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 YPFT 5

||||

6 YPFT 9

Db

## RESULT 20

US-09-996-288-16

; Sequence 16, Application US/09996288

; Patent No. US20020177126A1

; GENERAL INFORMATION:

; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxi

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996,288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-288-16

Query Match

Best Local Similarity 40.0%; Score 4; DB 10; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 YPFT 5

||||

6 YPFT 9

Db

## RESULT 21

US-09-996-288-61

; Sequence 61, Application US/09996288

; Patent No. US20020177126A1

; GENERAL INFORMATION:

; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

Query Match

Best Local Similarity 40.0%; Score 4; DB 10; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-996-288-61

Query Match          40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5
DB 6 YPFT 9

RESULT 22
US-09-940-727B-21
; Sequence 21, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
; US-09-940-727B-21

Query Match          40.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5
DB 6 YPFT 9

RESULT 23
US-09-940-727B-24
; Sequence 24, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
; US-09-940-727B-24

Query Match          40.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5
DB 6 YPFT 9

RESULT 24
US-09-940-727B-27
; Sequence 27, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
; US-09-940-727B-27

Query Match          40.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5
DB 6 YPFT 9

RESULT 25
US-09-940-727B-30
; Sequence 30, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
; US-09-940-727B-30

Query Match          40.0%; Score 4; DB 11; Length 9;
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Best Local Similarity 100.0%; Pred. No. 6.1e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;  
QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 26  
US-09-940-727B-81  
; Sequence 81, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 81  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: mouse  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: any amino acid  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: any amino acid  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: any amino acid  
US-09-940-727B-81

Query Match 40.0%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 27  
US-09-996-265-6  
; Sequence 6, Application US/09996265  
; Publication No. US20030091584A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-048-999  
; CURRENT APPLICATION NUMBER: US/09/996,265  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-265-6

Query Match 40.0%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 28  
US-09-996-265-16  
; Sequence 16, Application US/09996265  
; Publication No. US20030091584A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-048-999  
; CURRENT APPLICATION NUMBER: US/09/996,265  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-265-16

Query Match 40.0%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 29  
US-09-996-265-61  
; Sequence 61, Application US/09996265  
; Publication No. US20030091584A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-048-999  
; CURRENT APPLICATION NUMBER: US/09/996,265  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 61  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-265-61

Query Match 40.0%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 30  
US-09-798-689-6  
; Sequence 6, Application US/09798689

Query Match 40.0%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 28  
US-09-996-265-16  
; Sequence 16, Application US/09996265  
; Publication No. US20030091584A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-048-999  
; CURRENT APPLICATION NUMBER: US/09/996,265  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-265-16

Query Match 40.0%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 29  
US-09-996-265-61  
; Sequence 61, Application US/09996265  
; Publication No. US20030091584A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-048-999  
; CURRENT APPLICATION NUMBER: US/09/996,265  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 61  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-265-61

Query Match 40.0%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 30  
US-09-798-689-6  
; Sequence 6, Application US/09798689

Publication No. US20030103973A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists  
; TITLE OF INVENTION: Combined With Radiation and Chemotherapy  
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP  
; CURRENT APPLICATION NUMBER: US/09/798,689  
; CURRENT FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 09/401,163  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: 08/967,113  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/706,804  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/476,533  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/326,552  
; PRIOR FILING DATE: 1994-10-20  
; PRIOR APPLICATION NUMBER: 08/196,041  
; PRIOR FILING DATE: 1994-02-10  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-798-689-6

Query Match 40.0%; Score 4; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 31  
US-10-022-066-543  
; Sequence 543, Application US/10022066  
; Publication No. US20030166057A1  
; GENERAL INFORMATION:  
; APPLICANT: HILDEBRAND, WILLIAM H.  
; APPLICANT: PRILLIMAN, KILSEY RAE  
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 6680,034  
; CURRENT APPLICATION NUMBER: US/10/022,066  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/256,410  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/256,409  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 09/465,321  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: 09/974,366  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 543  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (9)  
; OTHER INFORMATION: Unknown amino acid  
US-10-022-066-543

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
Db 2 PFTG 5

RESULT 32  
US-10-020-354-6  
; Sequence 6, Application US/10020354  
; Publication No. US20030190311A1  
; GENERAL INFORMATION:  
; APPLICANT: DALL'ACQUA, WILLIAM  
; APPLICANT: JOHNSON, LESLIE  
; APPLICANT: WARD, ELIZABETH SALLY  
; TITLE OF INVENTION: MOLECULES WITH EXTENDED HALF-LIVES, COMPOSITIONS AND USES THEREOF.  
; FILE REFERENCE: 10271-027  
; CURRENT APPLICATION NUMBER: US/10/020,354  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/254,884  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/238,760  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-020-354-6

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 33  
US-10-020-354-16  
; Sequence 16, Application US/10020354  
; Publication No. US20030190311A1  
; GENERAL INFORMATION:  
; APPLICANT: DALL'ACQUA, WILLIAM  
; APPLICANT: JOHNSON, LESLIE  
; APPLICANT: WARD, ELIZABETH SALLY  
; TITLE OF INVENTION: MOLECULES WITH EXTENDED HALF-LIVES, COMPOSITIONS AND USES THEREOF.  
; FILE REFERENCE: 10271-027  
; CURRENT APPLICATION NUMBER: US/10/020,354  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/254,884  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/238,760  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-020-354-16

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 34  
US-10-020-354-61  
; Sequence 61, Application US/10020354  
; Publication No. US20030190311A1  
; GENERAL INFORMATION:  
; APPLICANT: DALL'ACQUA, WILLIAM  
; APPLICANT: JOHNSON, LESLIE  
; APPLICANT: WARD, ELIZABETH SALLY  
; TITLE OF INVENTION: MOLECULES WITH EXTENDED HALF-LIVES, COMPOSITIONS AND USES THEREOF  
; FILE REFERENCE: 10271-027  
; CURRENT APPLICATION NUMBER: US/10/020,354  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/254,884  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/238,760  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 61  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-020-354-61

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 35  
US-10-144-644-47  
; Sequence 47, Application US/10144644  
; Publication No. US20030059429A1  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp  
; STREET: P.O. Box 1539-UW2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/144,644  
; FILING DATE: 2002-08-08  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/470110  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/467420  
; FILING DATE: 2002-08-08  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/363131  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION: INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: US 08/467420  
; FILING DATE: 06-JUN-1995

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/363131  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION: INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50282-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5024  
; TELEFAX: 610-270-5090  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-10-144-644-47  
Query Match 40.0%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YPFT 5  
Db 6 YPFT 9  
RESULT 36  
US-10-144-644-48  
; Sequence 48, Application US/10144644  
; Publication No. US20030059429A1  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp  
; STREET: P.O. Box 1539-UW2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/144,644  
; FILING DATE: 2002-08-08  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/470110  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/467420  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/363131  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION: INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50282-2



TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5024  
TELEFAX: 610-270-5030  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-10-144-644-48

Query Match 40.0%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

## RESULT 37

US-10-162-889-17  
Sequence 17, Application US/10162889  
Publication No. US20030077252A1  
GENERAL INFORMATION:  
APPLICANT: SOLOMON, Beka  
APPLICANT: HANAN, Eilat  
TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME  
TITLE OF INVENTION: USEFUL IN DIAGNOSING  
TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES  
FILE REFERENCE: SOLOMON-2B  
CURRENT APPLICATION NUMBER: US/10/162,889  
CURRENT FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US/09/629,971  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: US 09/473,653  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: US 60/152,417  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 17  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-162-889-17

Query Match 40.0%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

## RESULT 38

US-10-162-889-19  
Sequence 19, Application US/10162889  
Publication No. US20030077252A1  
GENERAL INFORMATION:  
APPLICANT: SOLOMON, Beka  
APPLICANT: HANAN, Eilat  
TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME  
TITLE OF INVENTION: USEFUL IN DIAGNOSING  
TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES  
FILE REFERENCE: SOLOMON-2B  
CURRENT APPLICATION NUMBER: US/10/162,889  
CURRENT FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US/09/629,971

PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: US 09/473,653  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: US 60/152,417  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 19  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-162-889-19

Query Match 40.0%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

## RESULT 39

US-10-232-187-10  
Sequence 10, Application US/10232187  
Publication No. US20030092091A1  
GENERAL INFORMATION:  
APPLICANT: ABRAHAMSON, Julie A.  
APPLICANT: BOCHNER, Bruce  
APPLICANT: ERICKSON-MILLER, Connie L.  
APPLICANT: KIKLY, Kristine K.  
APPLICANT: SCHLEIMER, Robert  
APPLICANT: NULKU, Turkan E.  
TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies  
FILE REFERENCE: GH50042-1  
CURRENT APPLICATION NUMBER: US/10/232,187  
CURRENT FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 60/187,595  
PRIOR FILING DATE: 2000-03-07  
PRIOR APPLICATION NUMBER: PCT/US01/07193  
PRIOR FILING DATE: 2001-03-05  
PRIOR APPLICATION NUMBER: 60/315,943  
PRIOR FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: 60/349,830  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: 60/394,741  
PRIOR FILING DATE: 2002-07-10  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-232-187-10

Query Match 40.0%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

## RESULT 40

US-10-135-636-10  
Sequence 10, Application US/10135636  
Publication No. US20030097974A1  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, LESLIE S  
APPLICANT: BRADEN, BRADFORD

;; TITLE OF INVENTION: CRYSTALS AND STRUCTURE OF SYNAGIS FAB  
;; FILE REFERENCE: 10271-011-999  
;; CURRENT APPLICATION NUMBER: US/10/135,636  
;; CURRENT FILING DATE: 2002-12-05  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 10  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of artificial sequence: Complementary determining region of Synagis light chain humanized antibody  
US-10-135-636-10

Query Match 40.0%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YPFT 5  
Db 6 YPFT 9

## RESULT 41

US-10-084-843-131  
;; Sequence 131, Application US/10084843  
;; Publication No. US20030143243A1

## GENERAL INFORMATION:

;; APPLICANT: Reed, Steven G.  
;; Skeiky, Yasir A.W.  
;; Dillon, Davin C.  
;; Campos-Neto, Antonio  
;; Houghton, Raymond  
;; Vedvick, Thomas S.  
;; Twardzik, Daniel R.  
;; Lodes, Michael J.  
;; Hendrickson, Ronald C.  
;; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS

;; NUMBER OF SEQUENCES: 355  
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: SEED and BERRY LLP  
;; STREET: 6300 Columbia Center, 701 Fifth Avenue  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: USA

;; ZIP: 98104-7092

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/084,843  
;; FILING DATE: 25-Feb-2002  
;; CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/09/072,967  
;; FILING DATE: 05-MAY-1998  
;; ATTORNEY/AGENT INFORMATION:

;; NAME: Maki, David J.  
;; REGISTRATION NUMBER: 31,392  
;; REFERENCE/DOCKET NUMBER: 210121.411C9  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031

## INFORMATION FOR SEQ ID NO: 131:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear

;; FEATURE:  
;; OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 131:  
US-10-084-843-131

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FTGP 7  
Db 4 FTGP 7

## RESULT 42

US-10-193-002-126  
;; Sequence 126, Application US/10193002  
;; Publication No. US20030135026A1

## GENERAL INFORMATION:

;; APPLICANT: Reed, Steven G.  
;; Skeiky, Yasir A.W.  
;; Dillon, Davin C.  
;; Campos-Neto, Antonio  
;; Houghton, Raymond  
;; Vedvick, Thomas S.  
;; Twardzik, Daniel R.  
;; Lodes, Michael J.  
;; Hendrickson, Ronald C.  
;; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS

;; NUMBER OF SEQUENCES: 350

## CORRESPONDENCE ADDRESS:

;; ADDRESSEE: SEED and BERRY LLP  
;; STREET: 6300 Columbia Center, 701 Fifth Avenue  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: USA  
;; ZIP: 98104-7092

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/193,002  
;; FILING DATE: 10-Jul-2002  
;; CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/09/072,596  
;; FILING DATE: 05-MAY-1998  
;; ATTORNEY/AGENT INFORMATION:

;; NAME: Maki, David J.  
;; REGISTRATION NUMBER: 31,392  
;; REFERENCE/DOCKET NUMBER: 210121.417C9

## TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031

## INFORMATION FOR SEQ ID NO: 126:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: <Unknown>  
;; TOPOLOGY: linear

## FEATURE:

;; OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 126:

## US-10-193-002-126

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTGP 7  
|||||  
Db 4 FTGP 7

## RESULT 43

US-09-572-270A-1079  
; Sequence 1079, Application US/09572270A  
; Publication No. US20030148368A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Inter- complementary peptide listing  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/572,270A  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 1144  
; SOFTWARE: Protpatent version 1.0  
; SEQ ID NO 1079  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Arabidopsis Thaliana  
; OTHER INFORMATION: Sequence located in CYP73A5 OR CYP73 OR T06B20.16. at 34-  
US-09-572-270A-1079

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GP1P 9  
|||||  
Db 3 GP1P 6

## RESULT 44

US-10-189-437-624  
; Sequence 624, Application US/10189437  
; Publication No. US20030194414A1  
; GENERAL INFORMATION:  
; APPLICANT: BOGOCH, SAMUEL  
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE  
; FILE REFERENCE: 09425/46905  
; CURRENT APPLICATION NUMBER: US/10/189,437  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: 10/105,232  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: 09/984,057  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 729  
; SOFTWARE: PatentIn 2.1  
; SEQ ID NO 624  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-189-437-624

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
|||||  
Db 3 PFTG 6

## RESULT 45

US-10-057-789-123  
; Sequence 123, Application US/10057789

Publication No. US20030082522A1  
; GENERAL INFORMATION:  
; APPLICANT: Paul Haynes  
; APPLICANT: Jing Wei  
; APPLICANT: John Yates  
; APPLICANT: Nancy Andon  
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE  
; FILE REFERENCE: NADII.022A  
; CURRENT APPLICATION NUMBER: US/10/057,789  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 60/264,576  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/305,232  
; PRIOR FILING DATE: 2001-07-13  
; NUMBER OF SEQ ID NOS: 311  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 123  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 1  
; OTHER INFORMATION: Xaa = Modified Cysteine  
US-10-057-789-123

Query Match 40.0%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
|||||  
Db 2 PFTG 5

## RESULT 46

US-10-212-628-123  
; Sequence 123, Application US/10212628  
; Publication No. US20030087329A1  
; GENERAL INFORMATION:  
; APPLICANT: Paul Haynes  
; APPLICANT: Jing Wei  
; APPLICANT: John Yates  
; APPLICANT: Nancy Andon  
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE  
; FILE REFERENCE: NADII.022CPI  
; CURRENT APPLICATION NUMBER: US/10/212,628  
; CURRENT FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 60/264,576  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/305,232  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 10/057,789  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 311  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 123  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 1  
; OTHER INFORMATION: Xaa = Modified Cysteine  
US-10-212-628-123

Query Match 40.0%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6

Db  
||||  
2 PFTG 5

RESULT 47

US-09-933-767-830  
; Sequence 830, Application US/09933767  
; Publication No. US20030181692A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P2  
; CURRENT APPLICATION NUMBER: US/09/933,767  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: PCT/US01/05614  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/184,836  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/193,170  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/205,258  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: PCT/US98/11422  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/048,885  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,375  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,881  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,880  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,896  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,020  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,876  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,895  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,884  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,894  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,971  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,882  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,899  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,893  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,900  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,901  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,892  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,915  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,972  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,019  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,970  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,972  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,916  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,373  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,875

; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,374  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,917  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,949  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,883  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,897  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,898  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,962  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,963  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,877  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,878  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/068,054  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,064  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,053  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/070,923  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/085,925  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/092,921  
; PRIOR FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: 60/094,657  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1245  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 830  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-933-767-830

Query Match 40.0%; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
Db 4 PFTG 7

RESULT 48

US-10-189-437-623  
; Sequence 623, Application US/10189437  
; Publication No. US2003019441A1  
; GENERAL INFORMATION:

APPLICANT: BOGOCH, SAMUEL  
APPLICANT: BOGOCH, ELENORE S.  
TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE  
FILE REFERENCE: 09425/46905  
CURRENT APPLICATION NUMBER: US/10/189,437  
CURRENT FILING DATE: 2002-07-08  
PRIOR APPLICATION NUMBER: 10/105,232  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: 09/984,057  
PRIOR FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: 60/303,396  
PRIOR FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: 60/278,761  
PRIOR FILING DATE: 2001-03-27  
NUMBER OF SEQ ID NOS: 729  
SOFTWARE: PatentIn 2.1  
SEQ ID NO 623  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Triticum aestivum  
US-10-189-437-623

Query Match 40.0%; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFTG 6  
Db 4 PFTG 7

RESULT 49  
US-10-057-789-190  
Sequence 190, Application US/10057789  
Publication No. US2003008252A1  
GENERAL INFORMATION:  
APPLICANT: Paul Haynes  
APPLICANT: Jing Wei  
APPLICANT: John Yates  
APPLICANT: Nancy Andon  
TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE  
TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES  
FILE REFERENCE: NADII.022A  
CURRENT APPLICATION NUMBER: US/10/057,789  
CURRENT FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: US 60/264,576  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: US 60/305,232  
PRIOR FILING DATE: 2001-07-13  
NUMBER OF SEQ ID NOS: 311  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 190  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: 9  
OTHER INFORMATION: Xaa = Modified Cysteine  
US-10-057-789-190

Query Match 40.0%; Score 4; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGPI 8  
Db 4 TGPI 7

RESULT 50  
US-10-212-628-190  
Sequence 190, Application US/10212628

Publication No. US20030087329A1  
GENERAL INFORMATION:  
APPLICANT: Paul Haynes  
APPLICANT: Jing Wei  
APPLICANT: John Yates  
APPLICANT: Nancy Andon  
TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE  
TITLE OF INVENTION: ANALYSIS OF COMPLEX PROTEIN MIXTURES  
FILE REFERENCE: NADII.022CPI  
CURRENT APPLICATION NUMBER: US/10/212,628  
CURRENT FILING DATE: 2002-08-01  
PRIOR APPLICATION NUMBER: US 60/264,576  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: US 60/305,232  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: US 10/057,789  
PRIOR FILING DATE: 2002-01-25  
NUMBER OF SEQ ID NOS: 311  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 190  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: 9  
OTHER INFORMATION: Xaa = Modified Cysteine  
US-10-212-628-190

Query Match 40.0%; Score 4; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGPI 8  
Db 4 TGPI 7

RESULT 51  
US-10-023-282-830  
Sequence 830, Application US/10023282  
Publication No. US20030092893A1  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: PZ007PI  
CURRENT APPLICATION NUMBER: US/10/023,282  
CURRENT FILING DATE: 2001-12-20  
EARLIER APPLICATION NUMBER: 09/205,258  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,919  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 830  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-023-282-830

Query Match 40.0%; Score 4; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PFTG 6  
DB 4 PFTG 7

RESULT 52

US-09-045-020-2  
Sequence 2, Application US/09045020  
Patent No. US20020025942A1  
GENERAL INFORMATION:  
APPLICANT: Ingram, Vernon M., Roder, Hanno M.  
TITLE OF INVENTION: No. US20020025942A1el Tau/Neurofilament Protein Kinases  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Massachusetts Institute of Technology  
STREET: 28 Carleton Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: United States of America  
ZIP: 02142  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM-compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,020  
FILING DATE: 20-Mar-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480,793  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 07/912,293  
FILING DATE: July 10, 1992  
APPLICATION NUMBER: 07/742,880  
FILING DATE: 9-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Gates, Edward R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: M0656/7008  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 2  
US-09-045-020-2

Query Match 40.0%; Score 4; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGPI 8  
DB 2 TGPI 5

RESULT 53

US-09-954-385-375  
Sequence 375, Application US/09954385  
Publication No. US20030100467A1  
GENERAL INFORMATION:  
APPLICANT: Aehle, Wolfgang  
APPLICANT: Baldwin, Toby L.  
APPLICANT: Van Gastel, Franciscus J.C.  
APPLICANT: Janssen, Giselle G.  
APPLICANT: Murray, Christopher J.  
APPLICANT: Wang, Huaming  
APPLICANT: Winetzkv, Deborah S.  
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
TITLE OF INVENTION: Complexes  
FILE REFERENCE: GC690  
CURRENT APPLICATION NUMBER: US/09/954,385  
CURRENT FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 433

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 375  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: binding peptide  
US-09-954-385-375

Query Match 40.0%; Score 4; DB 11; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTGP 7  
DB 9 FTGP 12

RESULT 54  
US-10-155-883B-31  
; Sequence 31, Application US/10155883B  
; Publication No. US20030148380A1  
; GENERAL INFORMATION:  
; APPLICANT: Belcher, Angela M.  
; TITLE OF INVENTION: MOLECULAR RECOGNITION OF MATERIALS  
; FILE REFERENCE: 119927-1049  
; CURRENT APPLICATION NUMBER: US/10/155,883B  
; CURRENT FILING DATE: 2002-05-24  
; PRIOR APPLICATION NUMBER: 60/296,013  
; PRIOR FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: peptide binding sequence retrieved from phage biopanning  
US-10-155-883B-31

Query Match 40.0%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
DB 9 PFTG 12

RESULT 55  
US-10-158-596A-31  
; Sequence 31, Application US/10158596A  
; Publication No. US20030068900A1  
; GENERAL INFORMATION:  
; APPLICANT: Belcher, Angela  
; APPLICANT: Flynn, Christine  
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLE NUCLEATION, SHAPE AND CRYSTAL  
; FILE REFERENCE: 119927-1052  
; CURRENT APPLICATION NUMBER: US/10/158,596A  
; CURRENT FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/296,013  
; PRIOR FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: peptide retrieved from phage biopanning  
US-10-158-596A-31

Query Match 40.0%; Score 4; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
DB 9 PFTG 12

RESULT 56  
US-10-094-401-141  
; Sequence 141, Application US/10094401  
; Publication No. US20030069395A1  
; GENERAL INFORMATION:  
; APPLICANT: Dyax Corp.  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Cohen, Edward H.  
; TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES  
; FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US  
; CURRENT APPLICATION NUMBER: US/10/094,401  
; CURRENT FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/331,352  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/292,975  
; PRIOR FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 271  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 141  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: albumin binding peptide  
US-10-094-401-141

Query Match 40.0%; Score 4; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
DB 5 YPFT 8

RESULT 57  
US-10-157-775B-31  
; Sequence 31, Application US/10157775B  
; Publication No. US20030073104A1  
; GENERAL INFORMATION:  
; APPLICANT: Belcher, Angela M.  
; APPLICANT: Lee, Seung-wuk  
; TITLE OF INVENTION: NANOSCALING ORDERING OF HYBRID MATERIALS USING GENETICALLY ENGINEERED  
; FILE REFERENCE: 119927-1051  
; CURRENT APPLICATION NUMBER: US/10/157,775B  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: 60/326,583  
; PRIOR FILING DATE: 2001-10-02  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: peptide recognition sequence retrieved from phage biopanning  
US-10-157-775B-31

Query Match 40.0%; Score 4; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6

```
Db          9 PFTG 12
|||||
RESULT 58
US-10-254-446A-31
; Sequence 31, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
; APPLICANT: Ryan, Bethel
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopan
US-10-254-446A-31

Query Match          40.0%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 PFTG 6
|||||
Db          9 PFTG 12

RESULT 59
US-09-815-156-6
; Sequence 6, Application US/09815156
; Patent No. US20020037514A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Elliot S.
; APPLICANT: Wang, Weizhan
; APPLICANT: Chandraratna, Roshantha A.S.
; TITLE OF INVENTION: Identification of Nuclear
; TITLE OF INVENTION: Receptor-Dependent
; TITLE OF INVENTION: Coregulator Recruitment
; FILE REFERENCE: P-AR 4650
; CURRENT APPLICATION NUMBER: US/09/815,156
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-815-156-6

Query Match          40.0%; Score 4; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 PFTG 10
|||||
Db          3 PFTG 6

RESULT 60
US-09-887-280-11
; Sequence 11, Application US/09887280
; Publication No. US20020197670A1
; GENERAL INFORMATION:
; APPLICANT: PRICE, THOMAS M.
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROGESTERONE RECEPTOR
; FILE REFERENCE: GHS-338
; CURRENT APPLICATION NUMBER: US/09/887,280
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/213,340
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VS
US-09-887-280-11

Query Match          40.0%; Score 4; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 PFTG 10
|||||
Db          3 PFTG 6

RESULT 61
US-09-791-393-44
; Sequence 44, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 14
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-44

Query Match          40.0%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 GPIP 9
|||||
Db          3 GPIP 6

RESULT 62
US-09-791-389-44
; Sequence 44, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
```



; APPLICANT: Terrett, Jonathan Alexander  
; APPLICANT: Tyson, Kerry Louise  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)  
; TITLE OF INVENTION: and Unipolar Depression  
; FILE REFERENCE: 2543-1-001 N2  
; CURRENT APPLICATION NUMBER: US/09/791,389  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: GB 0004412.3  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: GB 0030050.9  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: US 60/254,830  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-09-791-389-44

Query Match 40.0%; Score 4; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIP 9  
|||  
Db 3 GPIP 6

RESULT 63  
US-10-076-047A-29  
; Sequence 29, Application US/10076047A  
; Publication No. US20030152935A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer  
; FILE REFERENCE: 2543-1-026  
; CURRENT APPLICATION NUMBER: US/10/076,047A  
; CURRENT FILING DATE: 2002-02-13  
; PRIOR APPLICATION NUMBER: GB 9919258.5  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: GB 0007754.5  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/GB00/031143  
; PRIOR FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 351  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-076-047A-29

Query Match 40.0%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIP 9  
|||  
Db 3 GPIP 6

RESULT 64  
US-10-306-903-16  
; Sequence 16, Application US/10306903  
; Publication No. US20030166014A1  
; GENERAL INFORMATION:  
; APPLICANT: Tlams, Kathy  
; TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY PROTEIN  
; FILE REFERENCE: 0994.00137

; CURRENT APPLICATION NUMBER: US/10/306,903  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 09/044,604  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 08/328,451  
; PRIOR FILING DATE: 1994-10-25  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 16  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Epitope  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(14)  
; OTHER INFORMATION: VS epitope  
US-10-306-903-16

Query Match 40.0%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIPN 10  
|||  
Db 3 PIPN 6

RESULT 65  
US-10-427-208-67  
; Sequence 67, Application US/10427208  
; Publication No. US20030200555A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: Hazuda, Daria J  
; APPLICANT: Chen Dodson, Elizabeth  
; APPLICANT: Lai, Ming-Tain  
; APPLICANT: Xu, Min  
; APPLICANT: Shi, Xiao-Ping  
; APPLICANT: Simon, Adam J.  
; APPLICANT: Wu, Guoxin  
; APPLICANT: Register, Robert B.  
; TITLE OF INVENTION: ASSAYS USING AMYLOID PRECURSOR PROTEINS WITH MODIFIED  
; TITLE OF INVENTION: BETA-SECRETASE CLEAVAGE SITES TO MONITOR BETA-SECRETASE ACTIVITY  
; FILE REFERENCE: 21052  
; CURRENT APPLICATION NUMBER: US/10/427,208  
; CURRENT FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: fusable polypeptide: VS  
US-10-427-208-67

Query Match 40.0%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIPN 10  
|||  
Db 3 PIPN 6

RESULT 66  
US-10-262-538-33  
; Sequence 33, Application US/10262538  
; Publication No. US2003011324A1  
; GENERAL INFORMATION:

; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: NEUROPILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37564  
; CURRENT APPLICATION NUMBER: US/10/262,538  
; CURRENT FILING DATE: 2002-09-30  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 33  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-262-538-33

Query Match 40.0%; Score 4; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIPN 10  
Db 3 PIPN 6  
|||||

## RESULT 67

US-09-785-770A-21  
; Sequence 21, Application US/09785770A  
; Patent No. US20020103360A1  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; APPLICANT: Barnes, Thomas M.  
; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN  
; FILE REFERENCE: 07334-328001  
; CURRENT APPLICATION NUMBER: US/09/785,770A  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: US 09/387,462  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: US 09/145,056  
; PRIOR FILING DATE: 1998-09-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 4.0  
; SEQ ID NO 21  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-785-770A-21

Query Match 40.0%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTGP 7  
Db 3 FTGP 6  
|||||

## RESULT 68

US-09-785-770A-23  
; Sequence 23, Application US/09785770A  
; Patent No. US20020103360A1  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; APPLICANT: Barnes, Thomas M.  
; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN  
; FILE REFERENCE: 07334-328001  
; CURRENT APPLICATION NUMBER: US/09/785,770A  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: US 09/387,462  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: US 09/145,056  
; PRIOR FILING DATE: 1998-09-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 4.0

; SEQ ID NO 23  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-785-770A-23

Query Match 40.0%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTGP 7  
Db 3 FTGP 6  
|||||

## RESULT 69

US-09-733-179A-2  
; Sequence 2, Application US/09733179A  
; Publication No. US20030073160A1  
; GENERAL INFORMATION:  
; APPLICANT: Boux, Heather A.  
; APPLICANT: Wong, Geraldine S.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING STRESS-INDUCIBLE PROTEINS  
; FILE REFERENCE: 12071-006001  
; CURRENT APPLICATION NUMBER: US/09/733,179A  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: WO US00/33341  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,535  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-733-179A-2

Query Match 40.0%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGPI 8  
Db 12 TGPI 15  
|||||

## RESULT 70

US-09-933-767-829  
; Sequence 829, Application US/09933767  
; Publication No. US20030181692A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P2  
; CURRENT APPLICATION NUMBER: US/09/933,767  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: PCT/US01/05614  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/184,836  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/193,170  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/205,258  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: PCT/US98/11422  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/048,885  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,375  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,881

; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,880  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,896  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,020  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,876  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,895  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,884  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,894  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,971  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,882  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,899  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,893  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,900  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,901  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,892  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,915  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,019  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,970  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,972  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,916  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,373  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,875  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,374  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,917  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,949  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,883  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,897  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,898  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,962  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,963  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,877  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,878  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/068,054  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,064  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,053  
; PRIOR FILING DATE: 1997-12-18

; PRIOR APPLICATION NUMBER: 60/070,923  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/085,925  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/092,921  
; PRIOR FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: 60/094,657  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1245  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 829  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-933-767-829  
  
Query Match 40.0%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 PFTG 6  
DB 5 PFTG 8  
  
RESULT 71  
US-10-273-541-47  
; Sequence 47, Application US/10273541  
; Publication No. US20030077277A1  
; GENERAL INFORMATION:  
; APPLICANT: Bayer Corporation  
; APPLICANT: Takeuchi, Toehi  
; TITLE OF INVENTION: Human Antibodies That Have MN Binding and Cell Adhesion-Neutrality  
; FILE REFERENCE: Activity  
; FILE REFERENCE: MSB-7289  
; CURRENT APPLICATION NUMBER: US/10/273,541  
; CURRENT FILING DATE: 2002-10-18  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 47  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-273-541-47  
  
Query Match 40.0%; Score 4; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 PFTG 6  
DB 2 PFTG 5  
  
RESULT 72  
US-10-273-541-48  
; Sequence 48, Application US/10273541  
; Publication No. US20030077277A1  
; GENERAL INFORMATION:

```
; APPLICANT: Bayer Corporation
; APPLICANT: Takeuchi Toshi
; TITLE OF INVENTION: Human Antibodies That Have MN Binding and Cell Adhesion-Neutraliz
; TITLE OF INVENTION: Activity
; FILE REFERENCE: MSB-7289
; CURRENT APPLICATION NUMBER: US/10/273,541
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-541-48

Query Match      40.0%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PFTG 6
      ||||
DB      2 PFTG 5

RESULT 73
US-10-023-282-829
; Sequence 829, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: US/10/023,282
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892

; APPLICANT: Bayer Corporation
; APPLICANT: Takeuchi Toshi
; TITLE OF INVENTION: Human Antibodies That Have MN Binding and Cell Adhesion-Neutraliz
; TITLE OF INVENTION: Activity
; FILE REFERENCE: MSB-7289
; CURRENT APPLICATION NUMBER: US/10/273,541
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-541-48

Query Match      40.0%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PFTG 6
      ||||
DB      2 PFTG 5

RESULT 74
US-08-424-550B-247
; Sequence 247, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
```

Query Match 40.0%; Score 4; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
|||  
DB 5 PFTG 8  
|||

RESULT 74  
US-08-424-550B-247  
; Sequence 247, Application US/08424550B  
; Publication No. US20020119447A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKER

APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550B  
FILING DATE:  
CLASSIFICATION: 435435  
ATTORNEY/AGENT INFORMATION:  
NAME: POREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 247:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-424-550B-247

Query Match 40.0%; Score 4; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GPIP 9  
Db 11 GPIP 14

RESULT 75  
US-10-161-791-174  
Sequence 174, Application US/10161791  
Publication No. US20030186863A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 174:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-174  
Query Match 40.0%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 GPIP 10  
Db 8 GPIP 11  
Search completed: November 25, 2003, 20:25:44  
Job time : 20.8936 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 10.9043 Seconds  
(without alignments)  
38.802 Million cell updates/sec

Title: US-09-641-801-18

Perfect score: 10

Sequence: 1 VYPFTGPIPN 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

Issued Patents\_AA:\*  
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3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/FCUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	4	US-09-641-803-18
2	4	40.0	6	5	PCT-US91-09152-6
3	4	40.0	8	3	US-08-444-818-453
4	4	40.0	8	3	US-08-444-818-454
5	4	40.0	8	3	US-08-444-818-455
6	4	40.0	8	3	US-08-444-818-456
7	4	40.0	8	3	US-08-444-818-457
8	4	40.0	8	5	PCT-US91-09152-7
9	4	40.0	9	1	US-08-438-123-3
10	4	40.0	9	1	US-08-467-420A-47
11	4	40.0	9	1	US-08-467-420A-48
12	4	40.0	9	1	US-08-470-110A-47
13	4	40.0	9	1	US-08-470-110A-48
14	4	40.0	9	1	US-08-667-769A-47
15	4	40.0	9	1	US-08-667-769A-48
16	4	40.0	9	2	US-08-940-371-47
17	4	40.0	9	2	US-08-940-371-48
18	4	40.0	9	2	US-08-672-345C-21
19	4	40.0	9	2	US-08-672-345C-24
20	4	40.0	9	2	US-08-672-345C-27
21	4	40.0	9	2	US-08-672-345C-30
22	4	40.0	9	2	US-08-672-345C-81
23	4	40.0	9	3	US-08-637-647-47
24	4	40.0	9	3	US-08-637-647-48
25	4	40.0	9	3	US-09-214-095D-21
26	4	40.0	9	3	US-09-214-095D-24
27	4	40.0	9	3	US-09-214-095D-27

28	4	40.0	9	3	US-09-214-095D-30	Sequence 30, Appl
29	4	40.0	9	3	US-09-214-095D-81	Sequence 81, Appl
30	4	40.0	9	4	US-09-406-532-20	Sequence 20, Appl
31	4	40.0	9	5	PCT-US95-17082A-47	Sequence 47, Appl
32	4	40.0	9	5	PCT-US95-17082A-48	Sequence 48, Appl
33	4	40.0	10	3	US-08-818-112-131	Sequence 131, Appl
34	4	40.0	10	4	US-08-818-111-126	Sequence 126, Appl
35	4	40.0	10	4	US-09-056-556-131	Sequence 131, Appl
36	4	40.0	10	4	US-09-072-596-126	Sequence 126, Appl
37	4	40.0	11	1	US-08-438-123-11	Sequence 11, Appl
38	4	40.0	11	4	US-09-208-258-830	Sequence 830, Appl
39	4	40.0	12	2	US-08-480-793-2	Sequence 2, Appl
40	4	40.0	12	5	PCT-US92-05825A-2	Sequence 2, Appl
41	4	40.0	14	4	US-09-400-564-16	Sequence 16, Appl
42	4	40.0	15	4	US-09-205-258-829	Sequence 829, Appl
43	4	40.0	16	3	US-08-602-999A-174	Sequence 174, Appl
44	4	40.0	16	4	US-09-500-124-174	Sequence 174, Appl
45	4	40.0	16	4	US-08-469-260A-247	Sequence 247, Appl
46	4	40.0	16	4	US-08-488-446-247	Sequence 247, Appl
47	4	40.0	16	4	US-08-467-344A-247	Sequence 247, Appl
48	4	40.0	17	4	US-09-355-398C-2	Sequence 2, Appl
49	4	40.0	18	4	US-09-355-398C-5	Sequence 5, Appl
50	4	40.0	19	1	US-07-924-753-12	Sequence 12, Appl
51	4	40.0	19	2	US-08-460-890A-55	Sequence 55, Appl
52	4	40.0	19	3	US-08-167-641C-55	Sequence 55, Appl
53	4	40.0	19	3	US-08-809-397-10	Sequence 10, Appl
54	4	40.0	19	3	US-08-460-971A-55	Sequence 55, Appl
55	4	40.0	19	3	US-08-462-040-55	Sequence 55, Appl
56	4	40.0	19	4	US-09-400-564-15	Sequence 15, Appl
57	4	40.0	19	4	US-09-425-597-10	Sequence 10, Appl
58	4	40.0	19	4	US-09-205-258-831	Sequence 831, Appl
59	4	40.0	19	5	PCT-US95-12502-10	Sequence 10, Appl
60	4	40.0	20	3	US-08-602-999A-136	Sequence 136, Appl
61	4	40.0	20	4	US-09-500-124-136	Sequence 136, Appl
62	4	40.0	20	4	US-09-355-398C-3	Sequence 3, Appl
63	3	30.0	4	1	US-08-358-160-172	Sequence 172, Appl
64	3	30.0	4	1	US-08-358-160-174	Sequence 174, Appl
65	3	30.0	4	2	US-08-824-109-2	Sequence 2, Appl
66	3	30.0	4	2	US-08-824-109-4	Sequence 4, Appl
67	3	30.0	4	2	US-08-824-109-6	Sequence 6, Appl
68	3	30.0	4	2	US-08-824-109-8	Sequence 8, Appl
69	3	30.0	4	2	US-08-747-137-162	Sequence 162, Appl
70	3	30.0	4	3	US-09-091-001-8	Sequence 8, Appl
71	3	30.0	4	3	US-09-091-001-8	Sequence 13, Appl
72	3	30.0	4	3	US-09-330-970-13	Sequence 13, Appl
73	3	30.0	4	3	US-09-330-970-31	Sequence 31, Appl
74	3	30.0	4	3	US-08-564-164A-15	Sequence 15, Appl
75	3	30.0	4	3	US-08-564-164A-17	Sequence 17, Appl
76	3	30.0	4	3	US-09-411-531A-1	Sequence 1, Appl
77	3	30.0	4	4	US-09-252-338-2	Sequence 2, Appl
78	3	30.0	4	4	US-09-252-338-4	Sequence 4, Appl
79	3	30.0	4	4	US-09-252-338-6	Sequence 6, Appl
80	3	30.0	4	4	US-09-252-338-8	Sequence 8, Appl
81	3	30.0	4	4	US-09-411-605A-1	Sequence 1, Appl
82	3	30.0	4	4	US-09-336-314-1	Sequence 1, Appl
83	3	30.0	4	6	5215966-14	Patent No. 5215966
84	3	30.0	5	1	US-07-729-099-12	Sequence 12, Appl
85	3	30.0	5	1	US-08-257-392-12	Sequence 12, Appl
86	3	30.0	5	2	US-08-642-045B-23	Sequence 23, Appl
87	3	30.0	5	2	US-08-627-173-9	Sequence 9, Appl
88	3	30.0	5	2	US-08-637-759B-93	Sequence 93, Appl
89	3	30.0	5	2	US-08-535-882A-9	Sequence 9, Appl
90	3	30.0	5	2	US-08-622-740-13	Sequence 13, Appl
91	3	30.0	5	3	US-08-770-035-12	Sequence 12, Appl
92	3	30.0	5	3	US-08-871-355A-93	Sequence 93, Appl
93	3	30.0	5	3	US-08-440-689-13	Sequence 13, Appl
94	3	30.0	5	3	US-09-039-308A-24	Sequence 24, Appl
95	3	30.0	5	3	US-09-005-546-9	Sequence 9, Appl
96	3	30.0	5	4	US-09-122-399-13	Sequence 13, Appl
97	3	30.0	5	4	US-09-201-945-93	Sequence 93, Appl
98	3	30.0	5	4	US-09-187-859-325	Sequence 325, Appl
99	3	30.0	5	4	US-09-187-859-2136	Sequence 2136, Appl
100	3	30.0	5	4	US-08-447-985-18	Sequence 18, Appl

## ALIGNMENTS

```
RESULT 1
US-09-641-803-18
; Sequence 18, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-18

Query Match          100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VYPFTGPIPN 10
Db      1 VYPFTGPIPN 10

RESULT 2
PCT-US91-09152-6
; Sequence 6, Application PC/TUS9109152
; GENERAL INFORMATION:
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Sharma, Satish K.
; TITLE OF INVENTION: Fusion Polypeptides
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Upjohn Company - Corp. Patents & Trademarks
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette (3M 3.5, DS double side 1.0 MB)
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09152
; FILING DATE: 19911212
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US07/626,727
; FILING DATE: 13/12/90
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US07/614,170
; FILING DATE: 14/11/90
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/02923
; FILING DATE: 30/05/90
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US07/368,231
; FILING DATE: 16/06/89
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US07/506,605
; FILING DATE: 09/04/90
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33229
; REFERENCE/DOCKET NUMBER: 4595
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616 385 5210
; TELEFAX: 616 385 6897
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: AMINO ACID
; TOPOLOGY: linear
PCT-US91-09152-6

Query Match          40.0%; Score 4; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e-05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GPIIP 9
Db      3 GPIIP 6

RESULT 3
US-08-444-818-453
; Sequence 453, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 453:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-453
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Query Match 40.0%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIP 9  
|||  
Db 5 GPIP 8

## RESULT 4

US-08-444-818-454  
; Sequence 454, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,818  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,590  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harbin, Alisa A.  
; REGISTRATION NUMBER: 33,895  
; REFERENCE/DOCKET NUMBER: 0110.002  
; TELEPHONE: (508)359-3876  
; TELEFAX: (508)359-3885  
; INFORMATION FOR SEQ ID NO: 454:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-444-818-454

Query Match 40.0%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIP 9  
|||  
Db 4 GPIP 7

## RESULT 5

US-08-444-818-455  
; Sequence 455, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,818  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,590  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Harbin, Alisa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 0110.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885  
INFORMATION FOR SEQ ID NO: 455:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-444-818-455

Query Match 40.0%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIP 9  
|||  
Db 3 GPIP 6

## RESULT 6

US-08-444-818-456  
; Sequence 456, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,818  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,590  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harbin, Alisa A.  
; REGISTRATION NUMBER: 33,895

REFERENCE/DOCKET NUMBER: 0110.002  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885  
INFORMATION FOR SEQ ID NO: 456:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-444-818-456

Query Match 40.0%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 GPIP 9  
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Db 2 GPIP 5

## RESULT 7

US-08-444-818-457  
Sequence 457, Application US/08444818  
Patent No. 6150087  
GENERAL INFORMATION:  
APPLICANT: Chien, David Y.  
APPLICANT: Rutter, William J.  
TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
NUMBER OF SEQUENCES: 777  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,818  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,590  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Harbin, Alisa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 0110.002  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885  
INFORMATION FOR SEQ ID NO: 457:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-444-818-457

Query Match 40.0%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 GPIP 9  
|||  
Db 1 GPIP 4

## RESULT 8

PCT-US91-09152-7  
Sequence 7, Application PC/TUS9109152  
GENERAL INFORMATION:  
APPLICANT: Kubiak, Teresa M.  
APPLICANT: Sharma, Satish K.  
TITLE OF INVENTION: Fusion Polypeptides  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Upjohn Company - Corp. Patents & Trademarks  
STREET: 301 Henrietta Street  
CITY: Kalamazoo  
STATE: Michigan  
COUNTRY: USA  
ZIP: 49001

COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette (3M 3.5, DS double side 1.0 MB)  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/09152  
FILING DATE: 19911212  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US07/626,727  
FILING DATE: 13/12/90

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US07/614,170  
FILING DATE: 14/11/90  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US90/02923  
FILING DATE: 30/05/90

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US07/368,231  
FILING DATE: 16/06/89

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US07/506,605  
FILING DATE: 09/04/90

ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33229  
REFERENCE/DOCKET NUMBER: 4595

TELEPHONE: 616 385 5210  
TELEFAX: 616 385 6897  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US91-09152-7

Query Match 40.0%; Score 4; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 GPIP 9  
|||  
Db 5 GPIP 8

## RESULT 9

US-08-438-123-3  
Sequence 3, Application US/08438123  
Patent No. 5552293  
GENERAL INFORMATION:  
APPLICANT: Lindholm et al  
TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lowe, Price, LeBlanc & Becker  
STREET: Suite 300, 99 Canal Center Plaza  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: DOS Text File  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,123  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/906,350  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: J.G. Mullins  
REGISTRATION NUMBER: 33073  
REFERENCE/DOCKET NUMBER: 149-011  
TELEPHONE: 703 684 1111  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Polypeptide  
US-08-438-123-3

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No.2.5e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 10  
US-08-467-420A-47  
Sequence 47, Application US/08467420A  
Patent No. 5683892  
GENERAL INFORMATION:  
APPLICANT: Ames, Robert S.  
APPLICANT: Appelbaum, Edward R.  
APPLICANT: Chaiken, Irwin M.  
APPLICANT: Cook, Richard M.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Holmes, Stephen D.  
APPLICANT: McMillan, Lynette J.  
APPLICANT: Theisen, Timothy W.  
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P. O. Box 1539-UM2220  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,420A

FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/363131  
FILING DATE: 23-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50282  
TELEPHONE: 610 270-5024  
TELEPHONE: 610 270-5024  
TELEPHONE: 610 270-5090  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-420A-47

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No.2.5e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 11  
US-08-467-420A-48  
Sequence 48, Application US/08467420A  
Patent No. 5683892  
GENERAL INFORMATION:  
APPLICANT: Ames, Robert S.  
APPLICANT: Appelbaum, Edward R.  
APPLICANT: Chaiken, Irwin M.  
APPLICANT: Cook, Richard M.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Holmes, Stephen D.  
APPLICANT: McMillan, Lynette J.  
APPLICANT: Theisen, Timothy W.  
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P. O. Box 1539-UM2220  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,420A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/363131  
FILING DATE: 23-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50282  
TELEPHONE: 610 270-5024  
TELEPHONE: 610 270-5090

; INFORMATION FOR SEQ ID NO: 48:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-467-420A-48

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Oy 2 YPFT 5

Db 6 YPFT 9

RESULT 12

US-08-470-110A-47

; Sequence 47, Application US/08470110A

; Patent No. 5693323

; GENERAL INFORMATION:

; APPLICANT: Ames, Robert S.

; APPLICANT: Appelbaum, Edward R.

; APPLICANT: Chaiken, Irwin M.

; APPLICANT: Cook, Richard M.

; APPLICANT: Gross, Mitchell S.

; APPLICANT: Holmes, Stephen D.

; APPLICANT: McMillan, Lynette J.

; APPLICANT: Theisen, Timothy W.

; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in

; TREATMENT OF IL5 MEDIATED DISORDERS

; NUMBER OF SEQUENCES: 74

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corp./Corporate

; ADDRESSEE: Intellectual Property

; STREET: P. O. Box 1539-UW2220

; CITY: King of Prussia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19406-0939

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,110A

; FILING DATE:

; CLASSIFICATION: 426

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/363131

; FILING DATE: 23-DEC-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028

; REFERENCE/DOCKET NUMBER: P50282

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610 270-5024

; TELEFAX: 610 270-5090

; INFORMATION FOR SEQ ID NO: 47:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-470-110A-47

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Oy 2 YPFT 5

Db 6 YPFT 9

RESULT 13

US-08-470-110A-48

; Sequence 48, Application US/08470110A

; Patent No. 5693323

; GENERAL INFORMATION:

; APPLICANT: Ames, Robert S.

; APPLICANT: Appelbaum, Edward R.

; APPLICANT: Chaiken, Irwin M.

; APPLICANT: Cook, Richard M.

; APPLICANT: Gross, Mitchell S.

; APPLICANT: Holmes, Stephen D.

; APPLICANT: McMillan, Lynette J.

; APPLICANT: Theisen, Timothy W.

; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in

; TREATMENT OF IL5 MEDIATED DISORDERS

; NUMBER OF SEQUENCES: 74

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corp./Corporate

; ADDRESSEE: Intellectual Property

; STREET: P. O. Box 1539-UW2220

; CITY: King of Prussia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19406-0939

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,110A

; FILING DATE:

; CLASSIFICATION: 426

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/363131

; FILING DATE: 23-DEC-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028

; REFERENCE/DOCKET NUMBER: P50282

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610 270-5024

; TELEFAX: 610 270-5090

; INFORMATION FOR SEQ ID NO: 48:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-470-110A-48

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Oy 2 YPFT 5

Db 6 YPFT 9

RESULT 14

US-08-667-769A-47

; Sequence 47, Application US/08667769A

; Patent No. 5783184

; GENERAL INFORMATION:

; APPLICANT: Ames, Robert S.

APPLICANT: Appelbaum, Edward R.  
APPLICANT: Chaiken, Irwin M.  
APPLICANT: Cook, Richard M.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Holmes, Stephen D.  
APPLICANT: McMillan, Lynette J.  
APPLICANT: Theisen, Timothy W.  
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSES: SmithKline Beecham Corp./Corporate  
STREET: P.O. Box 1539-UW2220  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/667,769A  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17082  
FILING DATE: 22-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470110  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/467420  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/363131  
FILING DATE: 23-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50503  
TELEPHONE: 610-270-5024  
TELEFAX: 610-270-5090  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-667-769A-47

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 15  
US-08-667-769A-48  
Sequence 48, Application US/08667769A  
Patent No. 5783184  
GENERAL INFORMATION:  
APPLICANT: Ames, Robert S.  
APPLICANT: Appelbaum, Edward R.  
APPLICANT: Chaiken, Irwin M.  
APPLICANT: Cook, Richard M.  
APPLICANT: Gross, Mitchell S.

APPLICANT: Holmes, Stephen D.  
APPLICANT: McMillan, Lynette J.  
APPLICANT: Theisen, Timothy W.  
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSES: SmithKline Beecham Corp./Corporate  
STREET: P.O. Box 1539-UW2220  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/667,769A  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17082  
FILING DATE: 22-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470110  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/467420  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/363131  
FILING DATE: 23-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50503  
TELEPHONE: 610-270-5024  
TELEFAX: 610-270-5090  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-667-769A-48

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
Db 6 YPFT 9

RESULT 16  
US-08-940-371-47  
Sequence 47, Application US/08940371  
Patent No. 5851525  
GENERAL INFORMATION:  
APPLICANT: Ames, Robert S.  
APPLICANT: Appelbaum, Edward R.  
APPLICANT: Chaiken, Irwin M.  
APPLICANT: Cook, Richard M.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Holmes, Stephen D.  
APPLICANT: McMillan, Lynette J.  
APPLICANT: Theisen, Timothy W.  
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in

;; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
;; NUMBER OF SEQUENCES: 74  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SmithKline Beecham Corp./Corporate  
;; ADDRESSES: Intellectual Property  
;; STREET: P. O. Box 1539-UM2220  
;; CITY: King of Prussia  
;; STATE: Pennsylvania  
;; COUNTRY: USA  
;; ZIP: 19406-0939  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/940,371  
;; FILING DATE:  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/470,110  
;; FILING DATE:  
;; APPLICATION NUMBER: US 08/363131  
;; FILING DATE: 23-DEC-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sutton, Jeffrey A.  
;; REGISTRATION NUMBER: 34,028  
;; REFERENCE/DOCKET NUMBER: P50282  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 610 270-5024  
;; TELEFAX: 610 270-5090  
;; INFORMATION FOR SEQ ID NO: 47:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
;; US-08-940-371-47

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 2 YPFT 5  
Db ||||  
6 YPFT 9

RESULT 17  
US-08-940-371-48  
; Sequence 48, Application US/08940371  
; Patent No. 5851525  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard W.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TREATMENT OF IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSES: Intellectual Property  
; STREET: P. O. Box 1539-UM2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/940,371  
;; FILING DATE:  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/470,110  
;; FILING DATE:  
;; APPLICATION NUMBER: US 08/363131  
;; FILING DATE: 23-DEC-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sutton, Jeffrey A.  
;; REGISTRATION NUMBER: 34,028  
;; REFERENCE/DOCKET NUMBER: P50282  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 610 270-5024  
;; TELEFAX: 610 270-5090  
;; INFORMATION FOR SEQ ID NO: 48:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
;; US-08-940-371-48

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 2 YPFT 5  
Db ||||  
6 YPFT 9

RESULT 18  
US-08-672-345C-21  
; Sequence 21, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids

;  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-21

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
|||  
Db 6 YPFT 9

## RESULT 19

US-08-672-345C-24  
; Sequence 24, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-24

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
|||  
Db 6 YPFT 9

## RESULT 20

US-08-672-345C-27  
; Sequence 27, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:

;  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-27

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
|||  
Db 6 YPFT 9

## RESULT 21

US-08-672-345C-30  
; Sequence 30, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-30

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 YPFT 5  
|||  
Db 6 YPFT 9

## RESULT 22

US-08-672-345C-81  
; Sequence 81, Application US/08672345C  
; Patent No. 5948658

;  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036

;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525

;  
; INFORMATION FOR SEQ ID NO: 81:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-81

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 YPFT 5  
|||  
Db 6 YPFT 9

## RESULT 23

US-08-637-647-47  
; Sequence 47, Application US/08637647  
; Patent No. 6129913

;  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.

;  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P. O. Box 1539-UM2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939

;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/637,647  
; FILING DATE: 19-JUN-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/363,131  
; FILING DATE:  
; CLASSIFICATION: 536

;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50282  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270-5024  
; TELEFAX: 610 270-5090

;  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-637-647-47

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 YPFT 5  
|||  
Db 6 YPFT 9

## RESULT 24

US-08-637-647-48  
; Sequence 48, Application US/08637647  
; Patent No. 6129913

;  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.

;  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P. O. Box 1539-UM2220  
; CITY: King of Prussia



STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/637,647  
FILING DATE: 19-JUN-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION NUMBER: US/08/363,131  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50282  
TELEPHONE: 610 270-5024  
TELEFAX: 610 270-5090  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-637-647-48

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
DB 6 YPFT 9

RESULT 25  
US-09-214-095D-21  
; Sequence 21, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 21  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-21

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
DB 6 YPFT 9

RESULT 26  
US-09-214-095D-24  
; Sequence 24, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:

APPLICANT: Landry, Donald  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
FILE REFERENCE: 51400-A-PCT-US  
CURRENT APPLICATION NUMBER: US/09/214,095D  
CURRENT FILING DATE: 1999-07-19  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 24  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Murinae gen. sp.  
US-09-214-095D-24

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
DB 6 YPFT 9

RESULT 27  
US-09-214-095D-27  
; Sequence 27, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 27  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-27

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
DB 6 YPFT 9

RESULT 28  
US-09-214-095D-30  
; Sequence 30, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 30  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-30

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5  
DB 6 YPFT 9

Db 6 YPFT 9

## RESULT 29

US-09-214-095D-81

; Sequence 81, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 81

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Murinae gen. sp.

; FEATURE:

; NAME/KEY: CHAIN

; LOCATION: (2)..(5)

; OTHER INFORMATION: X at positions 2, 4 and 5 represents any amino acid

US-09-214-095D-81

Query Match 40.0%; Score 4; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

Db 6 YPFT 9

## RESULT 30

US-09-406-532-20

; Sequence 20, Application US/09406532A

; Patent No. 6365154

; GENERAL INFORMATION:

; APPLICANT: Connie L. Erickson-Miller

; APPLICANT: Stephen D. Holmes

; APPLICANT: James D. Winkler

; TITLE OF INVENTION: TIE2 Agonist Antibodies

; FILE REFERENCE: P50843

; CURRENT APPLICATION NUMBER: US/09/406,532A

; CURRENT FILING DATE: 1999-09-27

; PRIOR APPLICATION NUMBER: 60/102,098

; PRIOR FILING DATE: 1998-09-28

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 20

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1)...(9)

; OTHER INFORMATION: light chain CDR 3

US-09-406-532-20

Query Match 40.0%; Score 4; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

Db 6 YPFT 9

## RESULT 31

PCT-US95-17082A-47

; Sequence 47, Application PC/TUS9517082A

; GENERAL INFORMATION:

; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; STREET: P.O. Box 1539-UM2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17082A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/470110  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/467420  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/363131  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50282-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5024  
; TELEFAX: 610-270-5090  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-17082A-47

Query Match 40.0%; Score 4; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPFT 5

Db 6 YPFT 9

## RESULT 32

PCT-US95-17082A-48

; Sequence 48, Application PC/TUS9517082A

; GENERAL INFORMATION:

; APPLICANT: Ames, Robert S.

; APPLICANT: Appelbaum, Edward R.

; APPLICANT: Chaiken, Irwin M.

; APPLICANT: Cook, Richard M.

; APPLICANT: Gross, Mitchell S.

; APPLICANT: Holmes, Stephen D.

; APPLICANT: McMillan, Lynette J.

; APPLICANT: Theisen, Timothy W.

;; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
;; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
;; NUMBER OF SEQUENCES: 76  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SmithKline Beecham Corp./Corporate  
;; STREET: P.O. Box 1539-WN2220  
;; CITY: King of Prussia  
;; STATE: Pennsylvania  
;; COUNTRY: USA  
;; ZIP: 19406-0939  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US95/17082A  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/470110  
;; FILING DATE: 06-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/467420  
;; FILING DATE: 06-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/363131  
;; FILING DATE: 23-DEC-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sutton, Jeffrey A.  
;; REGISTRATION NUMBER: 34,028  
;; REFERENCE/DOCKET NUMBER: P50282-2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 610-270-5024  
;; TELEFAX: 610-270-5090  
;; INFORMATION FOR SEQ ID NO: 48:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
PCT-US95-17082A-48  
Query Match 40.0%; Score 4; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;  
QY 2 YPFT 5  
Db 6 YPFT 9  
RESULT 33  
US-08-818-112-131  
; Sequence 131, Application US/08818112  
; Patent No. 6290969  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Campos-Neto, Antonio  
; APPLICANT: Houghton, Raymond  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Twardzik, Daniel R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington

;; COUNTRY: USA  
;; ZIP: 98104-7092  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/818,112  
;; FILING DATE: 13-MAR-1997  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Maki, David J.  
;; REGISTRATION NUMBER: 31,392  
;; REFERENCE/DOCKET NUMBER: 210121.411C6  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;; INFORMATION FOR SEQ ID NO: 131:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; FEATURE:  
;; OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"  
US-08-818-112-131  
Query Match 40.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No. 98;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 FTGP 7  
Db 4 FTGP 7  
RESULT 34  
US-08-818-111-126  
; Sequence 126, Application US/08818111  
; Patent No. 6338852  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Campos-Neto, Antonio  
; APPLICANT: Houghton, Raymond  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Twardzik, Daniel R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF  
; NUMBER OF SEQUENCES: 148  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818,111  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.417C6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 126:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"  
US-08-818-111-126

Query Match 40.0%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FTGP 7  
Db 4 FTGP 7

RESULT 35  
US-09-056-556-131  
; Sequence 131, Application US/09056556  
; Patent No. 6350456  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Dillon, Davin C.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND  
; NUMBER OF SEQUENCES: 241  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056,556  
; FILING DATE: 07-APR-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.457  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 131:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

US-09-056-556-131  
Query Match 40.0%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FTGP 7  
Db 4 FTGP 7

RESULT 36

US-09-072-596-126  
; Sequence 126, Application US/09072596  
; Patent No. 6458366  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Campos-Neto, Antonia  
; APPLICANT: Houghton, Raymond  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Twardzik, Daniel R.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Hendrickson, Ronald C.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF  
; NUMBER OF SEQUENCES: 350  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/072,596  
; FILING DATE: 05-MAY-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.417C9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 126:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

US-09-072-596-126  
Query Match 40.0%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FTGP 7  
Db 4 FTGP 7

RESULT 37  
US-08-438-123-11  
; Sequence 11, Application US/08438123  
; Patent No. 5552293  
; GENERAL INFORMATION:  
; APPLICANT: Lindholm et al  
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lowe, Price, Leblanc & Becker  
; STREET: Suite 300, 99 Canal Center Plaza  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: DOS Text File  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,123  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/906,350  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: J.G. Mullins  
REGISTRATION NUMBER: 33073  
REFERENCE/DOCKET NUMBER: 149-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703 684 1111  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Polypeptide  
US-08-438-123-11

Query Match 40.0%; Score 4; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YPFT 5  
Db 6 YPFT 9

RESULT 38  
US-09-205-258-830  
Sequence 830, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 830  
LENGTH: 11  
TYPE: PPT  
ORGANISM: Homo sapiens  
US-09-205-258-830

Query Match 40.0%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PFTG 6  
Db 4 PFTG 7

RESULT 39  
US-08-480-793-2  
Sequence 2, Application US/08480793  
Patent No. 5955444

GENERAL INFORMATION:  
APPLICANT: Ingram, Vernon M., Roder, Hanno M.  
TITLE OF INVENTION: No. 5955444el Tau/Neurofilament Protein  
REGISTRATION NUMBER: Kinases  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Massachusetts Institute of Technology  
STREET: 28 Carleton Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: United States of America  
ZIP: 02142  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM-compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,793  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/912,293  
FILING DATE: July 10, 1992  
APPLICATION NUMBER: 07/742,880  
FILING DATE: 9-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Gates, Edward R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: M0656/7008  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-480-793-2

Query Match 40.0%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGPI 8  
Db 2 TGPI 5

RESULT 40  
PCT-US92-05825A-2  
Sequence 2, Application PC/TUS9205825A  
GENERAL INFORMATION:  
APPLICANT: Ingram, Vernon M., Roder, Hanno M.  
TITLE OF INVENTION: Novel Tau/Neurofilament Protein  
REGISTRATION NUMBER: Kinases  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Massachusetts Institute of Technology  
STREET: 28 Carleton Street  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: United States of America  
ZIP: 02142  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM-compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05825A  
FILING DATE: 19920710  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/742,880

FILING DATE: 9-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Gates, Edward R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: M0656/7008  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US92-05825A-2

Query Match 40.0%; Score 4; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGPI 8  
Db 2 TGPI 5

RESULT 41  
US-09-400-564-16  
Sequence 16, Application US/09400564  
Patent No. 6350574  
GENERAL INFORMATION:  
APPLICANT: Montelaro, Ronald C.  
APPLICANT: Tencza, Sarah B.  
APPLICANT: Jolley, Michael E.  
APPLICANT: Nasir, Mohammad S.  
TITLE OF INVENTION: A Fluorescence Polarization-Based Diagnostic Assay  
FILE REFERENCE: Case No. 6350574 99,579  
CURRENT APPLICATION NUMBER: US/09/400,564  
CURRENT FILING DATE: 1999-09-21  
EARLIER APPLICATION NUMBER: US 60/101,553  
NUMBER OF SEQ ID NOS: 21  
SEQ ID NO 16  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Equine infectious anemia virus  
US-09-400-564-16

Query Match 40.0%; Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GPIIP 9  
Db 9 GPIIP 12

RESULT 42  
US-09-205-258-829  
Sequence 829, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: PZ007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 829

LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-829  
Query Match 40.0%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 PPTG 6  
Db 5 PPTG 8  
RESULT 43  
US-08-602-999A-174  
Sequence 174, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602.999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 174:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-174  
Query Match 40.0%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 PIPN 10  
Db 8 PIPN 11  
RESULT 44  
US-09-500-124-174  
Sequence 174, Application US/09500124

Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 174:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-174

Query Match 40.0%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIPN 10  
DB 8 PIPN 11

RESULT 45  
US-08-469-260A-247  
Sequence 247, Application US/08469260A  
Patent No. 6451578  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHROFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
REAGENTS AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,260A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 247:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-260A-247

Query Match 40.0%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIIP 9  
DB 11 GPIIP 14

RESULT 46  
US-08-488-446-247  
Sequence 247, Application US/08488446  
Patent No. 6558898  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHROFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-446-247

Query Match 40.0%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIIP 9
DB 11 GPIIP 14

RESULT 47
US-08-467-344A-247
; Sequence 247, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATIAS
; GEORGE J. DANSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUERHOFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-344A-247

Query Match 40.0%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIIP 9
DB 11 GPIIP 14

RESULT 48
US-09-355-398C-2
; Sequence 2, Application US/09355398C
; Patent No. 6461618
; GENERAL INFORMATION:
; APPLICANT: Chen, Dexiang
; APPLICANT: VanderWeid, Karl R.
; APPLICANT: McMichael, John C.
; APPLICANT: Barniak, Vicki L.
; TITLE OF INVENTION: The 74-Kilodalton Outer Membrane Protein From Moraxella
; TITLE OF INVENTION: Catarhalis
; FILE REFERENCE: 33251-00
; CURRENT APPLICATION NUMBER: US/09/355,398C
; CURRENT FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Moraxella catarhalis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1
; OTHER INFORMATION: uncertainties in the sequence
; US-09-355-398C-2

Query Match 40.0%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PIPN 10
DB 14 PIPN 17

RESULT 49
US-09-355-398C-5
; Sequence 5, Application US/09355398C
; Patent No. 6461618
; GENERAL INFORMATION:
; APPLICANT: Chen, Dexiang
; APPLICANT: VanderWeid, Karl R.
; APPLICANT: McMichael, John C.
; APPLICANT: Barniak, Vicki L.
; TITLE OF INVENTION: The 74-Kilodalton Outer Membrane Protein From Moraxella
; TITLE OF INVENTION: Catarhalis
; FILE REFERENCE: 33251-00
; CURRENT APPLICATION NUMBER: US/09/355,398C
; CURRENT FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
```

;  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Moraxella catarrhalis  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 1  
; OTHER INFORMATION: uncertainties in the sequence  
US-09-355-398C-5

Query Match 40.0%; Score 4; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 P1P10  
Db 14 P1P17

RESULT 50  
US-07-924-753-12  
; Sequence 12, Application US/07924753  
; Patent No. 5270303  
; GENERAL INFORMATION:  
; APPLICANT: Fujio SUZUKI et al.  
; TITLE OF INVENTION: CHONDROMODULIN-II PROTEIN  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/924,753  
FILING DATE: 19920804  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE: internal fragment  
ORIGINAL SOURCE:  
ORGANISM: bovine  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPOTYPE:  
TISSUE TYPE: fetal cartilage  
CELL TYPE:  
CELL LINE:  
ORGANELLE:

;  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-07-924-753-12

Query Match 40.0%; Score 4; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFTG 6  
Db 2 PFTG 5

RESULT 51  
US-08-460-890A-55  
; Sequence 55, Application US/08460890A  
; Patent No. 5994109  
; GENERAL INFORMATION:  
; APPLICANT: Woo, Savio L.C.  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Cristiano, Richard J.  
; APPLICANT: Gottchalk, Stephen  
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
; METHODS OF USE  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,890A  
FILING DATE: June 5, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/167,641  
FILING DATE: December 14, 1993  
APPLICATION NUMBER: 07/855,389  
FILING DATE: March 20, 1992  
APPLICATION NUMBER: PCT/US93/02725  
FILING DATE: March 19, 1993  
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/066  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-890A-55

Query Match 40.0%; Score 4; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPP 4  
Db 6 VYPP 9

RESULT 52  
US-08-167-641C-55  
Sequence 55, Application US/08167641C  
Patent No. 6033884  
GENERAL INFORMATION:  
APPLICANT: Woo, Savio L.C.  
APPLICANT: Smith, Louis C.  
APPLICANT: Cristiano, Richard J.  
APPLICANT: Gottchalk, Stephen  
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
METHODS OF USE  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/167,641C  
FILING DATE: December 14, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/855,389  
FILING DATE: March 20, 1992  
APPLICATION NUMBER: PCT/US93/02725  
FILING DATE: March 19, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/012  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-167-641C-55

Query Match 40.0%; Score 4; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPP 4  
Db 6 VYPP 9

RESULT 53  
US-08-809-397-10  
Sequence 10, Application US/08809397  
Patent No. 6127170  
GENERAL INFORMATION:  
APPLICANT: Boutin, Raymond H.  
TITLE OF INVENTION: Multifunctional Molecular Complexes for Gene Transfer  
METHODS OF USE  
FILE REFERENCE: ahplaua  
CURRENT APPLICATION NUMBER: US/08/809,397  
CURRENT FILING DATE: 1997-03-21  
EARLIER APPLICATION NUMBER: WO 9610038  
EARLIER FILING DATE: 1995-09-28  
EARLIER APPLICATION NUMBER: US 08/314,060  
EARLIER FILING DATE: 1994-09-28  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 10  
LENGTH: 19  
TYPE: PRT  
ORGANISM: SPV virus  
US-08-809-397-10

Query Match 40.0%; Score 4; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPP 4  
Db 6 VYPP 9

RESULT 54  
US-08-460-971A-55  
Sequence 55, Application US/08460971A  
Patent No. 6150168  
GENERAL INFORMATION:  
APPLICANT: Woo, Savio L.C.  
APPLICANT: Smith, Louis C.  
APPLICANT: Cristiano, Richard J.  
APPLICANT: Gottchalk, Stephen  
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
METHODS OF USE  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,971A

; FILING DATE: June 5, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167,641  
; FILING DATE: December 14, 1993  
; APPLICATION NUMBER: 07/855,389  
; FILING DATE: March 20, 1992  
; APPLICATION NUMBER: PCT/US93/02725  
; FILING DATE: March 19, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 212/063  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-460-971A-55

Query Match 40.0%; Score 4; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPF 4  
DB 6 VYPF 9

RESULT 55  
US-08-462-040-55  
; Sequence 55, Application US/08462040  
; Patent No. 6177554  
; GENERAL INFORMATION:  
; APPLICANT: Woo, Savio L.C.  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Cristiano, Richard J.  
; APPLICANT: Gortchalk, Stephen  
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
; TITLE OF INVENTION: METHODS OF USE  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FASTSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,040  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167,641  
; FILING DATE: December 14, 1993  
; APPLICATION NUMBER: 07/855,389  
; FILING DATE: March 20, 1992  
; APPLICATION NUMBER: PCT/US93/02725  
; FILING DATE: March 19, 1993  
; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 212/078  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-462-040-55

Query Match 40.0%; Score 4; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPF 4  
DB 6 VYPF 9

RESULT 56  
US-09-400-564-15  
; Sequence 15, Application US/09400564  
; Patent No. 6350574  
; GENERAL INFORMATION:  
; APPLICANT: Montelaro, Ronald C.  
; APPLICANT: Tencza, Sarah B.  
; APPLICANT: Jolley, Michael E.  
; APPLICANT: Nasir, Mohammad S.  
; TITLE OF INVENTION: A Fluorescence Polarization-Based Diagnostic Assay  
; TITLE OF INVENTION: for Equine Infectious Anemia Virus  
; FILE REFERENCE: Case No. 6350574 99,579  
; CURRENT APPLICATION NUMBER: US/09/400,564  
; CURRENT FILING DATE: 1999-09-21  
; EARLIER APPLICATION NUMBER: US 60/101,553  
; NUMBER OF SEQ ID NOS: 21  
; SEQ ID NO 15  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Equine infectious anemia virus  
US-09-400-564-15

Query Match 40.0%; Score 4; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GPIP 9  
DB 14 GPIP 17

RESULT 57  
US-09-425-597-10  
; Sequence 10, Application US/09425597  
; Patent No. 6379965  
; GENERAL INFORMATION:  
; APPLICANT: Boutin, Raymond H.  
; TITLE OF INVENTION: Multifunctional Molecular Complexes for Gene Transfer  
; FILE REFERENCE: ahplause  
; CURRENT APPLICATION NUMBER: US/09/425,597  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 08/809,397  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: WO 9610038  
; PRIOR FILING DATE: 1995-09-28  
; PRIOR APPLICATION NUMBER: US 08/314,060  
; PRIOR FILING DATE: 1994-09-28

; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: SFV virus  
US-09-423-597-10

Query Match 40.0%; Score 4; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYPF 4  
Db 6 VYPF 9

## RESULT 58

US-09-203-258-831  
; Sequence 831, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,885  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,896  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,020  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,895  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,884  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,894  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,971  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,882  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,899  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,893  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,900  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,901  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,892  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,915  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,019  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,970  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,972  
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,916  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,373  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,875  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,374  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,917  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,949  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,883  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,897  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,898  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,962  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,963  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,877  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,878  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/070,923  
; EARLIER FILING DATE: 1997-12-18  
; EARLIER APPLICATION NUMBER: 60/092,921  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1227  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 831  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-203-258-831

Query Match 40.0%; Score 4; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPTG 6  
Db 8 PPTG 11

## RESULT 59

PCT-US95-12502-10  
; Sequence 10, Application PC/TUS9512502  
; GENERAL INFORMATION:  
; APPLICANT: Boutin, Raymond H.  
; TITLE OF INVENTION: Multifunctional Molecular Complexes For  
; TITLE OF INVENTION: Gene Transfer To Cells  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris  
; STREET: One Liberty Place 46th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/12502

;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA: US 08/314,060  
;; APPLICATION NUMBER: 28-SEP-1994  
;; FILING DATE: 28-SEP-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Deluca, Mark  
;; REGISTRATION NUMBER: 33,229  
;; REFERENCE/DOCKET NUMBER: APOL-0216  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 215-568-3100  
;; TELEFAX: 215-568-3439  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 19 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
PCT-US95-12502-10

Query Match 40.0%; Score 4; DB 5; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYPF 4  
DB 6 VYPF 9

RESULT 60  
US-08-602-999A-136  
; Sequence 136, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 136:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid

;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-08-602-999A-136  
Query Match 40.0%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 PIPN 10  
DB 10 PIPN 13  
RESULT 61  
US-09-500-124-136  
; Sequence 136, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 136:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-136

Query Match 40.0%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 PIPN 10  
DB 10 PIPN 13  
RESULT 62

```
US-09-355-398C-3
; Sequence 3, Application US/09355398C
; Patent No. 6461618
; GENERAL INFORMATION:
; APPLICANT: Chen, Dexiang
; APPLICANT: VanderWeid, Karl R.
; APPLICANT: McMichael, John C.
; APPLICANT: Barniak, Vicki L.
; TITLE OF INVENTION: The 74-Kilodalton Outer Membrane Protein From Moraxella
; TITLE OF INVENTION: Catarrhalis
; FILE REFERENCE: 33251-00
; CURRENT APPLICATION NUMBER: US/09/355,398C
; CURRENT FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1
; OTHER INFORMATION: uncertainties in the sequence
US-09-355-398C-3
Query Match 40.0%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PIPN 10
DB 14 PIPN 17
RESULT 63
US-08-358-160-172
; Sequence 172, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEV, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; APPLICATION NUMBER: US 07/487,063

US-09-641-801-18.oligo.ra1
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEV=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 172:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-172
Query Match 30.0%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGP 7
DB 2 TGP 4
RESULT 64
US-08-358-160-174
; Sequence 174, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEV, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; APPLICATION NUMBER: US 07/487,063
```

;; FILING DATE: 02-MAR-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/240,160  
;; FILING DATE: 02-SEP-1988  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Cooper, Iver P.  
;; REGISTRATION NUMBER: 28,005  
;; REFERENCE/DOCKET NUMBER: LEV=1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-628-5197  
;; TELEFAX: 202-737-3528  
;; TELEX: 248633  
;; INFORMATION FOR SEQ ID NO: 174:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-358-160-174

Query Match 30.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGP 7  
|||  
Db 2 TGP 4

RESULT 65  
US-08-824-109-2  
; Sequence 2, Application US/08824109  
; Patent No. 5885958  
; GENERAL INFORMATION:  
; APPLICANT: Zadina, James E.  
; APPLICANT: Kastin, Abba J.  
; APPLICANT: Hackler, Laszlo  
; TITLE OF INVENTION: Mu-Opiate Receptor Peptides  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White and Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC-compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/824,109  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kammerer, Patricia A.  
; REGISTRATION NUMBER: 29,775  
; REFERENCE/DOCKET NUMBER: TUMC:009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/787-1400  
; TELEFAX: 713-789-2679  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified site  
; LOCATION: 4  
; LOCATION: Phe-NH2 (phenylalanine amide)

US-08-824-109-2  
Query Match 30.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 YPF 4  
|||  
Db 1 YPF 3

RESULT 66  
US-08-824-109-4  
; Sequence 4, Application US/08824109  
; Patent No. 5885958  
; GENERAL INFORMATION:  
; APPLICANT: Zadina, James E.  
; APPLICANT: Kastin, Abba J.  
; APPLICANT: Hackler, Laszlo  
; TITLE OF INVENTION: Mu-Opiate Receptor Peptides  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White and Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC-compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/824,109  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kammerer, Patricia A.  
; REGISTRATION NUMBER: 29,775  
; REFERENCE/DOCKET NUMBER: TUMC:009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/787-1400  
; TELEFAX: 713-789-2679  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-824-109-4

Query Match 30.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YPF 4  
|||  
Db 1 YPF 3

RESULT 67  
US-08-824-109-6  
; Sequence 6, Application US/08824109  
; Patent No. 5885958  
; GENERAL INFORMATION:  
; APPLICANT: Zadina, James E.  
; APPLICANT: Kastin, Abba J.  
; APPLICANT: Hackler, Laszlo  
; TITLE OF INVENTION: Mu-Opiate Receptor Peptides  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White and Durkee



STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC-compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/824,109  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kammerer, Patricia A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: TUMC:009  
TELEPHONE: 713/787-1400  
TELEFAX: 713-789-2679  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified site  
LOCATION: 4  
LOCATION: D-Phe-NH2 (D-phenylalanine amide)  
US-08-824-109-6

Query Match 30.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPF 4  
Db 1 YPF 3

RESULT 68  
US-08-824-109-8  
Sequence 8, Application US/08824109  
Patent No. 5885958  
GENERAL INFORMATION:  
APPLICANT: Zadina, James E.  
APPLICANT: Kastin, Abba J.  
APPLICANT: Hackler, Laszlo  
TITLE OF INVENTION: Mu-Opiate Receptor Peptides  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White and Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC-compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/824,109  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kammerer, Patricia A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: TUMC:009  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/787-1400  
TELEFAX: 713-789-2679  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified site  
LOCATION: 4  
LOCATION: pNO2-Phe-NH2 (p-nitrophenylalanine amide)  
US-08-824-109-8

Query Match 30.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YPF 4  
Db 1 YPF 3

RESULT 69  
US-08-747-137-162  
Sequence 162, Application US/08747137  
Patent No. 5945033  
GENERAL INFORMATION:  
APPLICANT: YEN, Richard C.K.  
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR  
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE  
NUMBER OF SEQUENCES: 184  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,137  
FILING DATE: 12-NOV-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212,546  
FILING DATE: 14-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/069,831  
FILING DATE: 01-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/959,560  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/641,720  
FILING DATE: 15-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 016197-000840US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
FEATURE:

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; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Pro-Amide"
US-08-747-137-162

Query Match      30.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YPF 4
Db      1 YPF 3

RESULT 70
US-08-973-539-1
; Sequence 1, Application US/08973539
; Patent No. 595885
; GENERAL INFORMATION:
; APPLICANT: Kagawa, Kyoichi
; APPLICANT: Matsutaka, Hisako
; APPLICANT: Fukushima, Chizuko
; APPLICANT: Fujino, Hiroaki
; APPLICANT: Numata, Masahiro
; APPLICANT: Honda, Kazuhisa
; APPLICANT: Nakamura, Toyoo
; TITLE OF INVENTION: A peptide inhibiting elevations of triglyceride levels
; TITLE OF INVENTION: in blood and an agent for inhibiting elevations of
; TITLE OF INVENTION: triglyceride levels in blood comprising the peptide as
; TITLE OF INVENTION: an active component
; FILE REFERENCE: 382.1014
; CURRENT APPLICATION NUMBER: US/08/973,539
; CURRENT FILING DATE: 1997-11-24
; EARLIER APPLICATION NUMBER: PCT/JP96/01570
; EARLIER FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Bos frontalis
US-08-973-539-1

Query Match      30.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVP 3
Db      2 YVP 4

RESULT 71
US-09-091-001-8
; Sequence 8, Application US/09091001
; Patent No. 6039959
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Treatment and Diagnosis of Infections due to
; TITLE OF INVENTION: Helicobacter pylori
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,001
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/02907
; FILING DATE:
; APPLICATION NUMBER: GB 9524934.8
```

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; FILING DATE: 06-DEC-1995
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-09-091-001-8

Query Match      30.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 TGP 7
Db      2 TGP 4

RESULT 72
US-09-330-970-13
; Sequence 13, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-13

Query Match      30.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 TGP 7
Db      1 TGP 3

RESULT 73
US-09-330-970-31
; Sequence 31, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-31
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Query Match 30.0%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGP 7  
Db 1 TGP 3

RESULT 74  
US-08-564-164A-15  
; Sequence 15, Application US/08564164A  
; Patent No. 6159947  
; GENERAL INFORMATION:  
; APPLICANT: Schweighoffer, Fabien  
; APPLICANT: Tocque, Bruno  
; TITLE OF INVENTION: Intracellular Binding Proteins and Use  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/564,164A  
; FILING DATE: 28-DEC-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR94/00714  
; FILING DATE: 15-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93/07241  
; FILING DATE: 16-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin F.  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: ST93030-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610)454-3816  
; TELEFAX: (610)454-3808  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-564-164A-15

Query Match 30.0%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
Db 2 FTG 4

RESULT 75  
US-08-564-164A-17  
; Sequence 17, Application US/08564164A  
; Patent No. 6159947  
; GENERAL INFORMATION:  
; APPLICANT: Schweighoffer, Fabien  
; APPLICANT: Tocque, Bruno  
; TITLE OF INVENTION: Intracellular Binding Proteins and Use

; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/564,164A  
; FILING DATE: 28-DEC-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR94/00714  
; FILING DATE: 15-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93/07241  
; FILING DATE: 16-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin F.  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: ST93030-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610)454-3816  
; TELEFAX: (610)454-3808  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-564-164A-17

Query Match 30.0%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FTG 6  
Db 2 FTG 4

Search completed: November 25, 2003, 20:16:15  
Job time : 11.9043 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 8.28191 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-19

Perfect score: 9

Sequence: 1 SLPQNILPL 9

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3893

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76:.\*  
1: pirl:.\*  
2: pirl:.\*  
3: pirl:.\*  
4: pirl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	44.4	9	S66636	alpha-2-macroglobu
2	4	44.4	10	F44644	neurotoxin-ascosia
3	4	44.4	13	G44644	neurotoxin-ascosia
4	3	33.3	6	A35039	hypothetical colla
5	3	33.3	8	I49404	prealbumin - weste
6	3	33.3	9	G58502	kidney and bladder
7	3	33.3	9	S66419	tetrameric protein
8	3	33.3	10	A61617	ecdysteroid UDPglu
9	3	33.3	10	C39398	Fc mu (IgM) recept
10	3	33.3	10	S68033	cytochrome P450 1A
11	3	33.3	11	I33098	173K exoantigen -
12	3	33.3	11	F33098	214K exoantigen (v
13	3	33.3	11	I52304	gene rSSTR4 protei
14	3	33.3	11	PC2390	trichorozin I - fu
15	3	33.3	11	PC2392	trichorozin III -
16	3	33.3	11	S62252	hypothetical prote
17	3	33.3	12	PQ0696	1,4-alpha-glucan b
18	3	33.3	12	B60228	Fc mu (IgM) recept
19	3	33.3	13	JZVHP1	crabrolin - Europe
20	3	33.3	13	S09019	hemolytic protein
21	3	33.3	14	JN0390	histamine-releasin
22	3	33.3	14	A44515	Trp EG leader pept
23	3	33.3	14	B36079	hypothetical prote
24	3	33.3	14	D61308	hemocyanin chain 5
25	3	33.3	15	S20410	protein kinase (EC
26	3	33.3	15	PS0455	superoxide dismuta
27	3	33.3	16	A54877	alpha-conotoxin Pn
28	3	33.3	16	B54877	alpha-conotoxin Pn
29	3	33.3	16	C39509	mannose-specific l

hypothetical prote  
excretory gland al  
interferon alpha (N4- (beta-N-acetyl)g  
u-plasminogen acti  
beta-Gliadin 13 -  
neurofibromatosis-  
H4-transferring tw  
glycogen(starch) a  
2-hydroxyglutaryl-  
S-locus specific g  
cell wall protein,  
hypothetical prote  
urotensin I precur  
lactase-phlorizin  
protein F45E6.5 (i  
hemocyanin subunit  
hemocyanin chain I  
hypothetical prote  
oxidoreductase - P  
jacalin beta chain  
hypothetical prote  
kallikrein (PK-120  
lysophospholipase  
82K protein - bovi  
class I histocompa  
tyrosine-melanocyt  
T-cell receptor be  
proctolin - Americ  
peptidyl-di-peptida  
flagellar protein  
neuropeptide - sea  
proctolin - Atlant  
T-cell receptor be  
T-cell receptor be  
N-formyl oligopept  
hypothetical prote  
hypothetical 6 pro  
Y protein - human  
pyruvate Kinase (E  
fatty-acid synthas  
MHC H2-K-k cell su  
T-cell receptor be  
T-cell receptor be  
T-cell receptor be  
galactose oxidase  
glutathione transf  
glutathione transf  
sex pheromone CAM3  
ribulose-bisphosph  
180K exoantigen -  
IC12 protein - Par  
Ig heavy chain CRD  
caldesquestrin, fas  
dihydrofolate redu  
DNA topoisomerase  
Ig H chain V-D-J r  
T-cell receptor be  
T-cell receptor be  
glutathione S-tran  
Na+-transporting A  
neuropeptide B - b  
tumor-associated a  
tumor-associated a  
hypothetical prote  
ipSP protein - Shi  
hypothetical prote  
205K exoantigen -  
Ig heavy chain CRD



A;Residues: 1-9 <BIN>  
A;Experimental source: human kidney stone, bladder stone  
A;Note: a secondary sequence AAKENPXD was also found

Query Match 33.3%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 1 SLP 3  
|||  
Db 1 SLP 3

## RESULT 7

S66419  
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)  
C;Species: Spinacia oleracea (spinach)  
C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 29-Aug-1997

C;Accession: S66419 #sequence\_revision 29-Aug-1997 #text\_change 29-Aug-1997

R;Kuwabara, T.

FEBS Lett. 371, 195-198, 1995

A;Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spinach  
A;Reference number: S66419; MUID:95402209; PMID:7672127

A;Accession: S66419

A;Molecule type: protein

A;Residues: 1-9 <KUM>

Query Match 33.3%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 6 ILP 8  
|||  
Db 3 ILP 5

## RESULT 8

A61617  
ecdysteroid UDPglucosyltransferase (EC 2.4.1.-) - Autographa californica nuclear polyhedrosis virus, ACKNPV  
C;Species: Autographa californica nuclear polyhedrosis virus, ACKNPV  
C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 28-Jul-1995

C;Accession: A61617

R;O'Reilly, D.R.; Brown, M.R.; Miller, L.K.

Insect Biochem. Mol. Biol. 22, 313-320, 1992

A;Title: Alteration of ecdysteroid metabolism due to baculovirus infection of the fall armyworm  
A;Reference number: A61617

A;Accession: A61617

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <OAR>

C;Genetics:

A;Gene: egt

C;Keywords: extracellular protein; glycosyltransferase; hexosyltransferase

Query Match 33.3%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 5 NIL 7  
|||  
Db 2 NIL 4

## RESULT 9

C93998

Fc mu (IgM) receptor surface complex gamma chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 20-Mar-1998

C;Accession: C93998

R;Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.

Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991

A;Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1 genes  
A;Reference number: A39398; MUID:91219496; PMID:2023945

A;Accession: C93998  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <CAM>

Query Match 33.3%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 7 LPL 9  
|||  
Db 4 LPL 6

## RESULT 10

S68033

cytochrome P450 1A1 - tilapia (fragment)

C;Species: Oreochromis niloticus x Oreochromis aureus (tilapia)

C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 29-Aug-1997

C;Accession: S68033

R;Ueng, Y.F.; Ueng, T.H.

Arch. Biochem. Biophys. 322, 347-356, 1995

A;Title: Induction and purification of cytochrome P450 1A1 from 3-methylcholanthrene-treated tilapia

A;Reference number: S68033; MUID:96032654; PMID:7574707

A;Accession: S68033

A;Molecule type: protein

A;Residues: 1-10 <UEN>

A;Experimental source: liver and gill

Query Match 33.3%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 6 ILP 8  
|||  
Db 1 ILP 3

## RESULT 11

I33098

173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C;Accession: I33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: I33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIC>

Query Match 33.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 7 LPL 9  
|||  
Db 6 LPL 8

## RESULT 12

F33098

214K exoantigen (version 3) - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C;Accession: F33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: F33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIC>

Query Match 33.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 6 ILP 8  
|||  
Db 2 ILP 4

# RESULT 13

152304

gene rSSTR4 protein - rat (fragment)

C;Species: Rattus sp. (rat)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 17-Mar-1999

C;Accession: 152304

R;Xu, Y.; Bruno, J.F.; Berelowitz, M.

Biochem. Biophys. Res. Commun. 206, 935-941, 1995

A;Title: Characterization of the proximal promoter region of the rat somatostatin receptor

A;Reference number: 152304; MUID:95134278; PMID:7832807

A;Accession: 152304

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:S75475; NID:9914315

C;Genetics:

A;Gene: rSSTR4

Query Match 33.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 7 LPL 9  
|||  
Db 7 LPL 9

# RESULT 14

PC2390

trichorozin I - fungus (Trichoderma harzianum)

C;Species: Trichoderma harzianum

C;Date: 17-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Oct-2000

C;Accession: PC2390

R;Iida, A.; Sanekata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai,

Chem. Pharm. Bull. 43, 392-397, 1995

A;Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichorozins I-IV,

A;Reference number: PC2390; MUID:95292356; PMID:7539721

A;Accession: PC2390

A;Status: unencoded polypeptide

A;Molecule type: protein

A;Residues: 1-11 <IID>

C;Keywords: antibiotic; unencoded polypeptide

F;1/Modified site: acetylated amino end #status experimental

F;1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental

F;11/Modified site: valinol #status experimental

Query Match 33.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 5 NIL 7  
|||  
Db 2 NIL 4

# RESULT 15

PC2392

trichorozin III - fungus (Trichoderma harzianum)

C;Species: Trichoderma harzianum

C;Date: 17-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Oct-2000

C;Accession: PC2392

R;Iida, A.; Sanekata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai,  
Chem. Pharm. Bull. 43, 392-397, 1995

A;Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichorozins I-IV,

A;Reference number: PC2390; MUID:95292356; PMID:7539721

A;Accession: PC2392

A;Status: unencoded polypeptide

A;Molecule type: protein

A;Residues: 1-11 <IID>

C;Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers

C;Keywords: antibiotic; unencoded polypeptide

F;1/Modified site: acetylated amino end #status experimental

F;1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental

F;11/Modified site: leucinol #status experimental

Query Match 33.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 5 NIL 7  
|||  
Db 2 NIL 4

# RESULT 16

S52252

hypothetical protein pco 5'-region - Escherichia coli plasmid pRJ1004 (fragment)

C;Species: Escherichia coli

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999

C;Accession: S70166; S52252

R;Brown, N.L.; Barrett, S.R.; Camakaris, J.; Lee, B.T.O.; Rouch, D.A.

Mol. Microbiol. 17, 1153-1166, 1995

A;Title: Molecular genetics and transport analysis of the copper-resistance determinant

A;Reference number: S70159; MUID:96130847; PMID:8594334

A;Accession: S70166

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-11 <BRO>

A;Cross-references: EMBL:X83541; NID:9619126; PIDN:CAA58524.1; PID:9619127

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

C;Comment: This is the hypothetical translation of a sequence that was not reported as a

C;Genetics:

A;Genome: plasmid pRJ1004

Query Match 33.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 5 NIL 7  
|||  
Db 2 NIL 4

# RESULT 17

PQ0696

1,4-alpha-glucan branching enzyme (EC 2.4.1.18) [imported] - rice (fragment)

C;Species: Oryza sativa [rice]

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C;Accession: PQ0696

R;Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension

A;Reference number: PQ0696

A;Accession: PQ0696

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <KOM>

C;Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 33.3%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 5 NIL 7



Db |||  
8 NIL 10

## RESULT 18

B60228  
Fc mu (IgM) receptor surface complex beta chain - mouse (fragment)  
N:Alternate names: membrane protein B29  
C:Species: Mus musculus (house mouse)  
C>Date: 08-Dec-1992 #sequence\_revision 08-Dec-1992 #text\_change 20-Mar-1998  
C:Accession: B60228; B39398  
R:Hombach, J.; Lottspeich, F.; Reth, M.  
Eur. J. Immunol. 20, 2795-2799, 1990  
A:Title: Identification of the genes encoding the IGM-alpha and Ig-beta components of the  
A:Reference number: A60228; MUID:91099432; PMID:2269334  
A:Accession: B60228  
A:Molecule type: protein  
A:Residues: 1-12 <HOM>  
R:Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991  
A:Title: IGM antigen receptor complex contains phosphoprotein products of B29 and mb-1 g  
A:Reference number: A39398; MUID:91219496; PMID:2023945  
A:Accession: B39398  
A:Molecule type: protein  
A:Residues: 'XX', 3-10 <CAM>  
C:Keywords: membrane protein

Query Match 33.3%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9  
|||  
Db 4 LPL 6

## RESULT 19

JZVHP1  
crabrolin - European hornet  
C:Species: Vespa crabro (European hornet)  
C>Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C:Accession: A01781  
R:Argiolas, A.; Pisano, J.J.  
J. Biol. Chem. 259, 10106-10111, 1984  
A:Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin,  
A:Reference number: A92441; MUID:84289390; PMID:6206053  
A:Accession: A01781  
A:Molecule type: protein  
A:Residues: 1-13 <ARG>  
C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; venom  
F:13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 33.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9  
|||  
Db 2 LPL 4

## RESULT 20

S09019  
hemolytic protein B9 - edible frog (fragment)  
C:Species: Rana esculenta (edible frog)  
C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
C:Accession: S09019  
R:Simmaco, M.; De Biase, D.; Severini, C.; Alta, M.; Erspamer, G.F.; Barra, D.; Bossa, F.  
Biochim. Biophys. Acta 1033, 318-323, 1990  
A:Title: Purification and characterization of bioactive peptides from skin extracts of R  
A:Reference number: S09018; MUID:90198965; PMID:2317508

A:Accession: S09019  
A:Molecule type: protein  
A:Residues: 1-13 <SIM>

Query Match 33.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9  
|||  
Db 2 LPL 4

## RESULT 21

JN0390  
histamine-releasing peptide II - oriental hornet  
N:Alternate names: venom protein HR-2  
C:Species: Vespa orientalis (oriental hornet)  
C>Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 23-Aug-1997  
C:Accession: JN0390; S10919  
R:Miroschnikov, A.I.; Sneshkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gus  
Bioorg. Khim. 7, 1467-1477, 1981  
A:Title: Structure and properties of histamine releasing peptides from the venom of Vespa  
A:Reference number: JN0389  
A:Accession: JN0390  
A:Molecule type: protein  
A:Residues: 1-14 <MIR>  
R:Tuichibaev, N.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.  
Biochemistry (N.Y.) 53, 183-190, 1988  
A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. St  
A:Reference number: S06445  
A:Accession: S10919  
A:Molecule type: protein  
A:Residues: 1-14 <TUT>  
C:Superfamily: crabrolin  
C:Keywords: amidated carboxyl end; venom  
F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9  
|||  
Db 2 LPL 4

## RESULT 22

A44515  
Trp EG leader peptide - Rhizobium meliloti  
C:Species: Rhizobium meliloti  
C>Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 12-Dec-1997  
C:Accession: A44515  
R:Bae, Y.M.; Holmgren, E.; Crawford, I.P.  
J. Bacteriol. 171, 3471-3478, 1989  
A:Title: Rhizobium meliloti anthranilate synthase gene: cloning, sequence, and expressio  
A:Reference number: A44515; MUID:89255120; PMID:2656657  
A:Accession: A44515  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-14 <BAE>  
A:Cross-references: EMBL:M22983  
C:Superfamily: unassigned leader peptides

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QNI 6  
|||  
Db 5 QNI 7

## RESULT 23

B36079  
 hypothetical protein insulin-like growth factor I 5'-region - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 30-Nov-1990 #sequence\_revision 13-Sep-1991 #text\_change 18-Aug-2000  
 C:Accession: B36079  
 R:Kajimoto, Y.; Rotwein, P.  
 Mol. Endocrinol. 4, 217-226, 1990  
 A:Title: Evolution of insulin-like growth factor I (IGF-I): structure and expression of  
 A:Reference number: A36079; MUID:90231335; PMID:2330002  
 A:Accession: B36079  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <KAJ>  
 A:Cross-references: GB:M9857; NID:9214287; PIDN:AAA70329.1; PID:g903887  
 A:Note: the authors translated the codon CAG for residue 4 as Gly  
 C:Superfamily: unassigned leader peptides

Query Match 33.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPQ 4

Db 2 LPQ 4

## RESULT 24

D61308  
 hemocyanin chain 5A - Sahara scorpion (fragment)  
 C:Species: Androctonus australis (Sahara scorpion)  
 C:Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
 C:Accession: D61308  
 R:Joilles, J.; Joilles, P.; Lamy, J.; Lamy, J.  
 FEBS Lett. 106, 289-291, 1979  
 A:Title: Structural characterization of seven different subunits in Androctonus australis  
 A:Reference number: A61308; MUID:80047238; PMID:499512  
 A:Accession: D61308  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <JOL>

Query Match 33.3%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9

Db 10 LPL 12

## RESULT 25

S20410  
 protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)  
 N:Alternate names: LHCI protein kinase  
 C:Species: chloroplast Spinacia oleracea (spinach)  
 C:Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
 C:Accession: S20410  
 R:Gal, A.; Herrmann, R.G.; Lottepeich, F.; Ohad, I.  
 FEBS Lett. 298, 33-35, 1992  
 A:Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome  
 A:Reference number: S20410; MUID:92183823; PMID:1544419  
 A:Accession: S20410  
 A:Molecule type: protein  
 A:Residues: 1-15 <GAL>  
 C:Genetics:  
 A:Genome: chloroplast  
 C:Function:  
 A:Description: is responsible for the regulation of energy distribution between photosyn  
 A:Note: does not exhibit redox-controlled activation  
 C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphot

Query Match 33.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILP 8

Db 3 ILP 5

## RESULT 26

PS0455  
 superoxide dismutase (EC 1.15.1.1) (Mn) - rice (strain Nihonbare) (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 05-Mar-1999  
 C:Accession: PS0455  
 R:Tsuigita, A.  
 submitted to JIPID, April 1993  
 A:Reference number: PS0206  
 A:Accession: PS0455  
 A:Molecule type: protein  
 A:Residues: 1-15 <TSU>  
 A:Experimental source: germ  
 C:Function:  
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
 C:Keywords: metalloprotein; oxidoreductase

Query Match 33.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILP 8

Db 8 ILP 10

## RESULT 27

A54877  
 alpha-conotoxin Pn1A [validated] - cone shell (Conus pennaceus)  
 N:Alternate names: alpha-CTX-Pn1A  
 C:Species: Conus pennaceus  
 C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
 C:Accession: A54877  
 R:Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlotk  
 Biochemistry 33, 9523-9529, 1994  
 A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rece  
 A:Reference number: A54877; MUID:94347719; PMID:8068627  
 A:Accession: A54877  
 A:Molecule type: protein  
 A:Residues: 1-16 <PAI>  
 R:Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.  
 submitted to the Brookhaven Protein Data Bank, January 1996  
 A:Reference number: A66355; PDB:1PEN  
 A:Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16  
 C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt

Query Match 33.3%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLP 3

Db 4 SLP 6

## RESULT 28

B54877  
 alpha-conotoxin Pn1B - cone shell (Conus pennaceus)  
 C:Species: Conus pennaceus  
 C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 23-May-1997  
 C:Accession: B54877  
 R:Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlotk

Biochemistry 33, 9523-9529, 1994  
 A;Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine release  
 A;Reference number: A54877; MUID:94347719; PMID:8068627  
 A;Accession: B54877  
 A;Molecule type: protein  
 A;Residues: 1-16 <PAI>  
 C;Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic neurotoxin  
 C;Superfamily: alpha-conotoxin  
 C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin  
 F;2-8,3-16/disulfide bonds: #status experimental  
 F;16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 33.3%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
 |||  
 Db 4 SLP 6

RESULT 29  
 C39509  
 mannose-specific lectin B-SJA-II chain b-1, bark - Japanese pagoda tree (fragment)  
 C;Species: Sophora japonica (Japanese pagoda tree)  
 C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993  
 C;Accession: C39509  
 R;Ueno, M.; Ogawa, H.; Matsumoto, I.; Seno, N.  
 J. Biol. Chem. 266, 3146-3153, 1991

A;Title: A novel mannose-specific and sugar specifically aggregatable lectin from the bark of Sophora japonica  
 A;Reference number: A39509; MUID:91131618; PMID:1993686  
 A;Accession: C39509  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-16 <UEN>

Query Match 33.3%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPQ 4  
 |||  
 Db 2 LPQ 4

RESULT 30  
 S61451  
 hypothetical protein 2 - Campylobacter jejuni (fragment)  
 C;Species: Campylobacter jejuni  
 C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 04-Mar-2000  
 C;Accession: S61451  
 R;Yao, R.; Burr, D.H.; Doig, P.; Trust, T.J.; Niu, H.; Querry, P.  
 Mol. Microbiol. 14, 883-893, 1994  
 A;Title: Isolation of motile and non-motile insertional mutants of Campylobacter jejuni  
 A;Reference number: 140776; MUID:95231295; PMID:7715450  
 A;Accession: S61451  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-17 <YAO>  
 A;Cross-references: GB:U09019; NID:g1177809; PIDN:AAA86823.1; PID:g1177811

Query Match 33.3%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NIL 7  
 |||  
 Db 7 NIL 9

RESULT 31  
 A59069  
 excretory gland allergen Ansl - nematode (Anisakis simplex) (fragment)

C;Species: Anisakis simplex  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C;Accession: A59069  
 R;Moneo, I.  
 submitted to the Protein Sequence Database, September 1999  
 A;Reference number: A59069  
 A;Accession: A59069  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-17 <MON>  
 A;Experimental source: strain L3

Query Match 33.3%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9  
 |||  
 Db 7 LPL 9

RESULT 32  
 I42753  
 interferon alpha (component 1) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 17-Mar-1999  
 C;Accession: I42753  
 R;Zoon, K.C.; Miller, D.; Bekisz, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu, J.

J. Biol. Chem. 267, 15210-15216, 1992  
 A;Title: Purification and characterization of multiple components of human lymphoblastoid interferon alpha (component 1)  
 A;Reference number: A42753; MUID:92340576; PMID:1634550  
 A;Accession: I42753  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-17 <ZOO>

Query Match 33.3%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPQ 4  
 |||  
 Db 3 LPQ 5

RESULT 33  
 S04229  
 N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)  
 N;Alternate names: glycosylasparaginase  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 30-Sep-1993  
 C;Accession: S04229  
 R;Tollersrud, O.K.; Aronson Jr., N.N.  
 Biochem. J. 260, 101-108, 1989

A;Title: Purification and characterization of rat liver glycosylasparaginase.  
 A;Reference number: S04228; MUID:89374025; PMID:2775174  
 A;Accession: S04229  
 A;Molecule type: protein  
 A;Residues: 1-18 <TOL>  
 C;Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase  
 C;Keywords: hydrolase

Query Match 33.3%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9  
 |||  
 Db 4 LPL 6

RESULT 34  
 I52614

u-plasminogen activator precursor - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000  
C;Accession: I52614  
R;Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.  
Blood 86, 624-635, 1995  
A;Title: A conserved TATA-less proximal promoter drives basal transcription from the urokinase-type plasminogen activator promoter  
A;Reference number: I52614; MUID:95329719; PMID:7605992  
A;Accession: I52614  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-18 <RES>  
A;Cross-references: GB:S78532; NID:g999307; PIDN:AAD14289.1; PID:g4561989  
C;Genetics:  
A;Gene: uPAR  
C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 33.3%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9  
|||  
Db 7 LPL 9

# RESULT 35

PN0149

beta-Gliadine 13 - Aegilops longissima (fragment)  
C;Species: Aegilops longissima  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: PN0149  
R;Odintsova, T.I.; Egorov, T.A.  
Biochimia 55, 509-516, 1990  
A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of gliadin  
A;Reference number: PN0146; MUID:90283493; PMID:2354218  
A;Accession: PN0149  
A;Molecule type: protein  
A;Residues: 1-18 <ODI>  
A;Experimental source: strain K-202  
C;Superfamily: gliadin

Query Match 33.3%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PQN 5  
|||  
Db 10 PQN 12

# RESULT 36

B35910  
neurofibromatosis-related protein NF1, long splice form - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 23-Oct-1990 #sequence\_revision 23-Oct-1990 #text\_change 29-Aug-1997  
C;Accession: B35910  
R;Cawthon, R.M.; Weiss, R.; Xu, G.; Viskochil, D.; Culver, M.; Stevens, J.; Robertson, M.  
Cell 62, 608b, 1990  
A;Reference number: A35910  
A;Accession: B35910  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-18 <CAW>  
C;Genetics:  
A;Gene: GDB:NFI  
A;Cross-references: GDB:120231; OMIM:162200  
A;Map position: 17q11.2-17q11.2  
C;Keywords: alternative splicing; tumor suppressor

Query Match 33.3%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLP 3  
|||  
Db 2 SLP 4

# RESULT 37

S60633  
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion (fragment)  
C;Species: mitochondrion Artemia sp. (brine shrimp)  
A;Variety: strain La Mata  
C;Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 03-Jun-2002  
C;Accession: S60633  
R;Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Matco, R.; Garesse, R.  
J. Mol. Evol. 38, 156-169, 1994  
A;Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic populations  
A;Reference number: S60624; MUID:94223692; PMID:8169960  
A;Accession: S60633  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-19 <PER>  
A;Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211  
A;Experimental source: strain La Mata  
A;Note: the source is designated as Artemia parthenogenetica  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992  
C;Genetics:  
A;Gene: ATP8

A;Genome: mitochondrion  
A;Genetic code: SGC4  
C;Superfamily: H+-transporting ATP synthase protein 8  
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 33.3%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9  
|||  
Db 5 LPL 7

# RESULT 38

S02269  
glycogen(starch) synthase (EC 2.4.1.11), skeletal muscle - rat (tentative sequence) (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 16-Aug-2002  
C;Accession: S02269  
R;Jaspers, S.R.; Rulfs, J.; Johnson, G.L.; Mole, J.E.; Miller Jr., T.B.  
Arch. Biochem. Biophys. 268, 630-636, 1989  
A;Title: Amino-terminal sequence analysis of rat heart and muscle glycogen synthase: homology with the alpha-1,4-glucosyltransferase  
A;Reference number: S02269; MUID:89117157; PMID:2492421  
A;Accession: S02269

A;Molecule type: protein  
A;Residues: 1-19 <JAS>  
A;Note: 10-Arg was also found

C;Function:  
A;Description: catalyzes the alpha-1,4-glucosylation of glycogen by UDPglucose producing UDPglucose-6-phosphate  
C;Superfamily: human UDPglucose-glycogen glucosyltransferase  
C;Keywords: glycogen/starch biosynthesis; glucosyltransferase; hexosyltransferase; muscle

Query Match 33.3%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLP 3  
|||  
Db 10 SLP 12

# RESULT 39

C48363  
2-hydroxyglutaryl-CoA dehydratase gamma chain - Fusobacterium nucleatum (fragment)  
C;Species: Fusobacterium nucleatum

C>Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995  
 C:Accession: C48363  
 R:Klees, A.G.; Linder, D.; Buckel, W.  
 Arch. Microbiol. 158, 294-301, 1992  
 A>Title: 2-Hydroxyglutaryl-CoA dehydratase from *Fusobacterium nucleatum* (subsp. *nucleatum*)  
 A:Reference number: A48363; MUID:93038007; PMID:14117419  
 A:Accession: C48363  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-19 <KLE>  
 A:Experimental source: subsp. *nucleatum*  
 A>Note: sequence extracted from NCBI backbone (NCBI:118485)

Query Match 33.3%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNI 6  
 |||  
 Db 1 QNI 3

RESULT 40  
 E5661  
 S-locus specific glycoprotein (allele S2) - wild cabbage (fragment)  
 C:Species: *Brassica oleracea* (wild cabbage)  
 C>Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
 C:Accession: E5661  
 R:Gaude, T.; Denoroy, L.; Dumas, C.  
 Electrophoresis 12, 646-653, 1991  
 A>Title: Use of a fast protein electrophoretic purification procedure for N-terminal sequencing  
 A:Reference number: A5661; MUID:92090397; PMID:1752245  
 A:Accession: E5661  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-19 <GAU>  
 A:Experimental source: stigma extracts, var. *albobolabra*  
 A>Note: This sequence extracted from NCBI backbone (NCBI:72299)  
 C:Comment: This glycoprotein, expressed only in stigmas, plays an important role in the  
 C:Keywords: glycoprotein; polymorphism

Query Match 33.3%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NIL 7  
 |||  
 Db 2 NIL 4

RESULT 41  
 S59486  
 cell wall protein, 22K - kidney bean (fragment)  
 C:Species: *Phaseolus vulgaris* (kidney bean)  
 C>Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
 C:Accession: S59486  
 R:Wojtaszek, P.; Tretthowan, J.; Bolwell, G.P.  
 Plant Mol. Biol. 28, 1075-1087, 1995  
 A>Title: Specificity in the immobilisation of cell wall proteins in response to different  
 A:Reference number: S59481; MUID:96011753; PMID:7548825  
 A:Accession: S59486  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-19 <WOJ>

Query Match 33.3%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQN 5  
 |||  
 Db 14 PQN 16

## RESULT 42

T22228

hypochemical protein F45E6.5 - *Caenorhabditis elegans* (fragment)C:Species: *Caenorhabditis elegans*

C&gt;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

A:Accession: T22228

R:McMurray, A.

submitted to the EMBL Data Library, November 1995

A:Reference number: Z19534

A:Accession: T22228

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-19 &lt;WIL&gt;

A:Cross-references: EMBL:Z68117; PIDN:CAA92179.1; GSPDB:GN00028; CESP:F45E6.5

A:Experimental source: clone F45E6

C:Genetics:

A:Gene: CESP:F45E6.5

A:Map position: X

Query Match 33.3%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NIL 7

|||

Db 1 NIL 3

## RESULT 43

B43978

urotensin I precursor - European flounder (fragment)

C:Species: *Platichthys flesus* (European flounder)

C&gt;Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text\_change 18-Jun-1993

C:Accession: B43978

R:Conlon, J.M.; Arnold-Reed, D.E.; Balmert, R.J.

Peptides 11, 891-895, 1990

A>Title: Urotensin I and its N-terminal flanking peptide from the flounder, *Platichthys*

A:Reference number: A43978

A:Accession: B43978

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 &lt;CON&gt;

Query Match 33.3%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NIL 7

|||

Db 16 NIL 18

## RESULT 44

B46592

lactase-phlorizin hydrolase 140K isoform - rat (fragment)

C:Species: *Rattus norvegicus* (Norway rat)

C&gt;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 01-Nov-1996

C:Accession: B46592

R:Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hutchens, T.W.; Nichols, B.L.; Rosenberger, J.

J. Biol. Chem. 268, 13609-13616, 1993

A&gt;Title: In vivo sucrose-isomaltase and lactase-phlorizin hydrolase turnover in the fed

A:Reference number: A46592; MUID:93293888; PMID:8514793

A:Accession: B46592

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 &lt;DUD&gt;

A&gt;Note: sequence extracted from NCBI backbone (NCBI:134560)

C:Keywords: carbohydrate digestion; intestine

Query Match 33.3%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
|||  
Db 4 SLP 6

RESULT 45  
G89669  
protein F45E6.5 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Nov-2001  
C:Accession: G89669  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: G89669  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-19 <STO>  
A:Cross-references: GB:chr\_X; PIDN:CAA921179.1; PID:g3877190; GSPDB:GN00028; CESP:F45E6.5  
C:Genetics:  
A:Gene: F45E6.5  
A:Map position: X

Query Match 33.3%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NIL 7  
|||  
Db 1 NIL 3

RESULT 46  
C20554  
hemocyanin subunit Iia - Atlantic horseshoe crab (fragment)  
C:Species: Limulus polyphemus (Atlantic horseshoe crab)  
C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-May-1997  
C:Accession: C20554  
R:Lamy, J.; Lamy, J.; Sizaret, P.Y.; Billiald, P.; Jolles, P.; Jolles, J.; Feldmann, R.J  
Biochemistry 22, 5573-5583, 1983  
A:Title: Quaternary structure of Limulus polyphemus hemocyanin.  
A:Reference number: A90478  
A:Accession: C20554  
A:Molecule type: protein  
A:Residues: 1-20 <LAM>  
C:Comment: Limulus polyphemus hemocyanin is an association of eight different subunits w  
C:Superfamily: hemocyanin

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
|||  
Db 18 SLP 20

RESULT 47  
S00493  
hemocyanin chain Ib - Japanese spiny lobster (fragment)  
C:Species: Panulirus japonicus (Japanese spiny lobster)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 01-Aug-1997  
C:Accession: S00493  
R:Makino, N.; Kimura, S.  
Eur. J. Biochem. 173, 423-430, 1988  
A:Title: Subunits of Panulirus japonicus hemocyanin. 1. Isolation and properties.  
A:Reference number: S00492; MUID:88196131; PMID:3360019  
A:Accession: S00493  
A:Molecule type: protein

A:Residues: 1-20 <MAK>  
C:Superfamily: hemocyanin  
C:Keywords: copper; hemolymph; hexamer; oxygen carrier

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNI 6  
|||  
Db 12 QNI 14

RESULT 48  
S08605  
hypothetical protein 1 estrogen receptor 5'-region - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 18-Aug-2000  
C:Accession: S08605  
R:Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.  
EMBO J. 5, 891-897, 1986  
A:Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oes  
A:Reference number: S07192; MUID:86247578; PMID:3755102  
A:Accession: S08605  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-20 <KRU>  
A:Cross-references: EMBL:X03805; NID:g63378; PIDN:CAA27431.1; PID:g63379  
A:Note: the authors translated the codon TTT for residue 5 as Gly and TTC for residue 16  
C:Superfamily: unassigned leader peptides

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQN 5  
|||  
Db 12 PQN 14

RESULT 49  
S45637  
oxidoreductase - Proteus vulgaris (fragment)  
C:Species: Proteus vulgaris  
C:Date: 10-Dec-1994 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S45637  
R:Trautwein, T.; Krauss, F.; Lottspeich, F.; Simon, H.  
Eur. J. Biochem. 222, 1025-1032, 1994  
A:Title: The (2R)-hydroxycarboxylate-viologen-oxidoreductase from Proteus vulgaris is a  
A:Reference number: S45637; MUID:94298804; PMID:8026480  
A:Accession: S45637  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <TRA>

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NIL 7  
|||  
Db 8 NIL 10

RESULT 50  
S29635  
jacalin beta chain - Artocarpus tonkinensis  
C:Species: Artocarpus tonkinensis  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C:Accession: S29635  
R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.  
Biochim. Biophys. Acta 1156, 219-222, 1993  
A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kt

A:Reference number: S29635; MUID:93152601; PMID:8427879  
A:Accession: S29635  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <NGO>

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNI 6  
|||  
DB 8 QNI 10

## RESULT 51

B30208

hypochemical protein 1 (cpc-1 5' region) - Neurospora crassa

C:Species: Neurospora crassa

C&gt;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 18-Jun-1993

A:Accession: B30208

R:Paluh, J.L.; Orbach, M.J.; Legerton, T.L.; Yanofsky, C.

Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988

A&gt;Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a protein

A:Reference number: A30208; MUID:88234499; PMID:2967496

A:Accession: B30208

A:Molecule type: DNA

A:Residues: 1-20 &lt;PAL&gt;

A:Cross-References: GB:J03262

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
|||  
DB 4 SLP 6

## RESULT 52

S10876

hypochemical protein - human

C:Species: Homo sapiens (man)

C&gt;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 18-Nov-1994

A:Accession: S10876

R:Assouline, Z.; Kerbirou-Nabias, D.M.; Pietu, G.; Thomas, N.; Bahnak, B.R.; Meyer, D.

Biochem. Biophys. Res. Commun. 153, 1159-1166, 1988

A&gt;Title: The human gene for von Willebrand factor. Identification of repetitive Alu sequences

A:Reference number: S10876; MUID:88268889; PMID:3260493

A:Accession: S10876

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-20 &lt;ASS&gt;

A:Cross-References: EMBL:X07258

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPQ 4  
|||  
DB 8 LPQ 10

## RESULT 53

S50175

kallikrein (PK-120) - human

C:Species: Homo sapiens (man)

C&gt;Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jul-1995

A:Accession: S50175

R:Pu, X.P.; Iwanoto, A.; Nishimura, H.; Nagasawa, S.

Biochim. Biophys. Acta 1208, 338-343, 1994

A&gt;Title: Purification and characterization of a novel substrate for plasma kallikrein (B

A:Reference number: S50175; MUID:95035036; PMID:7947966  
A:Accession: S50175  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <FOX>

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILP 8  
|||  
DB 14 ILP 16

## RESULT 54

S27350

lysophospholipase - human

C:Species: Homo sapiens (man)

C&gt;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 07-May-1999

A:Accession: S27350

R:Garsetti, D.; Holtsberg, F.; Steiner, M.R.; Egan, R.W.; Clark, M.A.

Biochem. J. 285, 831-837, 1992

A&gt;Title: Butyric acid-induced differentiation of HL-60 cells increases the expression of

A:Reference number: S27350; MUID:93111958; PMID:1471998

A:Accession: S27350

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 &lt;GAR&gt;

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
|||  
DB 5 SLP 7

## RESULT 55

S31220

82K protein - bovine

C:Species: Bos primigenius taurus (cattle)

C&gt;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 17-Mar-1999

A:Accession: S31220

R:Castillo, G.M.; Templeton, D.M.

FEBS Lett. 318, 292-296, 1993

A&gt;Title: Subunit structure of bovine ESF (extracellular-matrix stabilizing factor(s)). A

A:Reference number: S31219; MUID:93178646; PMID:7680011

A:Accession: S31220

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 &lt;CAS&gt;

Query Match 33.3%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
|||  
DB 1 SLP 3

## RESULT 56

A60897

class I histocompatibility antigen H-2K(d) alpha chain, alternate splice form - mouse (F

C:Species: Mus musculus (house mouse)

C&gt;Date: 04-Nov-1994 #sequence\_revision 04-Nov-1994 #text\_change 07-May-1999

A:Accession: A60897

R:Abu-Hadid, M.M.; Fuji, H.; Sood, A.K.

Mol. Immunol. 25, 739-749, 1988

A&gt;Title: Identification of an alternatively spliced K(d) and the Qa-6(d) mRNAs by using

A:Reference number: A60897; MUID:89039921; PMID:3141798

A:Accession: A60897  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-20 <ABU>

Query Match 33.3%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SL 3  
 ||  
 Db 7 SL 9

## RESULT 57

A32039  
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 18-Aug-2000  
 C:Accession: A32039

R:Horvath, A.; Kastin, A.J.  
 J. Biol. Chem. 264, 2175-2179, 1989  
 A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor  
 A:Reference number: A32039; MUID:89123285; PMID:2563371

A:Accession: A32039  
 A:Molecule type: protein  
 A:Residues: 1-4 <HOR>  
 A:Experimental source: brain  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end  
 F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 22.2%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PL 9  
 ||  
 Db 2 PL 3

## RESULT 58

PT0645  
 T-cell receptor beta chain V-D-J region (111-1A1) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0645; PT0626

R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0645  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-4 <PEE>  
 A:Experimental source: newborn thymus, strain BALB/c, 111-1A1  
 A:Accession: PT0626  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-4 <PE2>  
 A:Experimental source: newborn thymus, strain BALB/c, 120-2CJ  
 C:Keywords: T-cell receptor

Query Match 22.2%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SL 2  
 ||  
 Db 3 SL 4

## RESULT 59

## HOROHA

proctolin - American cockroach  
 C:Species: Periplaneta americana (American cockroach)  
 C:Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 23-Aug-1996  
 C:Accession: A01644  
 R:Starratt, A.N.; Brown, B.E.  
 Life Sci. 17, 1253-1256, 1975  
 A:Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects  
 A:Reference number: A93048; MUID:76074708; PMID:576

A:Accession: A01644  
 A:Molecule type: protein  
 A:Residues: 1-5 <STA>

A:Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmacological properties as the natural peptide.  
 R:O'Shea, M.; Adams, M.E.  
 Science 213, 567-569, 1981  
 A:Title: Pentapeptide (proctolin) associated with an identified neuron.  
 A:Reference number: A94260; MUID:81225865; PMID:6113690  
 A:Contents: annotation; biological source  
 C:Comment: This peptide is found in the lateral white neurons, which occur (in the cockroach) innervate the striated hindgut muscles in insects and stimulate contraction of these muscles.  
 C:Superfamily: proctolin  
 C:Keywords: neuropeptide

Query Match 22.2%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LP 3  
 ||  
 Db 3 LP 4

## RESULT 60

JN0860  
 peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito  
 C:Species: Sarda orientalis (striped bonito)

C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C:Accession: JN0860  
 R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
 A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide  
 A:Reference number: JN0859; MUID:94080036; PMID:7764272

A:Accession: JN0860  
 A:Molecule type: protein  
 A:Residues: 1-5 <MAT>  
 A:Experimental source: intestine  
 C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme inhibitory peptide  
 C:Superfamily: bradykinin-potentiating peptide  
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 22.2%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LP 3  
 ||  
 Db 2 LP 3

## RESULT 61

E42364  
 flagellar protein flir - Salmonella typhimurium (fragment)  
 C:Species: Salmonella typhimurium

C:Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 30-Sep-1993  
 C:Accession: E42364  
 R:Vogler, A.P.; Honma, M.; Irikura, V.M.; Macnab, R.M.  
 J. Bacteriol. 173, 3564-3572, 1991

A:Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion  
 A:Reference number: A42364; MUID:91258342; PMID:1646201  
 A:Accession: E42364  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-5 <VOG>



A;Cross-references: GB:M62408

Query Match 22.2%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LP 3  
||  
Db 4 LP 5

#### RESULT 62

A60803  
neuropeptide - sea anemone (*Anthopleura elegantissima*)  
C;Species: *Anthopleura elegantissima*  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: A60803  
R;Graff, D.; Grimmelikhuijzen, C.J.P.  
Brain Res. 442, 354-358, 1988  
A;Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemones.  
A;Reference number: A60803; MUID:88222764; PMID:2897223  
A;Accession: A60803

A;Molecule type: protein  
A;Residues: 1-5 <GRA>  
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 22.2%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SL 2  
||  
Db 2 SL 3

#### RESULT 63

A60411  
proctolin - Atlantic horseshoe crab  
C;Species: *Limulus polyphemus* (Atlantic horseshoe crab)  
C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 17-Mar-1999  
C;Accession: A60411  
R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, D.  
Peptides 11, 205-211, 1990  
A;Title: Identification of proctolin in the central nervous system of the horseshoe crab  
A;Reference number: A60411; MUID:90287800; PMID:2356151  
A;Accession: A60411

A;Molecule type: protein  
A;Residues: 1-5 <GRO>

C;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse  
C;Keywords: neuropeptide

Query Match 22.2%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LP 3  
||  
Db 3 LP 4

#### RESULT 64

PT0624  
T-cell receptor beta chain V-D-J region (120-1K) - mouse (fragment)  
C;Species: *Mus musculus* (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0624  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0624

A;Status: translation not shown

A;Molecule type: mRNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 22.2%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SL 2  
||  
Db 3 SL 4

#### RESULT 65

PT0625  
T-cell receptor beta chain V-D-J region (120-2S) - mouse (fragment)  
C;Species: *Mus musculus* (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0625  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0625

A;Status: translation not shown

A;Molecule type: mRNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 22.2%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SL 2  
||  
Db 3 SL 4

#### RESULT 66

PT0713  
T-cell receptor beta chain V-D-J region (165-3C) - mouse (fragment)  
C;Species: *Mus musculus* (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0713  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0713

A;Status: translation not shown

A;Molecule type: DNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 22.2%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SL 2  
||  
Db 3 SL 4

#### RESULT 67

A60986  
N-formyl oligopeptide - *Escherichia coli* (fragment)  
C;Species: *Escherichia coli*  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Dec-1993  
C;Accession: A60986

R:Broom, M.F.; Mellor, D.M.; Chadwick, V.S.

Experientia 45, 1097-1099, 1989

A>Title: Purification and amino acid sequencing of naturally occurring N-formyl-methionyl peptides from *Streptomyces clavuligerus*

A;Reference number: A60986; MUID:90092408; PMID:2689204

A;Accession: A60986

A;Molecule type: protein

A;Residues: 1-6 <BRO>

C;Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.

F;1/Modified site: N-formylmethionine #status experimental

Query Match 22.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7

DB 4 IL 5

RESULT 68

A37765

hypothetical protein (csmA 5' region) - *Chloroflexus aurantiacus* (fragment)

C;Species: *Chloroflexus aurantiacus*

C;Date: 31-May-1991 #sequence\_revision 31-May-1991 #text\_change 30-Sep-1993

C;Accession: A37765

R;Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.

J. Bacteriol. 172, 4497-4504, 1990

A>Title: Gene encoding the 5.7-kilodalton chlorosome protein of *Chloroflexus aurantiacus*

A;Reference number: A37765; MUID:90330558; PMID:2376566

A;Accession: A37765

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-6 <THE>

A;Cross-references: GB:M33964

Query Match 22.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQ 4

DB 1 PQ 2

RESULT 69

PC4127

hypothetical 6 protein - *Streptomyces clavuligerus* (fragment)

C;Species: *Streptomyces clavuligerus*

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C;Accession: PC4127

R;Rodriguez-Garcia, A.; Martin, J.F.; Liras, P.

Gene 167, 9-15, 1995

A>Title: The argG gene of *Streptomyces clavuligerus* has low homology to unstable argG fr

A;Reference number: JC4548; MUID:96144242; PMID:8566818

A;Accession: PC4127

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-6 <ROD>

A;Cross-references: EMBL:Z49111

Query Match 22.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QN 5

DB 2 QN 3

RESULT 70

I37263

Y protein - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999

C;Accession: I37263

R;Haerber, G.; Habener, J.F.

Endocrinology 131, 2010-2015, 1992

A>Title: Novel testis germ cell-specific transcript of the CREB gene contains an alterna

A;Reference number: I37263; MUID:93010691; PMID:1396344

A;Accession: I37263

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-6 <RES>

A;Cross-references: EMBL:X68994; NID:G396171; PIDN:CAA48780.1; PID:G579816

C;Genetics:

A;Gene: CREB

Query Match 22.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2

DB 1 SL 2

RESULT 71

A11490

pyruvate kinase (EC 2.7.1.40) - pig (fragment)

C;Species: *Sus scrofa domestica* (domestic pig)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 03-Mar-1995

C;Accession: A11490

R;Hjeltnist, G.; Andersson, J.; Edlund, B.; Engstrom, L.

Biochem. Biophys. Res. Commun. 61, 559-563, 1974

A>Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate kinase ph

A;Reference number: A11490; MUID:75127438; PMID:4375989

A;Accession: A11490

A;Molecule type: protein

A;Residues: 1-6 <HJE>

A;Experimental source: liver

C;Keywords: glycolysis; phosphotransferase

Query Match 22.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2

DB 5 SL 6

RESULT 72

A20186

fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 05-May-2000

C;Accession: A20186

R;McCarthy, A.D.; Aitken, A.; Hardie, G.; Santikarn, S.; Williams, D.H.

FEBS Lett. 160, 296-300, 1983

A>Title: Amino acid sequence around the active serine in the acyl transferase domain of

A;Reference number: A20186; MUID:83287768; PMID:6554204

A;Accession: A20186

A;Molecule type: protein

A;Residues: 1-6 <MCC>

C;Keywords: acyltransferase; coenzyme A

Query Match 22.2%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2

DB 1 SL 2

RESULT 73

I67345  
MHC H2-K-k cell surface glycoprotein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I67345  
R:Archibald, A.L.; Thompson, N.A.; Kvist, S.  
EMBO J. 5, 957-965, 1986  
A:Title: A single nucleotide difference at the 3' end of an intron causes differential splicing of the H2-K-k gene  
A:Reference number: 153243; MUID:86247587; PMID:3013627  
A:Accession: I67345  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-References: GB:M26859; NID:g199439; PIDN:AAA39612.1; PID:g387458  
C:Genetics:  
A:Introns: 6/1  
C:Keywords: glycoprotein

Query Match 22.2%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
||  
Db 1 LP 2

RESULT 74  
PT0519  
T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0519  
R:Peeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0519  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FEE>  
A:Experimental source: adult thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 22.2%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2  
||  
Db 3 SL 4

RESULT 75  
PT0621  
T-cell receptor beta chain V-D-J region (111-1M) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0621  
R:Peeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0621  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FEE>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 22.2%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2  
||  
Db 3 SL 4

Search completed: November 25, 2003, 18:28:25  
Job time : 8.28191 secs

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TEJA\_RANJA

RESULT 2

ALL6\_CVDPO

ID ALL6\_CVDPO STANDARD; PRT; 8 AA.

AC PB2157;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE Cydiaastatin 6.

OS Cydia pomonella (Codling moth).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.

OX NCBI\_TaxID=82600;

RN [1]

RP SEQUENCE.

RC MEDLINE=98054539; PubMed=9392829;

RX Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,

RA Duve H., East P.D., Thorpe A.;

RT "Lepidopteran peptides of the allatostatin superfamily.";

RL Peptides 18:1301-1309(1997).

CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

KW Neuropeptide; Amidation.

FT MOD RES 8

SQ SEQUENCE 8 AA; 936 MW; 082879C45B573767 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9

DB 1 LPL 3

TEJA\_RANJA

RESULT 3

EFG\_CLOPA

ID EFG\_CLOPA STANDARD; PRT; 11 AA.

AC PB1350;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Elongation factor G (EF-G) (CP 5) (Fragment).

GN FUSA.

OS Clostridium pasteurianum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OX NCBI\_TaxID=1501;

RN [1]

RP SEQUENCE.

RC STRAIN=W5;

RX MEDLINE=98291870; PubMed=9629918;

RA Flengrud R., Skjeldal L.;

RT "Two-dimensional gel electrophoresis separation and N-terminal

RL sequence analysis of proteins from Clostridium pasteurianum W5.";

CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of

CC the nascent protein chain from the A-site to the P-site of the

CC ribosome.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

CC EF-G/EF-2 SUBFAMILY.

DR InterPro; IPR000795; EF\_GTPbind.

DR PROSITE; PS00301; EFATOR\_GTP; PARTIAL.

KW Elongation factor; Protein biosynthesis; GTP-binding.

FT NON TER 11

SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNI 6

DB 8 QNI 10

TM2A\_METMA

RESULT 4

TM2A\_METMA STANDARD; PRT; 12 AA.

AC PB0652;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit

DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin-coenzyme M

DE methyltransferase 28 kDa subunit) (Fragment).

OS Methanosarcina mazel (Methanosarcina frisia).

OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;

OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.

OX NCBI\_TaxID=2209;

RN [1]

RP SEQUENCE.

RC STRAIN=Goel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;

RX MEDLINE=96370840; PubMed=8774736;

RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;

RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:

RT coenzyme M methyltransferase from Methanosarcina mazel G01

RT reconstituted in ether lipid liposomes.";

RL Eur. J. Biochem. 239:857-864(1996).

CC -1- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN

CC METHANOGNESIS, THE FORMATION OF METHYL-COENZYME M AND

CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-

CC TETRAHYDROMETHANOPTERIN.

CC -1- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-

CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-

CC (methylthio)ethanesulfonate.

CC -1- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 33.3%; Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9  
 |||  
 Db 8 LPL 10

RESULT 5  
 CRBL\_VESCR STANDARD; PRT; 13 AA.  
 AC PO1518;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Crabrolin  
 OS Vespa crabro (European hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID=7445;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Venom;  
 RX MEDLINE=84289390; PubMed=6206053;  
 RA Argiolas A., Pisano J.J.;  
 RT "Isolation and characterization of two new peptides, mastoparan C and  
 crabrolin, from the venom of the European hornet, *Vespa crabro*.";  
 RL J. Biol. Chem. 259:10106-10111(1984).  
 RN [2]

RP SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.  
 RX MEDLINE=97419326; PubMed=9273892;  
 RA Krishnakumari V., Nagaraj R.;  
 RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue  
 peptide from the venom of the European hornet, *Vespa crabro*, and its  
 analogs.";  
 RL J. Pept. Res. 50:88-93(1997).  
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 of neutrophils. Has antimicrobial and hemolytic activity.  
 CC PIR: A01781; JZVHP1.  
 KW Mast cell degranulation; Chemotaxis; Amidation; Antibiotic.  
 FT MOD RES 13 13  
 SQ SEQUENCE 13 AA; 1497 MW; 515EF8FCEA8D2407 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9  
 |||  
 Db 2 LPL 4

RESULT 6  
 HPB9\_RANES STANDARD; PRT; 13 AA.  
 AC P12416;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Hemolytic protein B9 (Fragment).  
 OS Rana esculenta (Edible frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
 OX NCBI\_TaxID=8401;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Skin secretion;  
 RX MEDLINE=9019865; PubMed=2317508;  
 RA Simmaco M., de Biase D., Severini C., Aita M., Erespaner G.F.,  
 RA Barra D., Bossa P.;  
 RT "Purification and characterization of bioactive peptides from skin  
 extracts of *Rana esculenta*.";  
 RL Biochim. Biophys. Acta 1033:318-323(1990).  
 CC -1- FUNCTION: Shows hemolytic activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 DR PIR: S09019; S09019.  
 KW Amphibian defense peptide; Amidation; Hemolysis.  
 FT MOD RES 13 13  
 FT NON TER 13 13  
 SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 33.3%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9  
 |||  
 Db 2 LPL 4

RESULT 7  
 SODM\_CANFA STANDARD; PRT; 13 AA.  
 AC P54712;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).  
 GN SOD2.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -1- FUNCTION: Destroys radicals which are normally produced within the  
 cells and which are toxic to biological systems.  
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
 CC -1- COFACTOR: Manganese (By similarity).  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE  
 FAMILY.

DR HSC-2DPAGE; P54712; DOG.  
 DR InterPro: IPR001189; SODismutase.  
 DR Pfam: PF00081; sodfe; 1.  
 DR PROSITE: PS00088; SOD\_MN; PARTIAL.  
 KW Oxidoreductase; Manganese; Mitochondrion.  
 FT MOD RES 13 13  
 FT NON TER 13 13  
 SQ SEQUENCE 13 AA; 1476 MW; 9C9651DE8BE0672A CRC64;

Query Match 33.3%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLP 3  
 |||  
 Db 3 SLP 5

RESULT 8  
 TEMA\_RANTE

```

ID  TEMA_RANTE      STANDARD;      PRT;      13 AA.
AC  P56917;
DT  30-MAY-2000 (Rel. 39, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Tempurin A.
OS  Rana temporaria (European common frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX  NCBI_TaxID=8407;
RN  [1]
RP  SEQUENCE AND SYNTHESIS.
RC  TISSUE=Skin secretion.
RX  MEDLINE=97175050; PubMed=9022710;
RA  Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA  Barra D.;
RT  "Temporin, antimicrobial peptides from the European red frog Rana
RT  temporaria.";
RL  Eur. J. Biochem. 242:788-792(1996).
CC  -1- FUNCTION: Has antibacterial activity against Gram-positive
CC  bacteria.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- TISSUE SPECIFICITY: Skin.
CC  -1- SIMILARITY: Belongs to the brevinin family.
KW  Amphibian defense peptide; Antibiotic; Amidation.
FT  MOD RES 13 13
SQ  SEQUENCE 13 AA; 1398 MW; 2653612B9DECD408 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9
Db 2 LPL 4

RESULT 9
ID  TEMP_RANTE      STANDARD;      PRT;      13 AA.
AC  P56921;
DT  30-MAY-2000 (Rel. 39, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Tempurin F.
OS  Rana temporaria (European common frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX  NCBI_TaxID=8407;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Skin secretion;
RX  MEDLINE=97175050; PubMed=9022710;
RA  Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA  Barra D.;
RT  "Temporins, antimicrobial peptides from the European red frog Rana
RT  temporaria.";
RL  Eur. J. Biochem. 242:788-792(1996).
CC  -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC  GRAM-POSITIVE BACTERIA.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- TISSUE SPECIFICITY: Skin.
CC  -1- SIMILARITY: Belongs to the brevinin family.
KW  Amphibian defense peptide; Antibiotic; Amidation.
FT  MOD RES 13 13
SQ  SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9
Db 2 LPL 4

ID  TEMP_RANTE      STANDARD;      PRT;      13 AA.
AC  P56921;
DT  30-MAY-2000 (Rel. 39, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Tempurin F.
OS  Rana temporaria (European common frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX  NCBI_TaxID=8407;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Skin secretion;
RX  MEDLINE=97175050; PubMed=9022710;
RA  Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA  Barra D.;
RT  "Temporins, antimicrobial peptides from the European red frog Rana
RT  temporaria.";
RL  Eur. J. Biochem. 242:788-792(1996).
CC  -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC  GRAM-POSITIVE BACTERIA.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- TISSUE SPECIFICITY: Skin.
CC  -1- SIMILARITY: Belongs to the brevinin family.
KW  Amphibian defense peptide; Antibiotic; Amidation.
FT  MOD RES 13 13
SQ  SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9
Db 2 LPL 4

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Db 2 LPL 4

RESULT 10
ID  CRBL_VESOR      STANDARD;      PRT;      14 AA.
AC  P17236;
DT  01-AUG-1990 (Rel. 15, Created)
DT  01-AUG-1990 (Rel. 15, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Histamine releasing peptide II (HR-II).
OS  Vespa orientalis (Oriental hornet).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidae;
OC  Vespidae; Vespinae; Vespa.
OX  NCBI_TaxID=7447;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Venom;
RA  Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA  Rozynov B.V., Gushchin I.S.;
RT  "Structure and properties of histamine releasing peptides from the
RT  venom of Vespa orientalis hornet.";
RL  Bioorg. Khim. 7:1467-1477(1981).
CC  -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC  of neutrophils.
DR  PIR; JN0390; JN0390.
KW  Mast cell degranulation; Chemotaxis; Amidation.
FT  MOD RES 14 14
SQ  SEQUENCE 14 AA; 1524 MW; 22015B4A6CEDFD38 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9
Db 2 LPL 4

RESULT 11
ID  LPW_RHIME      STANDARD;      PRT;      14 AA.
AC  P18854;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Trp operon leader peptide.
GN  TRPL OR R02387.1 OR SMC02725.1.
OS  Rhizobium meliloti (Sinorhizobium meliloti).
OC  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC  Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX  NCBI_TaxID=382;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89255120; PubMed=2656657;
RA  Bae Y.M., Holmgren E., Crawford I.P.;
RT  "Rhizobium meliloti antranilate synthase gene: cloning, sequence,
RT  and expression in Escherichia coli.";
RL  J. Bacteriol. 171:3471-3478(1989).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1021;
RX  MEDLINE=21396507; PubMed=11481430;
RA  Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA  Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA  Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA  Pohl T., Portetelle D., Puehler A., Purnelle B., Rampeger U.,
RA  Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT  "Analysis of the chromosome sequence of the legume symbiont
RT  Sinorhizobium meliloti strain 1021.";
RL  Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC  -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS

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DR EMBL; M22983; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; AL591790; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A44515; A44515.  
 KW Tryptophan biosynthesis; Leader peptide; Complete proteome.  
 SQ SEQUENCE 14 AA; 1777 MW; 05BFD63BC52A7CB0 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNI 6  
 |||  
 DB 5 QNI 7

RESULT 12  
 MCA2\_RHOOP STANDARD; PRT; 15 AA.  
 ID MCA2\_RHOOP STANDARD; PRT; 15 AA.  
 AC P56870;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative maleylacetate reductase II (EC 1.3.1.32) (Fragment).  
 OS Rhodococcus opacus (Nocardia opaca).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Nocardiaceae; Rhodococcus.  
 OX NCBI\_TaxID=37919;  
 [1]  
 RP SEQUENCE.  
 RC STRAIN=1CP;  
 RX MEDLINE=98324954; PubMed=9657989;  
 RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;  
 RT "Characterization of a maleylacetate reductase encoding region from  
 RT Rhodococcus opacus 1CP.";  
 RL J. Bacteriol. 180:3503-3508 (1998).  
 CC -|- CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P)(+) = 2-maleylacetate +  
 CC NAD(P)H.  
 CC -|- PATHWAY: 3-chlorocatechol degradation (beta-ketoadipate pathway).  
 CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC  
 CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL  
 CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.  
 CC -|- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE  
 CC FAMILY.  
 DR Interpro; IPR001670; Fe-ADH.  
 DR PROSITE; PS00913; ADH IRON 1; PARTIAL.  
 DR PROSITE; PS00060; ADH IRON 2; PARTIAL.  
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;

Query Match 33.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPQ 4  
 |||  
 DB 8 LPQ 10

RESULT 13  
 MILT\_ONCKE STANDARD; PRT; 15 AA.  
 ID MILT\_ONCKE PRT; 15 AA.  
 AC P81037;

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Miltpain (EC 3.4.22.-) (Fragment).  
 OS Oncorhynchus keta (Chum salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8018;  
 [1]  
 RN SEQUENCE, AND CHARACTERIZATION.  
 RP MEDLINE=97397031; PubMed=9253183;  
 RA Kawabata C., Ichishima E.;  
 RT "Miltpain, new cysteine proteinase from the milt of chum salmon,  
 RT Oncorhynchus keta.";  
 RL Comp. Biochem. Physiol. 117B:445-452 (1997).  
 CC -|- FUNCTION: CYSTEINE PROTEINASE THAT HYDROLYZES BASIC PROTEINS.  
 CC HYDROLYZE BASIC PROTEINS SUCH AS HISTONE, SALMINE AND CLOPAINE BUT  
 CC NOT MILK CASEIN.  
 CC -|- CATALYTIC ACTIVITY: Preferential cleavage with basic residues at  
 CC P2 and P1.  
 DR MEROPS; C01.093; -;  
 KW Hydrolase.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1730 MW; 766B771C0F88BE7 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NIL 7  
 |||  
 DB 13 NIL 15

RESULT 14  
 ODP3\_SOLTU STANDARD; PRT; 15 AA.  
 ID ODP3\_SOLTU STANDARD; PRT; 15 AA.  
 AC P81420;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 55 kDa dihydrolipoamide acetyltransferase component of pyruvate  
 DE dehydrogenase complex (EC 2.3.1.12) (E2) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Romano; TISSUE=Tuber;  
 RX MEDLINE=98399821; PubMed=9729464;  
 RA Millar A.H., Knorrpp C., Leaver C.J., Hill S.A.;  
 RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and  
 RT identification of catalytic components in potato.";  
 RL Biochem. J. 334:571-576 (1998).  
 CC -|- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall  
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains  
 CC multiple copies of three enzymatic components: pyruvate  
 CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and  
 CC lipoamide dehydrogenase (E3).  
 CC -|- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-  
 CC acetyldihydrolipoamide.  
 CC -|- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL  
 CC COFACTOR.  
 CC -|- SUBUNIT: FORMS A 60-POLYPEPTIDE STRUCTURAL CORE (BY SIMILARITY).  
 CC -|- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 KW Glycolysis; Transferrase; Acyltransferase; Lipoyl; Mitochondrion.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1447 MW; EA28B063799BE825 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLP 3  
|||  
DB 5 SLP 7

RESULT 15  
SODM ENTAE  
ID SODM ENTAE STANDARD; PRT; 15 AA.  
AC P22759;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).  
SODA.  
GN Enterobacter aerogenes (Aerobacter aerogenes).  
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxID=548;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91248479; PubMed=1368658;  
RA Kim S.W., Lee S.O., Lee T.H.;  
RT "Purification and characterization of superoxide dismutase from  
RT Aerobacter aerogenes.";  
RL Agric. Biol. Chem. 55:101-108(1991).  
CC -1- FUNCTION: Destroys radicals which are normally produced within the  
CC cells and which are toxic to biological systems.  
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
CC -1- COFACTOR: IRON.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE  
CC FAMILY.  
DR PIR; P0615; P0615.  
DR InterPro; IPR001189; SODismutase.  
DR Pfam; PF00081; sodfe; 1.  
DR PROSITE; PS00088; SOD\_MW; PARTIAL.  
KW Oxidoreductase; Iron.  
FT NON TER 15 15  
SQ SEQUENCE 15 AA; 1756 MW; 352F3D949202E642 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LPQ 4  
|||  
DB 4 LPQ 6

RESULT 16  
AHPP ACICA  
ID AHPP ACICA STANDARD; PRT; 16 AA.  
AC P82955;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Alkyl hydroperoxide reductase subunit F (EC 1.6.4.-) (Fragment).  
GN AHPP.  
OS Acinetobacter calcoaceticus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Moraxellaceae; Acinetobacter.  
OX NCBI\_TaxID=471;  
RN [1]  
RP SEQUENCE, AND INDUCTION.  
RC STRAIN=69-V;  
RX MEDLINE=21318969; PubMed=11425483;  
RA Benndorf D., Loffhagen N., Babel W.;  
RT "Protein synthesis patterns in Acinetobacter calcoaceticus induced by  
RT phenol and catechol show specificities of responses to chemotress.";  
RL FEMS Microbiol. Lett. 200:247-252(2001).

-1- FUNCTION: Serves to protect the cell against DNA damage by alkyl  
hydroperoxides. It can use either NADH or NADPH as electron donor  
for direct reduction of redox dyes or of alkyl hydroperoxides when  
combined with the AHPC protein (By similarity).  
-1- COFACTOR: FAD (By similarity).  
-1- SUBUNIT: Homodimer (By similarity).  
-1- INDUCTION: By oxidative stress and catechol, and very weakly by  
heat shock.  
-1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE  
OXIDOREDUCTASES CLASS-II.  
DR InterPro; IPR000103; Pyridine\_redox\_2.  
DR PROSITE; PS00573; PYRIDINE\_REDOX\_2; PARTIAL.  
KW Redox-active center; Oxidoreductase; NADP; NAD; Flavoprotein; FAD;  
KW Heat shock.  
FT NON TER 16 16  
SQ SEQUENCE 16 AA; 1928 MW; E070754AEFCBED15 CRC64;

Query Match 33.3%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 QNI 6  
|||  
DB 4 QNI 6

RESULT 17  
CXAA CONPE  
ID CXAA CONPE STANDARD; PRT; 16 AA.  
AC P50984;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Alpha-conotoxin Pn1A.  
OS Conus pennaceus (Feathered cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=37335;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=94347719; PubMed=8068627;  
RA Fainzilber M., Hesson A., Oren R., Burlingame A.L., Gordon D.,  
RA Spira M.E., Zlotkin E.;  
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal  
RT acetylcholine receptors.";  
RL Biochemistry 33:9523-9529(1994).  
RN [2]  
RP SULFATION OF TYR-15.  
RX MEDLINE=99242956; PubMed=10226369;  
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,  
RA Baldwin M.A., Burlingame A.L.;  
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins  
RT alpha-Pn1A and alpha-Pn1B: further investigation of labile sulfo- and  
RT phosphopeptides by electrospray, matrix-assisted laser  
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass  
RT spectrometry.";  
RL J. Mass Spectrom. 34:447-454(1999).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).  
RX MEDLINE=96311277; PubMed=8740364;  
RA Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,  
RA Martin J.L.;  
RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor  
RT antagonist, alpha-conotoxin Pn1A from Conus pennaceus.";  
RL Structure 4:417-423(1996).  
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE  
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS  
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.  
CC -1- SUBCELLULAR LOCATION: Secreted.



GN FGB.  
OS Ovis aries (Sheep), and  
OS Capra hircus (Goat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940, 9925;  
RN [1]  
RP SEQUENCE.  
RA Blomback B., Blomback M., Grondahl N.J.;  
RT "Studies on fibrinopeptides from mammals. ";  
RL Acta Chem. Scand. 19:1789-1791(1965).  
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COPACTOR IN PLATELET  
CC AGGREGATION.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR InterPro; IPR002181; Fibrinogen C.  
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma; Sulfation.  
FT PEPTIDE 1 20 FIBRINOPEPTIDE B.  
FT MOD\_RES 5 5 SULFATION.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2338 MW; FCF5B6FF0DEC6627 CRC64;  
Query Match 33.3%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 LPL 9  
Db 15 LPL 17  
RESULT 21  
HCYB PANJA  
ID -HCYB PANJA STANDARD; PRT; 20 AA.  
AC P82311;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hemocyanin subunit 1b (Fragment).  
OS Panulirus japonicus (Japanese spiny lobster).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;  
OC Palinuroidea; Palinuridae; Panulirus.  
OX NCBI\_TaxID=6736;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Serum;  
RX MEDLINE=88196131; PubMed=3360019;  
RA Makino N., Kimura S.;  
RT "Subunits of Panulirus japonicus hemocyanin. 1. Isolation and  
RT properties. ";  
RL Eur. J. Biochem. 173:423-430(1988).  
CC -!- FUNCTION: Hemocyanins are copper-containing oxygen carriers  
CC occurring freely dissolved in the hemolymph of many mollusks and  
CC arthropods.  
CC -!- SUBUNIT: Composed of 3 major subunits (IB, II and III) and 1 minor  
CC subunit (IA) which form homohexamers and heterohexamers. May also  
CC form larger structures.  
CC -!- SUBCELLULAR LOCATION: Extracellular.  
CC -!- TISSUE SPECIFICITY: Hemolymph.  
CC -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN  
CC SUBFAMILY.  
DR PIR; S00493; S00493.  
DR InterPro; IPR000896; Hemocyanin.  
DR InterPro; IPR002227; Tyrosinase.  
DR PROSITE; PS00209; HEMOCYANIN\_1; PARTIAL.

DR PROSITE; PS00210; HEMOCYANIN 2; PARTIAL.  
DR PROSITE; PS00497; TYROSINASE\_1; PARTIAL.  
DR PROSITE; PS00498; TYROSINASE\_2; PARTIAL.  
KW Transport; Oxygen transport; Copper; Hemolymph.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2206 MW; C408238C38610416 CRC64;  
Query Match 33.3%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 QNI 6  
Db 12 QNI 14  
RESULT 22  
LPP2 HUMAN  
ID -LPP2 HUMAN STANDARD; PRT; 20 AA.  
AC P56642;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lysophospholipase HL-60 peak 2 (EC 3.1.1.5) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Leukemia;  
RX MEDLINE=93111958; PubMed=1471598;  
RA Garsetti D., Hotsberg P., Steiner M.R., Egan R.W., Clark M.A.;  
RT "Butyric acid-induced differentiation of HL-60 cells increases the  
RT expression of a single lysophospholipase. ";  
RL Biochem. J. 288:831-837(1992).  
CC -!- FUNCTION: DEGRADATION OF LYSOPHOSPHOLIPIDS. MAY PLAY AN IMPORTANT  
CC ROLE IN PROTECTING THESE CELLS FROM THE CYTOLYTIC EFFECTS OF THE  
CC LYSOPHOSPHOLIPIDS PRODUCED BY THE ACTIVATION OF PHOSPHOLIPASE A2.  
CC -!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =  
CC glycerophosphocholine + a fatty acid anion.  
CC -!- INDUCTION: INCREASED BY DIFFERENTIATION OF THE CELLS.  
CC -!- PTM: THE N-TERMINUS IS BLOCKED.  
DR PIR; S27350; S27350.  
DR GO; GO:0004622; F:lysophospholipase activity; IDA.  
KW Hydrolyase; Lipid degradation.  
FT NON\_TER 1 1  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2138 MW; 15B38F6D23D89567 CRC64;  
Query Match 33.3%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SLP 3  
Db 5 SLP 7  
RESULT 23  
M117 BOVIN  
ID -M117 BOVIN STANDARD; PRT; 20 AA.  
AC P35451;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE 17 kDa milk glycoprotein (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]

RP SEQUENCE.  
 RC TISSUE=Milk;  
 RX MEDLINE=93308294; PubMed=8320368;  
 RA Soerensen E.S., Petersen T.E.;  
 RT "Purification and characterization of three proteins isolated from  
 the protease pepone fraction of bovine milk.";  
 RL J. Dairy Res. 60:189-197(1993).  
 CC -1- PTM: N-GLYCOSYLATED.  
 CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.  
 KW Glycoprotein; Milk.  
 FT NON\_TER 1 1  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2233 MW; 4CCAS89404C62C27 CRC64;  
 Query Match 33.3%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred.No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LPL 9  
 Db 12 LPL 14

RESULT 24  
 PRCT PERAM STANDARD; PRT; 5 AA.  
 AC P01373;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Proctolin.  
 OS Periplaneta americana (American cockroach);  
 OS Limulus polyphemus (Atlantic horseshoe crab), and  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978, 6850, 6759;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=76074708; PubMed=576;  
 RA Stazratt A.N., Brown B.E.;  
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
 in insects.";  
 RL Life Sci. 17:1253-1256(1975).  
 RN [2]  
 RP BIOLOGICAL SOURCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=81225865; PubMed=6113690;  
 RA O'Shea M., Adams M.E.;  
 RT "Pentapeptide (proctolin) associated with an identified neuron.";  
 RL Science 213:567-569(1981).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=L.polyphemus;  
 RX MEDLINE=90287800; PubMed=2356151;  
 RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,  
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,  
 RA Shabanowitz J.;  
 RT "Identification of proctolin in the central nervous system of the  
 horseshoe crab, Limulus polyphemus.";  
 RL Peptides 11:205-211(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=C.maenas;  
 RX MEDLINE=86232789; PubMed=2872661;  
 RA Stangier J., Dirksen H., Keller R.;  
 RT "Identification and immunocytochemical localization of proctolin in  
 pericardial organs of the shore crab, Carcinus maenas.";  
 RL Peptides 7:67-72(1986).  
 CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.  
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.

CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
 THE CRAB PERICARDIAL ORGANS.  
 DR PIR: A01644; HOROHA.  
 DR PIR: A60411; A60411.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LP 3  
 Db 3 LP 4

RESULT 25  
 TRPI\_PSEPU STANDARD; PRT; 6 AA.  
 AC P36414;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE TRPA operon transcriptional activator (fragment).  
 GN TRPI.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PPG1 C1S;  
 RX MEDLINE=89335826; PubMed=2503057;  
 RA Eberly L., Crawford I.P.;  
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas  
 putida.";  
 RL Biochimie 71:521-531(1989).  
 CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPA GENES ENCODING  
 THE TWO TRYPTOPHAN SYNTHASE SUBUNITS, IN THE ABSENCE OF THE  
 INDUCER (INDOLEGLYCEROL PHOSPHATE) TRPI BINDS UPSTREAM OF THE  
 TRPA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
 CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
 REGULATORS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC  
 DR EMBL: X13299; CAA31660.1; -.  
 DR InterPro: IPR000847; HTH\_LySR.  
 DR PROSITE: PS00044; HTH\_LYSR FAMILY; PARTIAL.  
 KW Tryptophan biosynthesis; Transcription regulation; Activator;  
 KW DNA-binding.  
 FT NON\_TER 6 6  
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LP 3  
 Db 5 LP 6

RESULT 26  
 VP19\_HSV1K STANDARD; PRT; 6 AA.  
 ID VP19\_HSV1K  
 AC P23210;

DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Capsid assembly and DNA maturation protein (Viron protein UL38)  
DE (Capsid protein VP19C) (Fragment).  
GN UL38.  
OS Herpes simplex virus (type 1 / strain KOS).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10306;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91101287; PubMed=1946198;  
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,  
RA Silverstein S., Wagner E.K.;  
RT "Analysis of the herpes simplex virus type 1 promoter controlling the  
RT expression of UL38, a true late gene involved in capsid assembly.";  
RL J. Virol. 65:769-786(1991).  
CC -1- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE  
CC EMBEDDED. BINDS DNA.  
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M57646; AAA45830.1; -;  
KW Capsid assembly; Coat protein; DNA-binding.  
FT NON TER  
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 PL 9  
Db |||  
5 PL 6  
  
RESULT 27  
C1A\_ENTFA ID - C1A\_ENTFA STANDARD; PRT; 7 AA.  
AC P11932;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=87005252; PubMed=3093276;  
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,  
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;  
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,  
RT CAM373";  
RL Lett. 206:69-72(1986).  
CC -1- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS  
CC HARBORING PAM373.  
CC -1- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR  
CC SPECIFICITY OF PHEROMONES TO PLASMIDS.  
CC -1- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.  
DR PIR; A25269; A25269.  
KW Pheromone.  
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 IL 7  
Db |||  
4 IL 5  
  
RESULT 28  
IGAO\_DACDE ID - IGAO\_DACDE STANDARD; PRT; 7 AA.  
AC P06294;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Galactose oxidase inhibitor.  
OS Dactylium dendroides (Ciadobotryum dendroides).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.  
OX NCBI\_TaxID=5132;  
RN [1]  
RP SEQUENCE.  
RA Avigad G., Markus Z.;  
RT "Identification of a peptide inhibitor of galactose oxidase from  
RT Dactylium dendroides";  
RL Fed. Proc. 31:447-447(1972).  
CC -1- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE  
CC GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY  
CC BINDING TO ITS PROSTHETIC COPPER GROUP.  
DR PIR; A01341; XEYDGD.  
KW Copper; Metalloenzyme inhibitor.  
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 QN 5  
Db |||  
3 QN 4  
  
RESULT 29  
MNPL\_LEPDE ID - MNPL\_LEPDE STANDARD; PRT; 7 AA.  
AC P42984;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Myotropic neuropeptide 1 (Led-MNP-I).  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;  
OC Chrysomelini; Leptinotarsa.  
OX NCBI\_TaxID=7539;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Head;  
RX MEDLINE=95380343; PubMed=7651886;  
RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,  
RA Grauwels L., van Leuven F., de Loof A.;  
RT "Identification, characterization, and immunological localization of  
RT a novel myotropic neuropeptide in the Colorado potato beetle,  
RT Leptinotarsa decemlineata";  
RL Peptides 16:365-374(1995).  
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE  
CC OVIDUCT.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PL 9  
DB 5 PL 6

RESULT 30  
UN06 PINPS STANDARD; PRT; 7 AA.  
AC P81675;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of needles (N141) (Fragment).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=71647;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Needle;  
RX MEDLINE=99274088; PubMed=10344291;  
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
RA Frigerio J.-M., Plomion C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins";  
RL Electrophoresis 20:1098-1108(1999).  
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.  
FT NON\_TER 1  
FT NON\_TER 7  
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3  
DB 5 LP 6

RESULT 31  
B44K\_PORGI STANDARD; PRT; 8 AA.  
AC P81886;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE 44 kDa immunogenic protein (Fragment).  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
OX NCBI\_TaxID=837;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=VPB 3492;  
RX MEDLINE=20198497; PubMed=10731616;  
RA Norris J.M., Love D.N.;  
RT "Serum antibody responses of cats to soluble whole cell antigens of  
RT feline Porphyromonas gingivalis";  
RL Vet. Microbiol. 73:37-49(2000).  
CC -I- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.  
KW Antigen.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PL 9  
DB 5 PL 6

QY 8 PL 9  
DB 5 PL 6

QY 5 NI 6  
DB 7 NI 8

RESULT 32  
CADI\_ENTFA STANDARD; PRT; 8 AA.  
AC P13268;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CADI.  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=85051889; PubMed=6437872;  
RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
RA Craig R.A., Clewell D.B., Suzuki A.;  
RT "Isolation and structure of the bacterial sex pheromone, CADI, that  
RT induces plasmid transfer in Streptococcus faecalis";  
RL FEBS Lett. 178:97-100(1984).  
CC -I- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
CC HEMOLYSIN PLASMID PAD1.  
KW Pheromone.  
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2  
DB 3 SL 4

RESULT 33  
COW2\_CONPU STANDARD; PRT; 8 AA.  
AC P58785;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leu-contryphan-P.  
OS Conus purpurascens (Purple cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=41690;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC STRAIN=Clipperton Island; TISSUE=Venom;  
RX MEDLINE=99388839; PubMed=10461743;  
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
RA Olivera B.M.;  
RT "A novel D-leucine-containing Conus peptide: diverse conformational  
RT dynamics in the contryphan family";  
RL J. Pept. Res. 54:93-99(1999).  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -I- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.  
CC -I- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.  
KW Toxin; Hydroxylation; D-amino acid.  
FT DISULFID 2  
FT MOD\_RES 4  
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 LP 3
      ||
Db      5 LP 6

RESULT 34
COXG_RAT
ID_COXG_RAT      STANDARD;      PRT;      8 AA.
AC P80430;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIB (EC 1.9.3.1) (AED) (Fragment).
GN COX6B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform";
RL Eur. J. Biochem. 230:235-241(1995).
CC -|- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT. THIS PROTEIN MAY BE ONE OF THE
CC HEME-BINDING SUBUNITS OF THE OXIDASE.
CC -|- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -|- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIB FAMILY.
DR PIR; S65381; S65381.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 1
SQ SEQUENCE 8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;

Query Match      22.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 QN 5
      ||
Db      1 QN 2

RESULT 35
NPB_BOVIN
ID_NPB_BOVIN      STANDARD;      PRT;      8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -|- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.

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KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D95C729 CRC64;

Query Match      22.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PQ 4
      ||
Db      5 PQ 6

RESULT 36
RT34_BOVIN
ID_RT34_BOVIN      STANDARD;      PRT;      8 AA.
AC P82929;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).
GN MRPS34.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -|- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -|- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 1
SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match      22.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 IL 7
      ||
Db      4 IL 5

RESULT 37
UPAA_HUMAN
ID_UPAA_HUMAN      STANDARD;      PRT;      8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).

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CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 7, ITS MW IS: 12 kDa.

DR SWISS-2DPAGE; P30096; HUMAN.  
 FT NON TER 1 5  
 FT VARIANT 5 5 F -> P.  
 FT NON TER 8 8 /FTID=VAR\_000004.

FT SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7  
 ||  
 Db 2 IL 3

RESULT 38  
 AL10\_CARNA  
 ID AL10\_CARNA STANDARD; PRT; 9 AA.

AC P81813;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 10.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubranchyura; Portunoidae; Portunidae; Carcinus.  
 ON NCBI\_TaxID=6759;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;

RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).

CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD RES 9  
 FT SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQ 4  
 ||  
 Db 2 PQ 3

RESULT 39  
 FARI\_CALVO  
 ID FARI\_CALVO STANDARD; PRT; 9 AA.

AC P41856;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE CalliprFamide 1.  
 OS Calliphora vomitoria (Blue blowfly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 CC Calliphoridae; Calliphora.  
 ON NCBI\_TaxID=27454;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliprFamides) from the blowfly  
 RT Calliphora vomitoria";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
 CC SALIVARY GLAND OF CALLIPHORA.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.

DR PIR; A41978; A41978  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 FT SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C67 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQ 4  
 ||  
 Db 2 PQ 3

RESULT 40  
 FAR5\_PENNO  
 ID FAR5\_PENNO STANDARD; PRT; 9 AA.

AC P83320;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP5 (SMPSLRFP-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 CC Penaeidae; Penaeus.  
 ON NCBI\_TaxID=6687;  
 RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,  
 RA Chaivuthangkura P., Sithigorngul W., Petsom A.;

RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn Penaeus monodon.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.

KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 FT SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2  
 ||  
 Db 4 SL 5

RESULT 41  
 FAR9\_ASCSU  
 ID FAR9\_ASCSU STANDARD; PRT; 9 AA.

AC P43172;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE FMRFamide-like neuropeptide AF9.  
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).  
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
 CC Ascarididae; Ascaris.

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OX NCBI_TaxID=6253;
RN [1]_
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRPamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PL 9
DB 6 PL 7

RESULT 42
FIBB MACFU STANDARD; PRT; 9 AA.
ID FIBB MACFU
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9543;
RN [1]_
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; C24180; C24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 1 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SL 2
DB 4 SL 5

RESULT 43.

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MGMT BOVIN
ID MGMT BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
DE methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP SEQUENCE.
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
CC IRREVERSIBLY INACTIVATED.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OCT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; transferase; Methyltransferase.
FT ACT SITE 1 1
FT NON_TER 1 1
FT NON_TER 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 IL 7
DB 5 IL 6

RESULT 44
OXVA SQUAC STANDARD; PRT; 9 AA.
ID OXVA SQUAC
AC P42959;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]_
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val9-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the

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RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PL 9
DB |||
7 PL 8

RESULT 45
OXYT_CYPCA
ID OXYT_CYPCA STANDARD; PRT; 9 AA.
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Vasotocin.
OS Cyprinus carpio (Common carp), and
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962, 7757;
RN [1]
RP SEQUENCE.
RC SPECIES=C. carpio; TISSUE=Pituitary;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishes.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=P. marinus; TISSUE=Pituitary;
RX MEDLINE=88225576; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawauchi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
RT (Petromyzon marinus): isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; B61364; B61364.
DR PIR; S06375; S06375.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QN 5
DB |||
4 QN 5

RESULT 46
OXYT_RABIT

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ID OXYT_RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit),
OS Hippopotamus amphibius (Hippopotamus),
OS Balanoptera physalus (Finback whale) (Common rorqual), and
OS Tachyglossus aculeatus aculeatus (Australian echidna), and
OS Hydrolagus collei (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=B. physalus;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
RN [4]
RP SEQUENCE.
RC SPECIES=A. aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Neurohypophyseal hormones and evolution of tetrapods.";
RL Nature New Biol. 244:124-126(1973).
RN [5]
RP SEQUENCE.
RC SPECIES=H. collei;
RX MEDLINE=70088110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophyseal hormone in the holocephalian
RT elasmobranch fish, Hydrolagus collei.";
RL J. Endocrinol. 45:597-606(1969).
CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC UTERUS AND OF THE MAMMARY GLAND.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A91466; A91466.
DR PIR; A92774; A92774.
DR PIR; A93147; A93147.
DR PIR; A93408; A93408.
DR PIR; B90667; B90667.
DR PDB; 1XY1; 15-OCT-90.
DR PDB; 1XY2; 15-OCT-90.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 QN 5
Db      ||
        4 QN 5

RESULT 47
OXYT_RAJCL
ID_OXYT_RAJCL STANDARD; PRT; 9 AA.
AC P42994;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glutitocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hynostomales; Pristigaster; Batoidae;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE=66123415; PubMed=5880565;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurohypophyseal peptides: isolation of a new hormone,
RT glutitocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,
RT the ray (Raja clavata).";
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -|- FUNCTION: ANTIDIURETIC HORMONE.
CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
PFam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB455804B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PQ 4
Db      ||
        7 PQ 8

RESULT 48
OXYV_SQUAC
ID_OXYV_SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=730311727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophyseal hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -|- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

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DR InterPro; IPR000981; Neurohyp_horm.
DR PFam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 QN 5
Db      ||
        4 QN 5

RESULT 49
RE42_LITRU
ID_RE42_LITRU STANDARD; PRT; 9 AA.
AC P82075; P82093;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.2/4.3.
OS Litoria rubella (Deepest tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OX Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinbörner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
RN [2]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -|- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -|- PM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-
CC terminal amidation.
CC -|- MASS SPECTROMETRY: MW=883; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 884 MW; 2C2D77205AA72728 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 IL 7
Db      ||
        6 IL 7

RESULT 50
RS10_SERMA
ID_RS10_SERMA STANDARD; PRT; 9 AA.
AC O68936;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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28-FEB-2003 (Rel. 41, Last annotation update)  
30S ribosomal protein S10 (Fragment).  
RPSJ.  
OS Serratia marcescens.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Serratia.  
OX NCBI\_TaxID=615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Noorani S.M., Lindahl L., Zengel J.M.;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By  
CC Similarity).  
CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF058451; AAC14294.1; -;  
DR HAMAP; MF\_00508; -; 1.  
DR InterPro; IPR001848; Ribosomal\_S10.  
DR PROSITE; PS00361; RIBOSOMAL\_S10; PARTIAL.  
KW Ribosomal protein.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1214 MW; D53944004416D456 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 4 QN 5  
Db 2 QN 3  
  
RESULT 51  
RT33\_BOVIN  
ID RT33\_BOVIN STANDARD; PRT; 9 AA.  
AC P82926;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).  
GN MRPS33.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP TISSUE=Liver;  
RC MEDLINE=21276436; PubMed=11279123;  
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;  
RT "The small subunit of the mammalian mitochondrial ribosome:  
RT Identification of the full complement of ribosomal proteins present."  
RL J. Biol. Chem. 276:19363-19374(2001).  
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit  
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
KW Ribosomal protein; Mitochondrion.  
FT NON\_TER 1  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 PL 9  
Db 6 PL 7  
  
RESULT 52  
SAMP MUSCA  
ID SAMP MUSCA STANDARD; PRT; 9 AA.  
AC P19095;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Serum amyloid P-component (SAP) (Fragment).  
OS Mustelus canis (Smooth dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;  
OC Mustelus.  
OX NCBI\_TaxID=7812;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=83160932; PubMed=6403520;  
RA Robey F.A., Tanaka T., Liu T.-Y.;  
RT "Isolation and characterization of two major serum proteins from the  
RT dogfish, Mustelus canis, C-reactive protein and amyloid P  
RT component."  
RL J. Biol. Chem. 258:3889-3894(1983).  
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID  
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND  
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
DR InterPro; IPR001759; Pentaxin.  
DR PROSITE; PS00289; PENTAXIN; PARTIAL.  
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.  
FT DOMAIN 1  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 SL 2  
Db 6 SL 7  
  
RESULT 53  
UPA3\_HUMAN  
ID UPA3\_HUMAN STANDARD; PRT; 9 AA.  
AC P30089;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.

DR SWISS-2DPAGE; P30089; HUMAN.  
 FT NON TER 1 9  
 FT NON TER 9 9  
 SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 8 PL 9  
 DB 2 PL 3  
 RESULT 54  
 UPA7 HUMAN STANDARD; PRT; 9 AA.  
 AC P30093;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=9302937; PubMed=1459097;  
 RA Hughes G.J., Fruiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RL "Plasma protein map: an update by microsequencing.";  
 RT Electrophoresis 13:707-714(1992).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.  
 DR SWISS-2DPAGE; P30093; HUMAN.  
 FT NON TER 1 1  
 FT UNSURE 5 5  
 FT NON TER 9 9  
 SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 SL 2  
 DB 1 SL 2  
 RESULT 55  
 AH3 PRUSE STANDARD; PRT; 10 AA.  
 AC P29261;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase  
 DE isozyme II) (AH II) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosida I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -1- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-

CC glucose.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 CC EMBRYONAL TISSUES.  
 CC -1- PTM: GLYCOSYLATED.  
 CC Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 SL 2  
 DB 9 SL 10  
 RESULT 56  
 ANG1 CHICK STANDARD; PRT; 10 AA.  
 ID ANG1 CHICK  
 AC P01018;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang  
 DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]  
 DE (Fragment).  
 GN AGT OR SERPIN A8.  
 OS Gallus gallus (Chicken), and  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031, 93934;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Chicken;  
 RX MEDLINE=74127845; PubMed=4361802;  
 RA Nakayama T., Nakajima T., Sokabe H.;  
 RT "Comparative studies on angiotensins. 3. Structure of fowl  
 RT angiotensin and its identification by DNS-method.";  
 RL Chem. Pharm. Bull. 21:2085-2087(1973).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=C.c.japonica;  
 RX MEDLINE=90284684; PubMed=2191893;  
 RA Takei Y., Hasegawa Y.;  
 RT "Vasopressor and depressor effects of native angiotensins and  
 RT inhibition of these effects in the Japanese quail.";  
 RL Gen. Comp. Endocrinol. 79:12-22(1990).  
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A60624; A60624.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT PEPTIDE 2 8 ANGIOTENSIN III.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2  
 DB 9 SL 10

RESULT 57  
 BPP2 BOTIN  
 ID BPP2 BOTIN STANDARD; PRT; 10 AA.  
 AC P30422;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -|- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 CC PIR; B37196; B37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QN 5  
 DB 1 QN 2

RESULT 58  
 BPP2 BOTJA  
 ID BPP2 BOTJA STANDARD; PRT; 10 AA.  
 AC P01022;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme inhibitor V-6-II).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=72118526; PubMed=4334402;  
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R., Kocy O.;  
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis.";  
 RL Biochemistry 10:4033-4039(1971).  
 CC -|- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A01255; XAVI6B  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QN 5  
 DB 1 QN 2

RESULT 59  
 BPP8 BOTIN  
 ID BPP8 BOTIN STANDARD; PRT; 10 AA.  
 AC P30426;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -|- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 CC PIR; B37196; B37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NI 6  
 DB 7 NI 8

RESULT 60  
 BRK ONCMY  
 ID BRK ONCMY STANDARD; PRT; 10 AA.  
 AC Q9PRZ1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lysyl-bradykinin-like.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94039817; PubMed=8224232;

RA Conlon J.M., Olson K.R.;  
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from  
RL trout plasma.";  
CC FEBS Lett. 334:75-78(1993).  
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR  
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.  
CC -!- SURCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Plasma.  
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
DR PIR; S39030; S39030.  
KW Bradykinin; Vasodilator.  
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 PL 9  
DB 8 PL 9  
  
RESULT 61  
CATB SHEEP  
ID CATB SHEEP STANDARD; PRT; 10 AA.  
AC P83205;  
DT 15-SEP-2003 (Rel. 42, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).  
GN CTSB.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=22394055; PubMed=12506352;  
RA El Amir B., Remy B., Sousa N.M., Joris B., Ottliers N.G., Perenyi Z.,  
RA Mboko H.B., Beckers J.-F.M.P.;  
RT "Isolation and partial characterization of three pregnancy-associated  
RT glycoproteins from the ewe placenta."  
RL Mol. Reprod. Dev. 64:199-206(2003).  
CC -!- FUNCTION: Thiol protease which is believed to participate in  
CC intracellular degradation and turnover of proteins. Has also been  
CC implicated in tumor invasion and metastasis.  
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in  
CC small molecule substrates (thus differing from cathepsin L). In  
CC addition to being an endopeptidase, shows peptidyl-dipeptidase  
CC activity, liberating C-terminal dipeptides.  
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked  
CC by a disulfide bond (By similarity).  
CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
DR InterPro; IPR000169; SHProt acsite.  
DR PROSITE; PS00640; THIOI\_PROTEASE ASN; PARTIAL.  
DR PROSITE; PS00139; THIOI\_PROTEASE\_CYS; PARTIAL.  
DR PROSITE; PS00639; THIOI\_PROTEASE\_HIS; PARTIAL.  
KW Hydrolase; Thiol protease; Lysosome.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 LP 3  
DB 1 LP 2

RESULT 62  
FAR6 PANRE  
ID FAR6 PANRE STANDARD; PRT; 10 AA.  
AC P82660;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE, FUNCTION, AND AMIDATION.  
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
RA Maule A.G.;  
RT "Isolation, characterization and pharmacology of FMRFamide-related  
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus."  
RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 10 10  
SQ SEQUENCE 10 AA; 1132 MW; CB13B4C9D776C76D CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 PQ 4  
DB 4 PQ 5  
  
RESULT 63  
GON1 PETMA  
ID GON1 PETMA STANDARD; PRT; 10 AA.  
AC P04378;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 20-MAR-1987 (Rel. 04, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I)  
DE (Luliberin I).  
OS Petromyzon marinus (Sea lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
OX NCBI\_TaxID=7757;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=86168192; PubMed=3514603;  
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;  
RT "Primary structure of gonadotropin-releasing hormone from lamprey  
RT brain."  
RL J. Biol. Chem. 261:4812-4819(1986).  
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
CC the secretion of both luteinizing and follicle-stimulating  
CC hormones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the GNRH family.  
DR PIR; A01412; RHLWGS.  
DR InterPro; IPR002012; GNRH.  
DR Pfam; PF00446; GNRH; 1.  
DR PROSITE; PS00473; GNRH; 1.  
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA; 1244 MW; 1B4B36237B1735AB CRC64;  
  
Query Match 22.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8e+03;



Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2

Db 4 SL 5

# RESULT 64

GON2\_CHEPR  
ID\_GON3\_CHEPR STANDARD; PRT; 10 AA.  
AC P80678;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)  
DE (Luliberin II).  
OS Chelyosoma productum.  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
OC Phlebobranchia; Corellidae; Chelyosoma.  
OX NCBI\_TaxID=71177;  
RN [1]  
RP SEQUENCE.

RA MEDLINE=96413669; PubMed=8816823;  
RA Powell J.F.F., Reeka-Skinner S.M., Prakash M.O., Fischer W.H.,  
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;  
RT "Two new forms of gonadotropin-releasing hormone in a protochordate  
and the evolutionary implications."  
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).

CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
CC the secretion of both luteinizing and follicle-stimulating  
CC hormones.

CC -!- SUBUNIT: Homodimer; disulfide-linked.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: GnRH neurons lie within blood sinuses close to  
CC the gonads and gonads in both juveniles and adults, implying  
CC that the neuropeptide is released into the bloodstream.

CC -!- MASS SPECTROMETRY: MW=1117.52; METHOD=MALDI.

CC -!- SIMILARITY: Belongs to the GnRH family.

DR InterPro: IPR002012; GnRH.

DR PROSITE; PS00473; GnRH; 1.  
KW Hormone; Amidation; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 6 6 INTERCHAIN.  
FT MOD RES 10 10 AMIDATION (BY SIMILARITY).

FT MOD RES 10 10 AMIDATION (BY SIMILARITY).  
SQ SEQUENCE 10 AA; 1135 MW; 284B38D1EB735A3 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2

Db 4 SL 5

# RESULT 65

GON3\_ONCKE  
ID\_GON3\_ONCKE STANDARD; PRT; 10 AA.  
AC P20367; P81751;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-  
RH III) (Luliberin III).  
GN GnRH3.  
OS Oncorhynchus keta (Chum salmon), and  
OS Clupea pallasii (Pacific herring).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8018, 30724;  
RN [1]  
RP SEQUENCE.

Query Match

Best Local Similarity

22.2%; Score 2; DB 1; Length 10;

100.0%; Pred. No. 8.8e+03;

RC

RE SPECIES=O.keta;

RE MEDLINE=83195140; PubMed=6341999;

RE Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;

RE "Characterization of a teleost gonadotropin-releasing hormone.";

RE Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).

RN [2]

RP SEQUENCE, AND FUNCTION.

RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;

RE MEDLINE=20114351; PubMed=10650929;

RE Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,

RE Chang J.P., Rivier J.E., Sherwood N.M.;

RE "Primary structure and function of three gonadotropin-releasing

RE hormones, including a novel form, from an ancient teleost, herring.";

RE Endocrinology 141:505-512(2000).

CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates

CC the secretion of both luteinizing and follicle-stimulating

CC hormones.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the GnRH family.

DR PIR; A21114; A21114.

DR InterPro: IPR002012; GnRH.

DR Pfam; PF00446; GnRH; 1.

DR PROSITE; PS00473; GnRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LP 3

Db 8 LP 9

# RESULT 66

GONL\_SQUAC

ID\_GONL\_SQUAC STANDARD; PRT; 10 AA.

AC P27429;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Gonadoliberin (Gonadotropin-releasing hormone) (GnRH) (LH-RH)

(Luliberin).

OS Squalus acanthias (Spiny dogfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.

OX NCBI\_TaxID=7797;

RN [1]

RP SEQUENCE.

RC TISSUE=Brain;

RE MEDLINE=92335300; PubMed=1631133;

RE Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,

RE Naboriak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;

RE "Distinct sequence of gonadotropin-releasing hormone (GnRH) in

RE dogfish brain provides insight into GnRH evolution.";

RE Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).

CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the GnRH family.

DR PIR; A46030; A46030.

DR InterPro: IPR002012; GnRH.

DR Pfam; PF00446; GnRH; 1.

DR PROSITE; PS00473; GnRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 10 10 AMIDATION

SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match

Best Local Similarity

22.2%; Score 2; DB 1; Length 10;

100.0%; Pred. No. 8.8e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LP 3

Db 8 LP 9

# RESULT 67

MOSEQ\_CLYJA  
ID MOSQ\_CLYJA STANDARD; PRT; 10 AA.  
AC P19962;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE [Gln6]-mosact.  
OS Clypeaster japonicus (Sand dollar).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;  
OC Clypeasteridae; Clypeaster.  
OX NCBI\_TaxID=7644;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Egg jelly;  
RA Suzuki N., Kurita M., Yoshino K., Kajiyura H., Nomura K., Yamaguchi M.;  
RT "Purification and structure of mosact and its derivatives from the  
RT egg jelly of the sea urchin Clypeaster japonicus";  
RL Zool. Sci. 4:649-656(1987).  
CC -!- FUNCTION: Stimulates sperm respiration and motility.  
DR PIR; JN0025; JN0025.  
SQ SEQUENCE 10 AA; 1019 MW; 9AFB032456DDC5BA CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.8e+03; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QN 5

Db 6 QN 7

# RESULT 68

NS1\_MYCTU  
ID NS1\_MYCTU STANDARD; PRT; 10 AA.  
AC P8135;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 30 kDa non-secretory protein 1 (Fragment).  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=H37Rv;  
RA Prasad H.K., Annapurna P.S.;  
RL Submitted (DEC-1997) to the SWISS-PROT data bank.  
CC -!- CAUTION: We are unable to find this protein in the translation of  
CC the genome of strain H37Rv.  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.8e+03; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PL 9

Db 4 PL 5

# RESULT 69

RRPL\_PHODV  
ID RRPL\_PHODV STANDARD; PRT; 10 AA.  
AC P35946;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)  
(L protein) (Fragment).  
GN L.  
OS Phocine distemper virus (PDV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
OX NCBI\_TaxID=11240;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Uster/88;  
RX MEDLINE=92268877; PubMed=1588321;  
RA Curran M.D., O'Loan D., Kennedy S., Rima B.K.;  
RT "Molecular characterization of phocine distemper virus: gene order  
RT and sequence of the gene encoding the attachment (H) protein.";  
RL J. Gen. Virol. 73:1189-1194(1992).  
CC -!- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY  
CC FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)  
CC SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAs. RNA EDITING OF THE P  
CC GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.  
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC (RNA) (N).  
CC -!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; D10371; BAA01208.1; -  
KW Transferase; RNA-directed RNA polymerase.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IL 7  
Db 9 IL 10

RESULT 70  
TEMK\_RANTE  
ID TEMK\_RANTE STANDARD; PRT; 10 AA.  
AC P56923;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Temporin K.  
OS Rana temporaria (European common frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8407;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=97175050; PubMed=9022710;  
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
RA Barra D.;  
RT "Temporins, antimicrobial peptides from the European red frog Rana  
RT temporaria";  
RL Eur. J. Biochem. 242:788-792(1996).  
CC -!- FUNCTION: Has antibacterial activity against Gram-positive

CC bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the brevinnin family.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 LP 3  
 Db 2 LP 3  
 RESULT 71  
 TKL2\_LOCMI STANDARD; PRT; 10 AA.  
 AC P16224;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Locustatachykinin II (TK-II).  
 OS Locusta migratoria (Migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=90184489; PubMed=2111766;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
 RT "Locustatachykinin I and II, two novel insect neuropeptides with  
 homology to peptides of the vertebrate tachykinin family.";  
 RL FEBS Lett. 261:397-401(1990).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE  
 CC OVIDUCT AND FOREGUT.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 PL 9  
 Db 2 PL 3  
 RESULT 72  
 TKL3\_LOCMI STANDARD; PRT; 10 AA.  
 AC P30249;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Locustatachykinin III (TK-III).  
 OS Locusta migratoria (Migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=91219696; PubMed=2132575;  
 RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,

de Loof A.;  
 RT "Locustatachykinin III and IV: two additional insect neuropeptides  
 with homology to peptides of the vertebrate tachykinin family.";  
 RL Regul. Pept. 31:199-212(1990).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE  
 CC OVIDUCT AND FOREGUT.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 DR PIR; A60073; ECIQ3M.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1065 MW; C452CD6B59C87DC6 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 PQ 4  
 Db 2 PQ 3  
 RESULT 73  
 TKL4\_LOCMI STANDARD; PRT; 10 AA.  
 AC P30250;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Locustatachykinin IV (TK-IV).  
 OS Locusta migratoria (Migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=91219696; PubMed=2132575;  
 RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,  
 RA de Loof A.;  
 RT "Locustatachykinin III and IV: two additional insect neuropeptides  
 with homology to peptides of the vertebrate tachykinin family.";  
 RL Regul. Pept. 31:199-212(1990).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE  
 CC OVIDUCT AND FOREGUT.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 DR PIR; B60073; ECIQ4M.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1040 MW; 9E52CD71E9C87735 CRC64;  
 Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SL 2  
 Db 3 SL 4  
 RESULT 74  
 TKN\_PHYBI STANDARD; PRT; 10 AA.  
 ID\_TKN\_PHYBI  
 AC P08610;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Phyllomedusa bicolor (Two-colored leaf frog).  
 OS Phyllomedusa bicolor (Two-colored leaf frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

OC Phylomedusinae; Phylomedusa.  
 OX NCBI\_TaxID=8393;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=70267748; PubMed=5452018;  
 RA Anastasi A., Erspamer G.F.;  
 RT "Occurrence of phylomedusin, a physalaemin-like decapeptide, in the  
 RL skin of Phylomedusa bicolor.";  
 RL Experimentia 26:866-867(1970).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; S07202; S07202.  
 DR InterPro; IPR002040; Tachykinin.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1189 MW; 3A257D7059D40457 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 QN 5  
 ||  
 DB 1 QN 2

RESULT 75  
 VEG6\_BACSU  
 ID\_VEG6\_BACSU STANDARD; PRT; 10 AA.  
 AC P80899;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Vegetative protein 6 (VEG6) (Fragment).  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=168 / IS58;  
 RX MEDLINE=97237728; PubMed=9084183;  
 RA Schmid R., Bernhardt J., Antelmann H., Voelker U., Mach H.,  
 RA Voelker A., Hecker M.;  
 RT "Identification of vegetative proteins for a two-dimensional protein  
 RL index of Bacillus subtilis.";  
 RL Microbiology 143:991-998(1997).  
 CC -!- CAUTION: Could not be found in the genome of B. subtilis 168.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 973 MW; 8793A6B2C8772861 CRC64;

Query Match 22.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 QN 5  
 ||  
 DB 9 QN 10

Search completed: November 25, 2003, 18:17:36  
 Job time : 4.35638 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 21.6862 Seconds  
(without alignments)  
107.095 Million cell updates/sec

Title: US-09-641-801-19

Perfect score: 9

Sequence: 1 SLPQNILPL 9

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_23.\*

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	44.4	10	2 Q9R5N6	Q9R5N6 clostridium
2	4	44.4	13	2 Q9R5N5	Q9R5N5 clostridium
3	4	44.4	13	4 Q16007	Q16007 homo sapien
4	4	44.4	17	11 Q9QUY6	Q9QUY6 rattus sp.
5	4	44.4	18	6 P83202	P83202 ovis aries
6	4	44.4	19	4 Q16184	Q16184 homo sapien
7	4	44.4	19	12 Q84863	Q84863 unidentified
8	4	44.4	19	12 Q84862	Q84862 unidentified
9	3	33.3	5	13 P83308	P83308 gallus gall
10	3	33.3	8	2 Q45615	Q45615 bacillus su
11	3	33.3	8	11 Q62527	Q62527 mus spretus
12	3	33.3	9	4 Q16220	Q16220 homo sapien
13	3	33.3	9	4 Q9UE09	Q9UE09 homo sapien
14	3	33.3	9	9 Q9XJN0	Q9XJN0 bacterioph
15	3	33.3	10	2 Q47651	Q47651 escherichia
16	3	33.3	10	2 Q9XBH3	Q9XBH3 bacillus ce

17	3	33.3	10	2 P83154	P83154 anabaena sp
18	3	33.3	10	4 Q9UJ48	Q9UJ48 homo sapien
19	3	33.3	10	11 Q9ESU5	Q9ESU5 mus musculus
20	3	33.3	10	12 Q86580	Q86580 simian para
21	3	33.3	11	2 Q47451	Q47451 escherichia
22	3	33.3	11	2 Q47569	Q47569 escherichia
23	3	33.3	11	4 Q9UELO	Q9UELO homo sapien
24	3	33.3	11	7 Q9TQB3	Q9TQB3 homo sapien
25	3	33.3	11	10 P82336	P82336 pisum sativ
26	3	33.3	13	2 Q9WW72	Q9WW72 enterococcu
27	3	33.3	13	2 Q9X514	Q9X514 enterococcu
28	3	33.3	13	2 Q9WW71	Q9WW71 enterococcu
29	3	33.3	13	2 Q8KHM6	Q8KHM6 streptococc
30	3	33.3	13	2 Q8KRA4	Q8KRA4 streptococc
31	3	33.3	13	8 Q95925	Q95925 porphyra pu
32	3	33.3	13	10 Q945C1	Q945C1 cryptobecodi
33	3	33.3	13	12 Q9WMG5	Q9WMG5 sigma virus
34	3	33.3	13	13 P82881	P82881 rana clamit
35	3	33.3	13	13 P82830	P82830 rana luteiv
36	3	33.3	14	2 Q9R8K0	Q9R8K0 chlamydia t
37	3	33.3	14	2 Q9R8M4	Q9R8M4 chlamydia t
38	3	33.3	14	2 Q9R8L0	Q9R8L0 chlamydia t
39	3	33.3	14	2 Q9R8K7	Q9R8K7 chlamydia t
40	3	33.3	14	2 Q9R8M1	Q9R8M1 chlamydia t
41	3	33.3	14	2 Q9R8L8	Q9R8L8 chlamydia t
42	3	33.3	14	2 Q9R8K2	Q9R8K2 chlamydia t
43	3	33.3	14	2 Q9R8M7	Q9R8M7 chlamydia t
44	3	33.3	14	2 Q9R8P2	Q9R8P2 chlamydia t
45	3	33.3	14	2 Q9R8J5	Q9R8J5 chlamydia t
46	3	33.3	14	2 Q85527	Q85527 chlamydia t
47	3	33.3	14	2 Q9R8N6	Q9R8N6 chlamydia t
48	3	33.3	14	2 Q9R8M8	Q9R8M8 chlamydia t
49	3	33.3	14	2 Q9R8L5	Q9R8L5 chlamydia t
50	3	33.3	14	2 Q9R8J7	Q9R8J7 chlamydia t
51	3	33.3	14	2 Q9R8N2	Q9R8N2 chlamydia t
52	3	33.3	14	2 Q9R8P6	Q9R8P6 chlamydia t
53	3	33.3	14	2 Q9R8M5	Q9R8M5 chlamydia t
54	3	33.3	14	2 Q9R8N9	Q9R8N9 chlamydia t
55	3	33.3	14	6 Q90061	Q90061 bos taurus
56	3	33.3	14	9 Q9XJN4	Q9XJN4 bacterioph
57	3	33.3	14	13 Q91777	Q91777 xenopus lae
58	3	33.3	15	2 Q9X637	Q9X637 klebsiella
59	3	33.3	15	2 Q9X635	Q9X635 escherichia
60	3	33.3	15	4 Q9UMY6	Q9UMY6 homo sapien
61	3	33.3	15	4 Q9UC60	Q9UC60 homo sapien
62	3	33.3	15	5 Q9TW86	Q9TW86 rapana thom
63	3	33.3	15	8 Q9T2K8	Q9T2K8 spinacia ol
64	3	33.3	15	8 Q8WK21	Q8WK21 bolidomonas
65	3	33.3	15	10 Q9SAP4	Q9SAP4 solanum tub
66	3	33.3	15	10 Q65177	Q65177 mesembryant
67	3	33.3	15	10 P82331	P82331 pisum sativ
68	3	33.3	16	2 Q30985	Q30985 rhodobacter
69	3	33.3	16	2 Q48387	Q48387 klebsiella
70	3	33.3	16	2 Q52901	Q52901 rhizobium m
71	3	33.3	16	4 Q9NNZ2	Q9NNZ2 homo sapien
72	3	33.3	16	4 Q8WXZ7	Q8WXZ7 homo sapien
73	3	33.3	16	8 Q8SL53	Q8SL53 aconium hie
74	3	33.3	16	11 Q9CW70	Q9CW70 mus musculus
75	3	33.3	16	12 Q918U2	Q918U2 human papil
76	3	33.3	16	12 Q918T1	Q918T1 human papil
77	3	33.3	16	12 Q918U8	Q918U8 human papil
78	3	33.3	16	12 Q918U6	Q918U6 human papil
79	3	33.3	16	12 Q918U4	Q918U4 human papil
80	3	33.3	16	12 Q918T9	Q918T9 human papil
81	3	33.3	17	2 Q46093	Q46093 campylobact
82	3	33.3	17	4 Q15276	Q15276 homo sapien
83	3	33.3	17	4 Q96P96	Q96P96 homo sapien
84	3	33.3	17	4 Q9NY39	Q9NY39 homo sapien
85	3	33.3	17	6 Q8MJ33	Q8MJ33 sus scrofa
86	3	33.3	18	2 Q50076	Q50076 mycobacteri
87	3	33.3	18	2 Q9LAP4	Q9LAP4 enterococcu
88	3	33.3	18	4 Q16244	Q16244 homo sapien
89	3	33.3	18	4 Q8WWHO	Q8WWHO homo sapien

Q9uc58 homo sapien  
O43834 homo sapien  
Q6wn06 bos taurus  
Q9tr90 bos taurus  
Q8sl29 aconium tab  
Q9s8n7 scenedesmus  
Q9qv84 rattus sp.  
Q90xc9 gallus galli  
Q78376 human immun  
Q9r596 fusobacteri  
Q8n5x1 homo sapien

## ALIGNMENTS

## RESULT 1

Q9RSN6 PRELIMINARY; PRT; 10 AA.  
AC Q9RSN6;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Neurotoxin type B HN+ 35 kDa SUBUNIT-BAND 3A (Fragment).  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92143938; PubMed=1781887;  
RA Somers E.; DasGupta B.R.;  
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or  
RT without hemagglutinating activity: do they share common amino acid  
RT sequences and genes?";  
RL J. Protein Chem. 10:415-425(1991).  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1169 MW; 00CF7E3AA4472054 CRC64;

Query Match 44.4%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QN1L 7  
Db 2 QN1L 5

## RESULT 2

Q9RSN5 PRELIMINARY; PRT; 13 AA.  
AC Q9RSN5;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Neurotoxin type B HN+ 35 kDa SUBUNIT-BAND 3B (Fragment).  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92143938; PubMed=1781887;  
RA Somers E.; DasGupta B.R.;  
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or  
RT without hemagglutinating activity: do they share common amino acid  
RT sequences and genes?";  
RL J. Protein Chem. 10:415-425(1991).  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1539 MW; 00DB6E78247E2054 CRC64;

Query Match 44.4%; Score 4; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QN1L 7  
Db 5 QN1L 8

## RESULT 3

Q16007 PRELIMINARY; PRT; 13 AA.  
AC Q16007;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE Lysosomal acid beta-galactosidase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91369478; PubMed=1909871;  
RA Morreau H.; Bonten E.; Zhou X.Y.; d'Azzo A.;  
RT "Organization of the gene encoding human lysosomal beta-  
RT galactosidase.";  
RL DNA Cell Biol. 10:495-504(1991).  
DR EMBL; S59584; AAB19814.1; -.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1482 MW; D70DAEE928194412 CRC64;

Query Match 44.4%; Score 4; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILPL 9  
Db 8 ILPL 11

## RESULT 4

Q9QUY6 PRELIMINARY; PRT; 17 AA.  
AC Q9QUY6;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Oligodendrocyte-specific UDP-galactose:ceramide galactosyltransferase  
DE (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96085162; PubMed=8521863;  
RA Schulte S.; Stoffel W.;  
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate  
RT transporter. Copurification, separation and characterization of the two  
RT glycoproteins.";  
RL Eur. J. Biochem. 233:947-953(1995).  
SQ SEQUENCE 17 AA; 2017 MW; 0F92A645FFD7F828 CRC64;

Query Match 44.4%; Score 4; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPQN 5  
Db 5 LPQN 8

## RESULT 5

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P83202
ID P83202 PRELIMINARY; PRT; 18 AA.
AC P83202;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 23, Last annotation update)
DE Pregnancy-associated glycoprotein 55 (EC 3.4.23.-) (ovPAG-55)
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE, AND TISSUE SPECIFICITY.
RC TISSUE=Placenta;
RA El Amir B., Remy B., Sousa N.M., Beckers J.-F.M.P.;
RT "Isolation and characterization of pregnancy-associated glycoproteins
RT extracted from sheep (Ovis aries) placentas.";
RL Mol. Reprod. Dev. 0:0-0(2002).
CC -!- TISSUE SPECIFICITY: PLACENTA.
CC -!- PTM: GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR InterPro; IPR001969; Asparticase site.
DR PROSITE; PS00141; ASP PROTEASE; PARTIAL.
KW Hydrolase; Aspartyl protease; Glycoprotein; Multigene family.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2128 MW; AA5F039CD95CA72A CRC64;

Query Match 44.4%; Score 4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILPL 9
DB 7 ILPL 10

RESULT 6
Q16184
ID Q16184 PRELIMINARY; PRT; 19 AA.
AC Q16184;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphofructokinase-M (EC 2.7.1.11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94311311; PubMed=8037209;
RA Sherman J.B., Raben N., Nicastri C., Argov Z., Nakajima H.,
RA Adams E.M., Eng C.M., Cowan T.M., Plotz P.H.;
RT "Common mutations in the phosphofructokinase-M gene in Ashkenazi
RT Jewish patients with glycogenesis VII--and their population
RT frequency.";
RL Am. J. Hum. Genet. 55:305-313(1994).
DR EMBL; S72312; AA831343.2; -.
KW Kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2081 MW; 20175220E0432A63 CRC64;

Query Match 44.4%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILPL 9
DB 10 ILPL 13

P83202
ID P83202 PRELIMINARY; PRT; 19 AA.
AC P83202;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 2.1 kDa protein (Fragment).
OS unidentified human poliovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=40278;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87169734; PubMed=3031313;
RA Kuge S., Saito I., Nomoto A.;
RT "Primary structure of poliovirus defective-interfering particle
RT genomes and possible generation mechanisms of the particles.";
RL J. Mol. Biol. 192:473-487(1986).
DR EMBL; M30221; AAA66829.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2106 MW; F774197992500AC8 CRC64;

Query Match 44.4%; Score 4; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILPL 9
DB 2 ILPL 5

RESULT 8
Q84862
ID Q84862 PRELIMINARY; PRT; 19 AA.
AC Q84862;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 2.0 kDa protein (Fragment).
OS unidentified human poliovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=40278;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87169734; PubMed=3031313;
RA Kuge S., Saito I., Nomoto A.;
RT "Primary structure of poliovirus defective-interfering particle
RT genomes and possible generation mechanisms of the particles.";
RL J. Mol. Biol. 192:473-487(1986).
DR EMBL; M30220; AAA66828.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 1995 MW; 6EADCC8296DDE139 CRC64;

Query Match 44.4%; Score 4; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILPL 9
DB 3 ILPL 6

RESULT 9
P83308
ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE FMRPamide-like neuropeptide (LPLRF-amide).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RX PubMed=613771;  
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
 RT "A novel active pentapeptide from chicken brain identified by  
 RT antibodies to FMRPamide."  
 RL Nature 305:328-330(1983).  
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;  
  
 Query Match 33.3%; Score 3; DB 13; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 7 LPL 9  
 Db 1 LPL 3  
  
 RESULT 10  
 Q45615 PRELIMINARY; PRT; 8 AA.  
 AC Q45615;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE GutB protein (Fragment).  
 GN GUTB.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=94253000; PubMed=8195086;  
 RA Ye R., Wong S.L.;  
 RT "Transcriptional regulation of the Bacillus subtilis glucitol  
 RT dehydrogenase gene."  
 RL J. Bacteriol. 176:3314-3320(1994).  
 DR EMBL; L16626; AAA20875.1; -.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;  
  
 Query Match 33.3%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 3 PON 5  
 Db 6 PON 8  
  
 RESULT 11  
 Q62527 PRELIMINARY; PRT; 8 AA.  
 AC Q62527;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE Transthyretin (Prealbumin) (Fragment).  
 GN TTR.

OS Mus spretus (Western wild mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10096;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRET/EI;  
 RX MEDLINE=94319082; PubMed=8043949;  
 RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,  
 RA Nadeau J.H.;  
 RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR."  
 RL Mamm. Genome 5:349-355(1994).  
 CC -!- FUNCTION: THYROID HORMONE-BINDING PROTEIN. PROBABLY TRANSPORTS  
 CC THYROXINE FROM THE BLOODSTREAM TO THE BRAIN.  
 CC -!- SUBUNIT: HOMOTETRAMER.  
 DR EMBL; U05689; AAB60461.1; -.  
 DR MGD; MGI:98865; Ttr.  
 KW Albumin; Transport; Retinol-binding; Vitamin A; Thyroid hormone.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 828 MW; 9156C76455A2D2CD CRC64;  
  
 Query Match 33.3%; Score 3; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 3 PON 5  
 Db 6 PON 8  
  
 RESULT 12  
 Q16220 PRELIMINARY; PRT; 9 AA.  
 AC Q16220;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
 DE HGRP protein (Fragment).  
 GN HGRP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94320083; PubMed=8044796;  
 RA Nagalla S.R., Spindel E.R.;  
 RT "Functional analysis of the 5'-flanking region of the human gastrin-  
 RT releasing peptide gene in small cell lung carcinoma cell lines."  
 RL Cancer Res. 54:4461-4467(1994).  
 DR EMBL; S73265; AAD14116.1; -.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1070 MW; 77FE37672B040864 CRC64;  
  
 Query Match 33.3%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 7 LPL 9  
 Db 6 LPL 8  
  
 RESULT 13  
 Q9UE09 PRELIMINARY; PRT; 9 AA.  
 AC Q9UE09;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Myristoyl-CoA:protein N-myristoyltransferase (Fragment).  
 GN NMT.  
 OS Homo sapiens (Human).



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98343933; PubMed=9677304;  
 RA McIlhinney R.A., Young K., Egerton M., Camble R., White A.,  
 RA Soloviev M.;  
 RT "Characterization of human and rat brain myristoyl-CoA:protein N-  
 RT myristoyltransferase: evidence for an alternative splice variant of  
 RT the enzyme.";  
 RL Biochem.J. 333:491-495 (1998).  
 DR EMBL; Y17208; CAA76685.1; -.  
 KW Transferase.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1030 MW; 097D0B1DC76735B4 CRC64;  
 Query Match 33.3%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 SLP 3  
 DB 3 SLP 5  
 RESULT 14  
 OXQXJNO  
 ID Q9XJNO PRELIMINARY; PRT; 9 AA.  
 AC Q9XJNO;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE P10 (Fragment).  
 OS Bacteriophage phi-10.  
 OC Viruses; dsRNA viruses; Cytoviridae; Cystovirus.  
 OX NCBI\_TaxID=90889;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99350412; PubMed=10419946;  
 RA Mindich L., Qiao X., Qiao J., Onodera S., Romantschuk M.,  
 RA Hoogstraaten D.;  
 RT "Isolation of additional bacteriophages with genomes of segmented  
 RT double-stranded RNA.";  
 RL J. Bacteriol. 181:4505-4508 (1999).  
 DR EMBL; AF125675; AAD22555.1; -.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1058 MW; 880E376AA720544A CRC64;  
 Query Match 33.3%; Score 3; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 NIL 7  
 DB 3 NIL 5  
 RESULT 15  
 ID Q47651 PRELIMINARY; PRT; 10 AA.  
 AC Q47651;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Trat protein (Fragment).  
 OS Escherichia coli.  
 OG Plasmid F.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=88118903; PubMed=3323526;  
 RA Jallajakumari M.B., Guidolin A., Buhj H.J., Manning P.A.;  
 RT "Surface exclusion genes tras and traf of the F sex factor of  
 RT Escherichia coli K-12 - Determination of the nucleotide sequence and  
 RT promoter and terminator activities.";  
 RL J. Mol. Biol. 198:1-11 (1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=92104498; PubMed=1761225;  
 RA Nomura N., Masai H., Inuzuka M., Miyazaki C., Ohtsubo E., Itoh T.,  
 RA Sasamoto S., Matsui M., Iehizaki R., Arai K.;  
 RT "Identification of eleven single-strand initiation sequences (ssi) for  
 RT priming of DNA replication in the F, R6K, R100 and ColE2 plasmids.";  
 RL Gene 108:15-22 (1991).  
 DR EMBL; D90177; BAA14207.1; -.  
 KW DNA replication; Plasmid.  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1070 MW; CC18014DD045B33D CRC64;  
 Query Match 33.3%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 NIL 7  
 DB 8 NIL 10  
 RESULT 16  
 OXQXBH3  
 ID Q9XBH3 PRELIMINARY; PRT; 10 AA.  
 AC Q9XBH3;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Celp-like protein (Fragment).  
 CN CELF.  
 OS Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1396;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 10987;  
 RX MEDLINE=99231848; PubMed=10217496;  
 RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;  
 RT "Genome organisation is not conserved between Bacillus cereus and  
 RT Bacillus subtilis.";  
 RL Microbiology 145:621-631 (1999).  
 DR EMBL; AJ000394; CAB40625.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1264 MW; D3757EC3339C9D6 CRC64;  
 Query Match 33.3%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 LPQ 4  
 DB 1 LPQ 3  
 RESULT 17  
 ID P83154 PRELIMINARY; PRT; 10 AA.  
 AC P83154;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Phycobilisome rod-core linker polypeptide cpcG3 (Fragment).  
 OS Anabaena sp. (strain L31).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
 OX NCBI\_TaxID=29412;  
 RN [1]  
 RP SEQUENCE.  
 RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;  
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF  
 CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.  
 CC -!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION  
 CC AND THE LOCATION OF THE DISK-SHAPED PHYCOBILIPROTEIN UNITS WITHIN  
 CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN  
 CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.  
 CC -!- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS  
 CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT  
 CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM  
 CC THE CORE.  
 CC -!- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.  
 CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.  
 KW Phycobilisome; Photosynthesis; Thylakoid; Membrane.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1144 MW; 299B662B5B172737 CRC64;  
 Query Match 33.3%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LPL 9  
 DB 2 LPL 4

RESULT 18  
 Q9UJ48 PRELIMINARY; PRT; 10 AA.  
 ID Q9UJ48;  
 AC Q9UJ48;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Latrophilin-2 (Fragment).  
 GN LPHH1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99153747; PubMed=10030676;  
 RA White G.R.M., Varley J.M., Heighway J.;  
 RT "Isolation and characterisation of a human homologue of the  
 RT latrophilin gene from a region of 1p31.1 implicated in breast  
 RT cancer.";  
 RL Oncogene 17:3513-3519(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20225451; PubMed=10760572;  
 RA White G.R.M., Varley J.M., Heighway J.;  
 RT "Genomic structure and expression profile of LPHH1, a 7TM gene  
 RT variably expressed in breast cancer cell lines.";  
 RL Biochim. Biophys. Acta 1491:75-92(2000).  
 DR EMBL; AJ244514; CAB60206.1; -;  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1112 MW; 06CC4C2720544724 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 NIL 7  
 DB 5 NIL 7

RESULT 19

Q9ESU5 PRELIMINARY; PRT; 10 AA.  
 ID Q9ESU5;  
 AC Q9ESU5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Fas death receptor (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C3H/He;  
 RX MEDLINE=20127858; PubMed=10660538;  
 RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,  
 RA Yonish-Rouach E., Reisdorf P.;  
 RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a  
 RT p53-responsive element that is activated by p53 mutants unable to  
 RT induce apoptosis.";  
 RL J. Biol. Chem. 275:3867-3872(2000).  
 DR EMBL; AF282865; AAG02410.1; -;  
 KW Receptor.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;  
 Query Match 33.3%; Score 3; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LPL 9  
 DB 8 LPL 10

RESULT 20  
 Q86580 PRELIMINARY; PRT; 10 AA.  
 ID Q86580;  
 AC Q86580;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Large protein (Fragment).  
 OS Simian parainfluenza virus 5.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.  
 OX NCBI\_TaxID=11207;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93224905; PubMed=8385701;  
 RA Higuchi Y., Miyahara Y., Kawano M., Tsurudome M., Matsumura H.,  
 RA Kusagawa S., Komada H., Nishio M., Ito Y.;  
 RT "Sequence analysis of the large (L) protein of simian virus 5.";  
 RL J. Gen. Virol. 74:789-789(1993).  
 DR EMBL; S57860; AAB26118.1; -;  
 FT NON TER 1 1  
 SQ SEQUENCE 10 AA; 1144 MW; 0C25A0D9C86776D4 CRC64;  
 Query Match 33.3%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QNI 6  
 DB 8 QNI 10

RESULT 21  
 Q47451 PRELIMINARY; PRT; 11 AA.  
 ID Q47451;  
 AC Q47451;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Plasmid pRJ1004 DNA (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PRJ1004;  
 RX MEDLINE=96130847; PubMed=8594334;  
 RA Brown N.L., Barrett S.R., Camakaris J., Lee B.T., Rouch D.A.;  
 RT "Molecular genetics and transport analysis of the copper-resistance  
 RT determinants (pcc) from Escherichia coli plasmid pRJ1004.";  
 RL Mol. Microbiol. 17:1153-1165(1995).  
 DR EMBL; X83541; CAA58524.1; -;  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1195 MW; 47D864F8ADCA1057 CRC64;  
  
 Query Match 33.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 NIL 7  
 DB 2 NIL 4  
  
 RESULT 22  
 Q47569 PRELIMINARY; PRT; 11 AA.  
 AC Q47569;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)  
 DE Hypothetical 1.3 kDa protein (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=N-12;  
 RX MEDLINE=94162733; PubMed=7764507;  
 RA Yamada M., Yanai S., Talkuder A.;  
 RT "Analysis of products of the Escherichia coli genomic genes and  
 RT regulation of their expressions: an applicable procedure for genomic  
 RT analysis of other microorganisms.";  
 RL Biosci. Biotechnol. Biochem. 58:117-120(1994).  
 DR EMBL; D21156; BAA04692.1; -;  
 KW Hypothetical protein.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1322 MW; C0B8E40E37672732 CRC64;  
  
 Query Match 33.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 7 LPL 9  
 DB 6 LPL 8  
  
 RESULT 23  
 Q9UELO PRELIMINARY; PRT; 11 AA.  
 AC Q9UELO;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE FAS antigen (CD95 antigen) (Fragment).  
 GN CD95.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=95355401; PubMed=7543095;  
 RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,  
 RA Nakanishi Y.;  
 RT "Transcription stimulation of the Fas-encoding gene by nuclear factor  
 RT for interleukin-6 expression upon influenza virus infection.";  
 RL J. Biol. Chem. 270:18007-18012(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Muschen M., Re D., Jungnickel B., Diehl V., Hansmann M.L., Diehl V.,  
 RA Kuppers R., Rajewsky K.;  
 RT "Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg  
 RT cells.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;  
 RT "Somatic mutations of the CD95 gene in human B cells as a side-effect  
 RT of the germinal center reaction.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22404279; PubMed=12516573;  
 RA Kurth J., Pernio A., Schmitz R., Iking-Konert C., Chiorazzi N.,  
 RA Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;  
 RT "Lack of deleterious somatic mutations in the CD95 gene of  
 RT plasmablasts from systemic lupus erythematosus patients and  
 RT autoantibody-producing cell lines.";  
 RL Eur. J. Immunol. 32:3785-3792(2002).  
 DR EMBL; D31968; BAA20850.1; -;  
 DR EMBL; AJ279011; CAC35539.1; -;  
 DR EMBL; AJ279012; CAC35540.1; -;  
 DR EMBL; AJ279013; CAC35541.1; -;  
 DR EMBL; AJ509179; CAD48929.1; -;  
 DR EMBL; AJ509180; CAD48930.1; -;  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;  
  
 Query Match 33.3%; Score 3; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 7 LPL 9  
 DB 8 LPL 10  
  
 RESULT 24  
 Q9TOB3 PRELIMINARY; PRT; 11 AA.  
 AC Q9TOB3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class I related protein 1 (Fragment).  
 GN MRI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98451457; PubMed=9780177;  
 RA Riegert P., Wanner V., Bahrman S.;  
 RT "Genomics, isoforms, expression, and phylogeny of the MHC class I-  
 RT related MRI gene.";  
 RL J. Immunol. 161:4066-4077(1998).  
 DR EMBL; AF039526; AAD02172.1; -;  
 FT NON\_TER 11 11

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SQ SEQUENCE 11 AA; 1235 MW; 5E71A31E29CDD697 CRC64;
Query Match 33.3%; Score 3; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
   |||
Db 9 LPL 11

RESULT 25
P82336
ID P82336 PRELIMINARY; PRT; 11 AA.
AC P82336;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SP07125) (Fragment).
OS Pisum sativum (Garden pea)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]_TaxID=3888;
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=99240351; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-342(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC PERIPHERY.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.8, ITS MW IS: 45.8 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1255 MW; 13511E6EDB1DDB10 CRC64;

Query Match 33.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNI 6
   |||
Db 8 QNI 10

RESULT 26
Q9WW72
ID Q9WW72 PRELIMINARY; PRT; 13 AA.
AC Q9WW72;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE VANS (Fragment).
GN VANSB.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]_TaxID=1351;
RP SEQUENCE FROM N.A.
RC STRAIN=TUH7-68, TUH1-75, TUH4-67, and TUH7-54;
RX MEDLINE=99240351; PubMed=10223921;
RA Dahl K.H., Simonsen G.S., Olsvik O., Sundsfjord A.;
RT "Heterogeneity in the vanB gene cluster of genomically diverse
RT clinical strains of vancomycin-resistant enterococci.";
RL Antimicrob. Agents Chemother. 43:1105-1110(1999).
DR EMBL; AF125553; AAD28596.1; -.
DR EMBL; AF125544; AAD28580.1; -.

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DR EMBL; AF125548; AAD28588.1; -.
DR EMBL; AF125551; AAD28592.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1518 MW; 8D0E282199B9672A CRC64;

Query Match 33.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
   |||
Db 7 LPL 9

RESULT 27
Q9X514
ID Q9X514 PRELIMINARY; PRT; 13 AA.
AC Q9X514;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE VANS (Fragment).
GN VANSB.
OS Enterococcus gallinarum.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1353;
RN [1]_TaxID=1353;
RP SEQUENCE FROM N.A.
RC STRAIN=TUH7-16;
RX MEDLINE=99240351; PubMed=10223921;
RA Dahl K.H., Simonsen G.S., Olsvik O., Sundsfjord A.;
RT "Heterogeneity in the vanB gene cluster of genomically diverse
RT clinical strains of vancomycin-resistant enterococci.";
RL Antimicrob. Agents Chemother. 43:1105-1110(1999).
DR EMBL; AF125550; AAD28590.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1518 MW; 8D0E282199B9672A CRC64;

Query Match 33.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
   |||
Db 7 LPL 9

RESULT 28
Q9WW71
ID Q9WW71 PRELIMINARY; PRT; 13 AA.
AC Q9WW71;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE VANS (Fragment).
GN VANSB.
OS Enterococcus faecium (Streptococcus faecium).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1352;
RN [1]_TaxID=1352;
RP SEQUENCE FROM N.A.
RC STRAIN=TUH7-55, TUH1-79, TUH2-18, and TUH4-54;
RX MEDLINE=99240351; PubMed=10223921;
RA Dahl K.H., Simonsen G.S., Olsvik O., Sundsfjord A.;
RT "Heterogeneity in the vanB gene cluster of genomically diverse
RT clinical strains of vancomycin-resistant enterococci.";
RL Antimicrob. Agents Chemother. 43:1105-1110(1999).
DR EMBL; AF125552; AAD28594.1; -.
DR EMBL; AF125545; AAD28582.1; -.
DR EMBL; AF125546; AAD28584.1; -.
DR EMBL; AF125547; AAD28586.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1518 MW; 8D0E282199B9672A CRC64;

```

Query Match 33.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9  
 |||  
 Db 7 LPL 9

## RESULT 29

Q8KHM6 PRELIMINARY; PRT; 13 AA.

AC Q8KHM6; 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Protein histidine kinase Vansb (Fragment).  
 GN VANSB.

OS Streptococcus gallolyticus.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=53354;  
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=4-C11, and 4-G10; TRANSPOSON=Tn5382-like;

RA Dahl K.H., Sundsfjord A.;

RT "vanB2 operons linked to Tn5382-like elements in Streptococcus strains from veal calves.";

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY035707; AAL07286.1; -.

DR EMBL; AY035708; AAL07290.1; -.

KW Kinase.

FT NON TER

SQ SEQUENCE 13 AA; 1518 MW; 8D0E282199B9672A CRC64;

Query Match 33.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9  
 |||  
 Db 7 LPL 9

## RESULT 30

Q8KRA4 PRELIMINARY; PRT; 13 AA.

AC Q8KRA4; 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)

DE Protein histidine kinase Vansb (Fragment).

GN VANSB.

OS Streptococcus lutetiensis.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI\_TaxID=150055;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=5-F9; TRANSPOSON=Tn5382-like;

RA Dahl K.H., Sundsfjord A.;

RT "vanB2 operons linked to Tn5382-like elements in Streptococcus strains from veal calves.";

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY035706; AAL07286.1; -.

KW Kinase.

FT NON TER

SQ SEQUENCE 13 AA; 1518 MW; 8D0E282199B9672A CRC64;

Query Match 33.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9  
 |||  
 Db 7 LPL 9

## RESULT 31

Q95925 PRELIMINARY; PRT; 13 AA.

AC Q95925; 01-FEB-1997 (TReMBLrel. 02, Created)

DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Cytochrome oxidase subunit 3 (Fragment).

GN COX3.

OS Porphyra purpurea.

OC Mitochondrion.

OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Porphyra.

OX NCBI\_TaxID=2787;

RN [1]

RP SEQUENCE FROM N.A.

RA Lang B.Franz., Goff L.J., Gray M.W.;

RT "A 5 S rRNA Gene is Present in the Mitochondrial Genome of the

RT Protist, Reclinomonas americana, but is Absent from Red Algal

RT Mitochondrial DNA.";

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U59763; AAB17951.1; -.

KW Mitochondrion.

FT NON TER

SQ SEQUENCE 13 AA; 1522 MW; 0831666D0B9C65B0 CRC64;

Query Match 33.3%; Score 3; DB 8; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
 |||  
 Db 1 SLP 3

## RESULT 32

Q945C1 PRELIMINARY; PRT; 13 AA.

AC Q945C1; 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Dip5 protein (Fragment).

OS Cryptocodinium cohnii (Dinoflagellate).

OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptocodiniaceae;

OC Cryptocodinium.

OX NCBI\_TaxID=2866;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21428164; PubMed=11545436;

RA Guillebault D., Derelle E., Bhaud Y., Moreau H.;

RT "Role of nuclear MW domains and proline-rich proteins in

RT dinoflagellate transcription.";

RL Protist 152:127-138(2001).

DR EMBL; AF417570; AAL15908.1; -.

FT NON TER

SQ SEQUENCE 13 AA; 1225 MW; 322FA05EE70CB327 CRC64;

Query Match 33.3%; Score 3; DB 10; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
 |||  
 Db 8 SLP 10

## RESULT 33

Q9WMG5  
ID Q9WMG5 PRELIMINARY; PRT; 13 AA.  
AC Q9WMG5;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
DE 3 protein (Fragment).  
GN GENE 3.  
OS Sigma virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Rhabdoviridae; unclassified Rhabdoviridae.  
OX NCBI\_TaxID=11301;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212481; PubMed=8384742;  
RA Teninges D., Bras F., Dezelee S.;  
RT "Genome organization of the sigma rhabdovirus: six genes and a gene overlap."  
RT overlap."  
RL Virology 193:1018-1023(1993).  
DR EMBL; S57850; AAD40700.1; -.  
FT NON TER 13  
SQ SEQUENCE 13 AA; 1456 MW; 9AFAF3FDE75E32D5 CRC64;  
Query Match 33.3%; Score 3; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 LPL 9  
Db 8 LPL 10  
RESULT 34  
P82881  
ID P82881 PRELIMINARY; PRT; 13 AA.  
AC P82881;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Tempurin-1CB.  
OS Rana clamitans (green frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.  
OX NCBI\_TaxID=145282;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin;  
RX MEDLINE=20283865; PubMed=10822101;  
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;  
RT "Purification and characterization of antimicrobial peptides from the skin of the North American green frog Rana clamitans."  
RT Peptides 21:469-476(2000).  
RL Peptides 21:469-476(2000).  
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM S. AUREUS.  
CC -!- SUBCELLULAR LOCATION: SECRETED.  
CC -!- MASS SPECTROMETRY: MW=1430.0; MW ERR=0.02; METHOD=ELECTROSPRAY.  
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN FAMILY.  
KW Antibiotic; Amidation.  
FT MOD RES 13  
SQ SEQUENCE 13 AA; 1432 MW; C4A71A765A8935BD CRC64;  
Query Match 33.3%; Score 3; DB 13; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 LPL 9  
Db 2 LPL 4  
RESULT 35  
P82830  
ID P82830 PRELIMINARY; PRT; 13 AA.  
AC P82830;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Tempurin-1LA.  
OS Rana luteiventris.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.  
OX NCBI\_TaxID=58176;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=SKIN;  
RX MEDLINE=20117700; PubMed=10651828;  
RA Corlay J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E., Conlon J.M.;  
RT "Peptides with antimicrobial activity from four different families isolated from the skins of the North American frogs Rana luteiventris, Rana berlandieri and Rana pipiens."  
RT Rana berlandieri and Rana pipiens."  
RL Eur. J. Biochem. 267:894-900(2000).  
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM S. AUREUS.  
CC -!- MASS SPECTROMETRY: MW=1366.8; METHOD=ELECTROSPRAY.  
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN FAMILY.  
KW Antibiotic; Amidation.  
FT MOD RES 13  
SQ SEQUENCE 13 AA; 1368 MW; 92541A7649A3D685 CRC64;  
Query Match 33.3%; Score 3; DB 13; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 LPL 9  
Db 2 LPL 4  
RESULT 36  
Q9R8K0  
ID Q9R8K0 PRELIMINARY; PRT; 14 AA.  
AC Q9R8K0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Major outer membrane protein (fragment).  
GN OMP-1.  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B4b;  
RA Hsieh Y.-H., Bobo L.D.;  
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia trachomatis in trachoma endemic villages, Kongwa, Tanzania."  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070297; AAC25267.1; -.  
FT NON TER 14  
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;  
Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 LPL 9  
Db 3 LPL 5  
RESULT 37  
Q9R8M4

```
ID Q9R8M4      PRELIMINARY;      PRT;      14 AA.
AC Q9R8M4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2f;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia
trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070261; AAC25231.1; -.
FT NON_TER 1
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match      33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
Db 3 LPL 5

RESULT 38
Q9R8L0
ID Q9R8L0      PRELIMINARY;      PRT;      14 AA.
AC Q9R8L0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2e;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia
trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070281; AAC25251.1; -.
FT NON_TER 1
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match      33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
Db 3 LPL 5

RESULT 39
Q9R8K7
ID Q9R8K7      PRELIMINARY;      PRT;      14 AA.
AC Q9R8K7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
```

```
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2f;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia
trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070285; AAC25255.1; -.
FT NON_TER 1
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match      33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
Db 3 LPL 5

RESULT 40
Q9R8M1
ID Q9R8M1      PRELIMINARY;      PRT;      14 AA.
AC Q9R8M1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2c;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia
trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070265; AAC25235.1; -.
FT NON_TER 1
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match      33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
Db 3 LPL 5

RESULT 41
Q9R8L8
ID Q9R8L8      PRELIMINARY;      PRT;      14 AA.
AC Q9R8L8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2d;
RA Hsieh Y.-H., Bobo L.D.;
```

RT "Diversity of major outer membrane protein (omp-1) of Chlamydia  
trachomatis in trachoma endemic villages, Kongwa, Tanzania.";  
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070269; AAC25239.1; -  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9

Db 3 LPL 5

#### RESULT 42

Q9R8K2 PRELIMINARY; PRT; 14 AA.  
AC Q9R8K2; (Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Major outer membrane protein (Fragment).  
GN OMP-1.  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B4;  
RA Hsieh Y.-H., Bobo L.D.;  
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia  
trachomatis in trachoma endemic villages, Kongwa, Tanzania.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070293; AAC25263.1; -  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9

Db 3 LPL 5

#### RESULT 43

Q9R8M7 PRELIMINARY; PRT; 14 AA.  
AC Q9R8M7; (Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Major outer membrane protein (Fragment).  
GN OMP-1.  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2;  
RA Hsieh Y.-H., Bobo L.D.;  
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia  
trachomatis in trachoma endemic villages, Kongwa, Tanzania.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070253; AAC25223.1; -  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9

Db 3 LPL 5

#### RESULT 44

Q9R8P2 PRELIMINARY; PRT; 14 AA.  
AC Q9R8P2; (Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Major outer membrane protein (Fragment).  
GN OMP-1.  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ref Ba;  
RA Hsieh Y.-H., Bobo L.D.;  
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia  
trachomatis in trachoma endemic villages, Kongwa, Tanzania.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070233; AAC25203.1; -  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1431 MW; 55D7E3FF812C06A7 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9

Db 3 LPL 5

#### RESULT 45

Q9R8J5 PRELIMINARY; PRT; 14 AA.  
AC Q9R8J5; (Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Major outer membrane protein (Fragment).  
GN OMP-1.  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B4;  
RA Hsieh Y.-H., Bobo L.D.;  
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia  
trachomatis in trachoma endemic villages, Kongwa, Tanzania.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070305; AAC25275.1; -  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9

Db 3 LPL 5



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Db          3 LPL 5
RESULT 46
O85527      PRELIMINARY;      PRT;      14 AA.
ID O85527;
AC O85527;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B3a;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070289; AAC25259.1; -.
FT NON_TER 1 14
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1399 MW; 39D7E3FF813466B7 CRC64;

Query Match      33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
Db 3 LPL 5

RESULT 47
Q9R8N6      PRELIMINARY;      PRT;      14 AA.
ID Q9R8N6;
AC Q9R8N6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B1a;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070241; AAC25211.1; -.
FT NON_TER 1 14
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match      33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
Db 3 LPL 5

RESULT 48
Q9R8M8      PRELIMINARY;      PRT;      14 AA.
ID Q9R8M8;
AC Q9R8M8;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B124a;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070249; AAC25219.1; -.
FT NON_TER 1 14
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match      33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
Db 3 LPL 5

RESULT 49
Q9R8L5      PRELIMINARY;      PRT;      14 AA.
ID Q9R8L5;
AC Q9R8L5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B24b;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070273; AAC25243.1; -.
FT NON_TER 1 14
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match      33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9
Db 3 LPL 5

RESULT 50
Q9R8J7      PRELIMINARY;      PRT;      14 AA.
ID Q9R8J7;
AC Q9R8J7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

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OX  NCBI_TaxID=813;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=B4c;
RA  Hsieh Y.-H., Bobo L.D.;
RT  "Diversity of major outer membrane protein (omp-1) of Chlamydia
RT  trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL  Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF070301; AAC2521.1; -.
FT  NON_TER 1
FT  NON_TER 14
SQ  SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9
Db 3 LPL 5

RESULT 51
Q9R8N2 ID Q9R8N2 PRELIMINARY; PRT; 14 AA.
AC Q9R8N2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B12a;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia
RT trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070245; AAC2521.1; -.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9
Db 3 LPL 5

RESULT 52
Q9R8P6 ID Q9R8P6 PRELIMINARY; PRT; 14 AA.
AC Q9R8P6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ref B;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia
RT trachomatis in trachoma endemic villages, Kongwa, Tanzania.";

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RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070229; AAC25199.1; -.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9
Db 3 LPL 5

RESULT 53
Q9R8M5 ID Q9R8M5 PRELIMINARY; PRT; 14 AA.
AC Q9R8M5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B24a;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia
RT trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070257; AAC2522.1; -.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPL 9
Db 3 LPL 5

RESULT 54
Q9R8N9 ID Q9R8N9 PRELIMINARY; PRT; 14 AA.
AC Q9R8N9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMP-1.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B;
RA Hsieh Y.-H., Bobo L.D.;
RT "Diversity of major outer membrane protein (omp-1) of Chlamydia
RT trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070237; AAC2520.1; -.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1415 MW; 55D7E3FF813466A7 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 14;

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Best Local Similarity 100.0%; Pred. No. 8.6e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0

QY 7 LPL 9  
|||  
DB 3 LPL 5

## RESULT 55

Q09061 Q09061 PRELIMINARY; PRT; 14 AA.  
AC Q09061;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE Hepatocyte growth factor activator (EC 3.4.21.-) (Serine protease) (Fragment).  
DE (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=FETAL SERUM;  
RX MEDLINE=93001906; PubMed=1368819;  
RA Shimomura T., Ochiai M., Kondo J., Morimoto Y.;  
RT "A novel protease obtained from FBS-containing culture supernatant, that processes single chain form hepatocyte growth factor to two chain form in serum-free culture.";  
RT Cytotechnology 8:219-229(1992).  
RL CC -!- FUNCTION: ACTIVATES HEPATOCYTE GROWTH FACTOR (HGF) BY CONVERTING IT FROM A SINGLE CHAIN TO A HETERODIMERIC FORM.  
CC -!- SUBUNIT: DIMER OF A SHORT CHAIN AND A LONG CHAIN LINKED BY A DISULFIDE BOND.  
CC -!- SUBCELLULAR LOCATION: SECRETED AS AN INACTIVE SINGLE-CHAIN PRECURSOR AND IS THEN ACTIVATED TO A HETERODIMERIC FORM.  
CC Hydrolase; Glycoprotein; Plasma; Serine protease; Zymogen.  
KW NON\_TER 14  
FT SEQUENCE 14 AA; 1395 MW; 9AFEE93979104A35 CRC64;  
SQ

Query Match 33.3%; Score 3; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
|||  
DB 7 SLP 9

## RESULT 56

Q09XJN4 Q09XJN4 PRELIMINARY; PRT; 14 AA.  
AC Q09XJN4;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE P10 (Fragment).  
OS Bacteriophage phi-9.  
OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.  
OX NCBI\_TaxID=90887;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99350412; PubMed=10419946;  
RA Mindich L., Qiao J., Onodera S., Romantschuk M.,  
RA Hoogstraaten D.;  
RT "Isolation of additional bacteriophages with genomes of segmented double-stranded RNA.";  
RL J. Bacteriol. 181:4505-4508(1999).  
DR EMBL: AF125678; AAD22559.1; -.  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1548 MW; 21AF9FA6CFD80E37 CRC64;

Query Match 33.3%; Score 3; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NIL 7  
|||  
DB 3 NIL 5

## RESULT 57

Q091777 Q091777 PRELIMINARY; PRT; 14 AA.  
AC Q091777;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE Hypothetical 1.6 kDa protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=90231335; PubMed=23300002;  
RA Kajimoto Y., Rotwein P.;  
RT "Evolution of insulin-like growth factor I (IGF-I): structure and expression of an IGF-I precursor from Xenopus laevis.";  
RL Mol. Endocrinol. 4:217-226(1990).  
DR EMBL: M29857; AAA70329.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 14 AA; 1627 MW; 3002F6B29B887BD7 CRC64;

Query Match 33.3%; Score 3; DB 13; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPQ 4  
|||  
DB 2 LPQ 4

## RESULT 58

Q09X637 Q09X637 PRELIMINARY; PRT; 15 AA.  
AC Q09X637;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Mert (Fragment).  
GN MERT.  
OS Klebsiella oxytoca.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=571;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=509H;  
RX MEDLINE=97208220; PubMed=9055422;  
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;  
RT "Phylogeny of mercury resistance (mer) operons of gram-negative bacteria isolated from the fecal flora of primates.";  
RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=509H;  
RX MEDLINE=98027386; PubMed=9361435;  
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
RT "Association of mercury resistance with antibiotic resistance in the gram-negative fecal bacteria of primates.";  
RL Appl. Environ. Microbiol. 63:4494-4503(1997).  
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN=509H;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
RL mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF131272; AAD37141.1; -.
DR InterPro: IPR003457; Transprt_MerT.
DR Pfam: PF02411; MerT; 1.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 33.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQN 5
DB 4 PQN 6

RESULT 59
QX635
ID Q9X635 PRELIMINARY; PRT; 15 AA.
AC Q9X635;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE MerT (Fragment).
GN MerT.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=390;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RL bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=390;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RL gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=390;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
RL mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF131271; AAD37139.1; -.
DR InterPro: IPR003457; Transprt_MerT.
DR Pfam: PF02411; MerT; 1.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1492 MW; 65BFCFC9827A585D CRC64;

Query Match 33.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQN 5
DB 4 PQN 6

RESULT 60

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Q9UMY6
ID Q9UMY6 PRELIMINARY; PRT; 15 AA.
AC Q9UMY6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE ABO glycosyltransferase (Fragment).
GN ABO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97318856; PubMed=9175793;
RA Olsson M.L., Guerreiro J.F., Zago M.A., Chester M.A.;
RT "Molecular analysis of the O alleles at the blood group ABO locus in
RL populations of different ethnic origin reveals novel crossing-over
RL events and point mutations.";
RL Biochem. Biophys. Res. Commun. 234:779-782 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Olsson M.L., Chester M.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF170890; AAD51650.1; -.
KW Transferase.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1762 MW; FB7670B69CC88D18 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3
DB 13 SLP 15

RESULT 61
Q9UC60
ID Q9UC60 PRELIMINARY; PRT; 15 AA.
AC Q9UC60;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE N-acetylmuramyl-L-alanine amidase (EC 3.5.1.28) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95392215; PubMed=7663175;
RA De Pauw P., Neyt C., Vanderwinkel E., Wattiez R., Palmagne P.;
RT "Characterization of human serum N-acetylmuramyl-L-alanine amidase
RL purified by affinity chromatography.";
RL Protein Expr. Purif. 6:371-378 (1995).
SQ SEQUENCE 15 AA; 1600 MW; 9016B00FF9E780A CRC64;

Query Match 33.3%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3
DB 1 SLP 3

RESULT 62
Q9TWR6
ID Q9TWR6 PRELIMINARY; PRT; 15 AA.
AC Q9TWR6;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Hemocyanin RH51 subunit (Fragment).  
 OS Rapana thomasi (Marine snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;  
 OC Neogastropoda; Muricoidae; Muricidae; Rapana.  
 OX NCBI\_TaxID=29165;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=94007762; PubMed=8403854;  
 RA Idakieva K., Severov S., Svendsen I., Genov N., Stoeva S.,  
 RA Beltramini M., Tognon G., Di Muro P., Salvato B.;  
 RT "Structural properties of Rapana thomasi glosse hemocyanin:  
 RT isolation, characterization and N-terminal amino acid sequence of two  
 RT different dissociation products.";  
 RL Comp. Biochem. Physiol. 108B:53-59(1993).  
 FT NON\_TER 1  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1735 MW; 78985413C9E90B6B CRC64;  
  
 Query Match 33.3%; Score 3; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 SLP 3  
 Db |||  
 1 SLP 3  
  
 RESULT 63  
 Q9T2K8 PRELIMINARY; PRT; 15 AA.  
 AC Q9T2K8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE LHCII kinase, 64 kDa kinase (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=92183823; PubMed=154419;  
 RA Gal A., Herrmann R.G., Lottspeich F., Ohad I.;  
 RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with  
 RT the cytochrome complex.";  
 RL FEBS Lett. 298:33-35(1992).  
 FT NON\_TER 1  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33E CRC64;  
  
 Query Match 33.3%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 ILP 8  
 Db |||  
 3 ILP 5  
  
 RESULT 64  
 Q8WK21 PRELIMINARY; PRT; 15 AA.  
 AC Q8WK21;  
 DT 01-MAY-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAY-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAY-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Putative proteolysis tag (Fragment).

OS Bolidomonas sp. OLI46SE.  
 OG Chloroplast.  
 OC Eukaryota; stramenopiles; Bolidophyceae; Bolidomonas.  
 OX NCBI\_TaxID=129302;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OLI46SE;  
 RA Williams K., Guillou L., Gueneau de Novoa P.;  
 RT "Small RNAs from non-green plastidial genomes.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF169626; AAL55606.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 15 AA; 1666 MW; OD578E9144198201 CRC64;  
  
 Query Match 33.3%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 NIL 7  
 Db |||  
 3 NIL 5  
  
 RESULT 65  
 Q9SAP4 PRELIMINARY; PRT; 15 AA.  
 AC Q9SAP4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Serine proteinase inhibitor (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Irish Cobbler;  
 RA Yamagishi K., Kikuta Y.;  
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X70376; CAA49837.1; -.  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1667 MW; 8093D41B4CA0D1EC CRC64;  
  
 Query Match 33.3%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 NIL 7  
 Db |||  
 5 NIL 7  
  
 RESULT 66  
 Q6S177 PRELIMINARY; PRT; 15 AA.  
 AC Q6S177;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Turgor responsive protein homolog (Fragment).  
 OS Mesembryanthemum crystallinum (Common ice plant).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.  
 OX NCBI\_TaxID=3544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Root;  
 RA Michalowski C.B., Bohnert H.J.;  
 RT "An expressed sequence tag from M. crystallinum.";

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF054444; AAC14178.1; -  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1607 MW; 4137ED0DF9B3FC21 CRC64;  
 Query Match 33.3%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LPL 9  
 DB 6 LPL 8

RESULT 67  
 P82331 PRELIMINARY; PRT; 15 AA.  
 AC P82331;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Unknown protein from 2nd page of thylakoid (SPOT114) (Fragment).  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
 OC NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
 RX MEDLINE=20181728; PubMed=10715320;  
 RA Pelier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
 RA Adamek I., van Wijk K.J.;  
 RT "Proteomics of the chloroplast: systematic identification and  
 targeting analysis of lumenal and peripheral thylakoid proteins.";  
 RL Plant Cell 12:319-341(2000).  
 CC -/- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR  
 CC PERIPHERY.  
 CC -/- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
 CC -/- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.7, ITS MW IS: 24.7 KDA.  
 KW Chloroplast; Thylakoid membrane.  
 FT DOMAIN 2 POLY-GLN.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 2000 MW; 2F1518C5051556D6 CRC64;  
 Query Match 33.3%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PQN 5  
 DB 8 PQN 10

RESULT 68  
 O30985 PRELIMINARY; PRT; 16 AA.  
 AC O30985;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Putative ammonia transporter (Fragment).  
 GN AMTB.  
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
 OC Rhodospirillaceae; Rhodospirillum.  
 OC NCBI\_TaxID=1063;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16PHC;  
 RX MEDLINE=98389683; PubMed=9721307;  
 RX Qian Y., Tabita F.R.;

RT "Expression of glnB and a glnB-like gene (glnK) in a ribulose  
 RT biphosphate carboxylase/oxygenase-deficient mutant of Rhodospirillum  
 RT rubrum.";  
 RL J. Bacteriol. 180:4644-4649(1998).  
 DR EMBL: AF023909; AAC34723.1; -  
 FT NON TER 16 16  
 SQ SEQUENCE 16 AA; 1812 MW; EDB859A962D6FEEA CRC64;  
 Query Match 33.3%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ILP 8  
 DB 12 ILP 14

RESULT 69  
 Q48387 PRELIMINARY; PRT; 16 AA.  
 AC Q48387;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribitol dehydrogenase rbtK (Fragment).  
 OS Klebsiella aerogenes.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OC NCBI\_TaxID=28451;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86050424; PubMed=2933028;  
 RA Loviny T., Norton P.M., Hartley B.S.;  
 RT "Ribitol dehydrogenase of Klebsiella aerogenes: Sequence of the  
 RT structural gene.";  
 RL Biochem. J. 230:579-585(1985).  
 DR EMBL: M25606; AAA25141.1; -  
 FT NON TER 16 16  
 SQ SEQUENCE 16 AA; 1657 MW; 3E240A779ABA6547 CRC64;  
 Query Match 33.3%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 QNI 6  
 DB 6 QNI 8

RESULT 70  
 Q52901 PRELIMINARY; PRT; 16 AA.  
 AC Q52901;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Nosy protein (Fragment).  
 GN NOSY.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium.  
 OC NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JJ1c10;  
 RX MEDLINE=96198150; PubMed=8626275;  
 RA Holloway P., McCormick W., Watson R.J., Chan Y.K.;  
 RT "Identification and analysis of the dissimilatory nitrous oxide  
 RT reduction genes, nosRZDFY, of Rhizobium meliloti.";  
 RL J. Bacteriol. 178:1505-1514(1996).  
 DR EMBL: U47133; AAC4026.1; -  
 FT NON TER 16 16  
 SQ SEQUENCE 16 AA; 1735 MW; 0CF7165CF62AA3B8 CRC64;

Query Match 33.3%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NIL 7  
 DB 3 NIL 5

RESULT 71  
 Q9NNZ2 PRELIMINARY; PRT; 16 AA.  
 AC Q9NNZ2;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
 DE Integrin alpha-2 subunit (Fragment).  
 GN ITGA2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98421383; PubMed=9746778;  
 RA Kritzik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,  
 RA Kunicki T.J.;  
 RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles  
 that are associated with differences in platelet alpha2 beta1  
 density.";  
 RL Blood 92:2382-2388(1998).  
 DR EMBL; AF062039; AAF77577.1; -.  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1635 MW; 6A5FC64F83370A9 CRC64;

Query Match 33.3%; Score 3; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9  
 DB 11 LPL 13

RESULT 72  
 Q8WXZ7 PRELIMINARY; PRT; 16 AA.  
 AC Q8WXZ7;  
 DT 01-MAR-2002 (TReMBLrel. 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Alpha-3-galactosylaminyltransferase (EC 2.4.1.40) (Fragment).  
 GN ABO.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2141478; PubMed=11520811;  
 RA Olsson M.L., Irshaid N.M., Hosseini-Maaf B., Hellberg A., Moulds M.K.,  
 RA Saraneva H., Chester M.A.;  
 RT "Genomic analysis of clinical samples with serologic ABO blood  
 grouping discrepancies: identification of 15 novel A and B subgroup  
 alleles.";  
 RL Blood 98:1585-1593(2001).  
 DR EMBL; AF324008; AAL37340.1; -.  
 KW Transferase; Glycosyltransferase.  
 FT NON TER 1  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1849 MW; 67BB7670F40CC8D CRC64;

Query Match 33.3%; Score 3; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
 DB 13 SLP 15

RESULT 73  
 Q8SL53 PRELIMINARY; PRT; 16 AA.  
 ID Q8SL53;  
 AC Q8SL53;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE PSBA (Fragment).  
 GN PSBA.  
 OS Aeonium hierrense.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Saxifragales; Crassulaceae; Aeonium.  
 OX NCBI\_TaxID=111151;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;  
 RT "Evolution and diversification of the Macaronesian clade of  
 Crassulaceae.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AY082204; AAM13948.1; -.  
 KW Chloroplast.  
 FT NON TER 1  
 SQ SEQUENCE 16 AA; 1652 MW; B08B1B6DAD4B853A CRC64;

Query Match 33.3%; Score 3; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9  
 DB 2 LPL 4

RESULT 74  
 Q9CW70 PRELIMINARY; PRT; 16 AA.  
 ID Q9CW70;  
 AC Q9CW70;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Adult male brain cDNA, RIKEN full-length enriched library,  
 DE clone:0710008B15, full insert sequence (fragment).  
 GN MAG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=Brain;  
 RC MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 403:685-690(2001).  
 DR EMBL; AK003029; BAB22519.1; -.  
 DR MGD; MGI:96912; Mag.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1867 MW; 65BB8C02CB69FDB5 CRC64;

Query Match 33.3%; Score 3; DB 11; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPL 9  
 |||  
 Db 7 LPL 9

## RESULT 75

Q918U2 PRELIMINARY; PRT; 16 AA.  
 AC Q918U2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE E1 protein (Fragment).  
 CN E1.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HPV16E2CC4;  
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
 RT "Sequence variation and physical state of human Papillomavirus type 16  
 cervical cancer isolates from Australia and New Caledonia."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF407217; AAL01397.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match 33.3%; Score 3; DB 12; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLP 3  
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 Db 1 SLP 3

Search completed: November 25, 2003, 18:25:45  
 Job time : 23.7362 secs



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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 29.1543 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-19

Perfect score: 9

Sequence: 1 SUPQNILPL 9

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	22	Colostrinin derive
2	9	100.0	9	22	Colostrinin peptid
3	9	100.0	9	22	Colostrinin peptid
4	9	100.0	9	22	Ewe colostrinin pe
5	9	100.0	9	23	Colostrinin consti
6	9	100.0	9	23	Colostrinin consti
7	9	100.0	9	23	Neural cell regula
8	7	77.8	7	11	Hypotensive peptid
9	6	66.7	19	21	Bioactive peptide

10	5	55.6	11	20	AAAY5198	STAT4 receptor pep
11	5	55.6	15	23	ABB83390	Human cell death r
12	5	55.6	23	23	ABG32207	Sheep colostrinin
13	4	44.4	6	20	AAAY2449	Monoclonal antibod
14	4	44.4	6	22	AAE09148	Bacteriophage pept
15	4	44.4	7	20	AAAY3141	Amino acid sequenc
16	4	44.4	7	21	AAAY8475	Uteroglobulin inter
17	4	44.4	8	19	AAW33806	Monoclonal antibod
18	4	44.4	8	20	AAAY2448	Human peptide #208
19	4	44.4	8	22	AAW98813	Human leucocyte an
20	4	44.4	9	17	AAW49282	HLA binding plu-1
21	4	44.4	9	20	AAAY5419	HLA binding plu-1
22	4	44.4	9	20	AAAY55430	Immunogenic peptid
23	4	44.4	9	20	AAAY46572	Human B99-2 HLA A1
24	4	44.4	9	21	AAAB45575	Human B99-2 HLA A*
25	4	44.4	9	21	AAAB45576	HIV A02 super moti
26	4	44.4	9	22	ABP13308	HIV A24 super moti
27	4	44.4	9	22	ABP15936	HIV B62 super moti
28	4	44.4	9	22	ABP18996	HIV peptide SEQ ID
29	4	44.4	9	22	AAAM2210	Porcine endogenous
30	4	44.4	9	23	AAO19008	N. meningitidis LO
31	4	44.4	9	23	ABP47492	Phosphopeptide #2
32	4	44.4	9	23	AAE20459	MHC binding peptid
33	4	44.4	9	24	ABJ20132	HLA protein 121P2A
34	4	44.4	9	24	ABP83653	HLA protein 121P2A
35	4	44.4	9	24	ABP83703	HLA protein 121P2A
36	4	44.4	9	24	ABP84035	HLA protein 121P2A
37	4	44.4	9	24	ABP84289	HLA protein 121P2A
38	4	44.4	9	24	ABP84573	HLA protein 121P2A
39	4	44.4	9	24	ABP84587	HLA protein 121P2A
40	4	44.4	9	24	ABP85175	HLA protein 121P2A
41	4	44.4	9	24	ABP85517	HLA protein 121P2A
42	4	44.4	9	24	ABP85775	HLA protein 121P2A
43	4	44.4	9	24	ABP85776	HLA protein 121P2A
44	4	44.4	9	24	ABP85857	HLA protein 121P2A
45	4	44.4	9	24	ABP86000	HLA protein 121P2A
46	4	44.4	9	24	ABP86064	HLA protein 121P2A
47	4	44.4	9	24	ABP86202	HLA protein 121P2A
48	4	44.4	9	24	ABP86278	HLA protein 121P2A
49	4	44.4	9	24	ABP86279	HLA protein 121P2A
50	4	44.4	9	24	ABP86394	HLA protein 121P2A
51	4	44.4	9	24	ABP86425	HLA protein 121P2A
52	4	44.4	9	24	ABP86449	HLA protein 121P2A
53	4	44.4	9	24	ABP86650	HLA protein 121P2A
54	4	44.4	9	24	ABP86679	HLA protein 121P2A
55	4	44.4	9	24	ABP86764	HLA protein 121P2A
56	4	44.4	9	24	ABP86870	HLA protein 121P2A
57	4	44.4	9	24	ABP86902	HLA protein 121P2A
58	4	44.4	9	24	ABP86978	HLA protein 121P2A
59	4	44.4	9	24	ABP87159	HLA protein 121P2A
60	4	44.4	9	24	ABP87242	HLA protein 121P2A
61	4	44.4	9	24	ABP87320	HLA protein 121P2A
62	4	44.4	9	24	ABP87402	HLA protein 121P2A
63	4	44.4	9	24	ABP87403	HLA protein 121P2A
64	4	44.4	9	24	ABP87537	HLA protein 121P2A
65	4	44.4	9	24	ABP87705	HLA protein 121P2A
66	4	44.4	9	24	ABP87729	HLA protein 121P2A
67	4	44.4	9	24	ABP87761	HLA protein 121P2A
68	4	44.4	9	24	ABP87883	HLA protein 121P2A
69	4	44.4	9	24	ABP87884	HLA protein 121P2A
70	4	44.4	9	24	ABP87956	HLA protein 121P2A
71	4	44.4	9	24	ABP88213	HLA protein 121P2A
72	4	44.4	9	24	ABP88298	HLA protein 121P2A
73	4	44.4	9	24	ABP88299	HLA protein 121P2A
74	4	44.4	9	24	ABP88346	HLA protein 121P2A
75	4	44.4	9	24	ABP88410	HLA protein 121P2A
76	4	44.4	9	24	ABP88411	HLA protein 121P2A
77	4	44.4	9	24	ABP88502	HLA protein 121P2A
78	4	44.4	9	24	ABP88651	HLA protein 121P2A
79	4	44.4	9	24	ABP88743	HLA protein 121P2A
80	4	44.4	9	24	ABP88744	HLA protein 121P2A
81	4	44.4	9	24	ABP88849	HLA protein 121P2A
82	4	44.4	9	24	ABP88850	HLA protein 121P2A

83 4 44.4 9 24 ABP88947 HLA protein 121P2A  
84 4 44.4 9 24 ABP88983 HLA protein 121P2A  
85 4 44.4 9 24 ABP89273 HLA protein 121P2A  
86 4 44.4 9 24 ABP89274 HLA protein 121P2A  
87 4 44.4 9 24 ABP89320 HLA protein 121P2A  
88 4 44.4 9 24 ABP89357 HLA protein 121P2A  
89 4 44.4 9 24 ABP89634 HLA protein 121P2A  
90 4 44.4 9 24 ABP89635 HLA protein 121P2A  
91 4 44.4 9 24 ABP89684 HLA protein 121P2A  
92 4 44.4 9 24 ABP89764 HLA protein 121P2A  
93 4 44.4 9 24 ABP89765 HLA protein 121P2A  
94 4 44.4 9 24 ABP90031 HLA protein 121P2A  
95 4 44.4 9 24 ABP90032 HLA protein 121P2A  
96 4 44.4 9 24 ABP90055 HLA protein 121P2A  
97 4 44.4 9 24 ABP90056 HLA protein 121P2A  
98 4 44.4 9 24 ABP90169 HLA protein 121P2A  
99 4 44.4 9 24 ABP90227 HLA protein 121P2A  
100 4 44.4 9 24 ABP90387 HLA protein 121P2A

ALIGNMENTS

RESULT 1  
AAB72264  
ID AAB72264 standard; peptide; 9 AA.  
XX  
AC AAB72264;  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Colostrinin derived cytokine inducing peptide SEQ ID 19.  
XX  
KW Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.  
XX  
OS Synthetic.  
XX  
PN WO20011937-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US22818.  
XX  
PR 17-AUG-1999; 99US-0149311.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (REG-) REGEN THERAPEUTICS PLC.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX  
DR WPI; 2001-202804/20.  
XX  
PT Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator -  
XX  
PS Claim 1; Page 34; 50pp; English.  
XX  
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The  
CC peptides have immune response modulatory activity, and are capable of  
CC inducing cytokines. Colostrinin and its derived peptides are useful for  
CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.

XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 9; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLPQNILPL 9  
Db 1 SLPQNILPL 9  
RESULT 2  
AAB72517  
ID AAB72517 standard; Peptide; 9 AA.  
XX  
AC AAB72517;  
XX  
DT 09-MAY-2001 (first entry)  
XX  
DE Colostrinin peptide #18.  
XX  
KW Dermatological; oxidative stress regulator; colostrinin.  
XX  
OS Unidentified.  
XX  
PN WO200112650-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US22665.  
XX  
PR 17-AUG-1999; 99US-0149310.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I;  
XX  
DR WPI; 2001-218342/22.  
XX  
PT Modulating oxidative stress level in a cell, involves contacting the  
PT cell with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations -  
XX  
PS Claim 6; Page 25; 48pp; English.  
XX  
CC The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidising species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient.  
XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 9; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLPQNILPL 9  
Db 1 SLPQNILPL 9  
RESULT 3  
AAB72549  
ID AAB72549 standard; Peptide; 9 AA.  
XX  
AC AAB72549;  
XX  
DT 09-MAY-2001 (first entry)  
XX

DE Colostrinin peptide #18.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 PN  
 XX  
 XX 22-FEB-2001.  
 PD  
 XX  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX  
 XX Boldogh I;  
 PI  
 XX  
 XX WPI; 2001-226545/23.  
 DR  
 XX  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 CC  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 100.0%; Score 9; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQNILPL 9  
 Db |||||  
 1 SLPQNILPL 9

RESULT 4  
 AAB59327  
 ID AAB59327 standard; Peptide; 9 AA.  
 XX  
 XX AAB59327;  
 AC  
 XX 21-MAR-2001 (first entry)  
 DT  
 XX Ewe colostrinin peptide fragment C-2.  
 DE  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 XX Ovis sp.  
 OS  
 XX WO200075173-A2.  
 PN  
 XX  
 XX 14-DEC-2000.  
 PD  
 XX  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF  
 XX  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI  
 XX WPI; 2001-071058/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 XX Claim 7; Page 27; 63pp; English.  
 PS  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 100.0%; Score 9; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQNILPL 9  
 Db |||||  
 1 SLPQNILPL 9

RESULT 5  
 AAE20246  
 ID AAE20246 standard; peptide; 9 AA.  
 XX  
 XX AAE20246;  
 AC  
 XX 18-JUN-2002 (first entry)  
 DT  
 XX Colostrinin constituent peptide #18.  
 DE  
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnery.  
 XX  
 XX Unidentified.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 9  
 FT /note= "Optionally C-terminal amide"  
 FT  
 XX WO200213850-A1.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2000; 2000WO-US22776.  
 PF  
 XX 17-AUG-2000; 2000WO-US22776.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 PI  
 XX WPI; 2002-269151/31.  
 DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 XX Claim 6; Page 25; 51pp; English.  
 PS  
 XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQNILPL 9  
 |||||  
 Db 1 SLPQNILPL 9

RESULT 6

AAM51053  
 ID AAM51053 standard; Peptide; 9 AA.

XX AC AAM51053;

DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide (casein amino acids 84-92).

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;

XX KW blood cell regulator; cytokine inducer; beta-casein; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 9

FT /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PA (REG-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX DR WPI; 2002-269150/31.

XX PT Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue

XX PS Claim 1; Page 34; 54pp; English.

XX CC The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. It is  
 CC classified as having a beta-casein homologue precursor, and  
 CC corresponds to casein amino acids 84-92. Methods are claimed for:  
 CC inducing a cytokine in a cell by contact with an immunological  
 CC regulator, where the cell is present in a cell culture, a tissue,  
 CC an organ or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide. Cytokines  
 CC induced by this peptide in human-leucocyte cultures include  
 CC interferon-gamma, tumour necrosis factor-alpha, interleukin-4 and  
 CC interleukin-10.

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQNILPL 9  
 |||||  
 Db 1 SLPQNILPL 9

RESULT 7

AAO14595

ID AAO14595 standard; peptide; 9 AA.

XX AC AAO14595;

XX DT 27-MAY-2002 (first entry)

XX DE Neutral cell regulatory colostrinin peptide 18.

XX KW Neutral cell differentiation; neural cell regulator; colostrinin peptide;

XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 9

FT /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX DR WPI; 2002-269152/31.

XX PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog

XX PS Claim 7; Page 21; 37pp; English.

XX CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the

CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.

SQ Sequence 9 AA;  
 Query Match 100.0%; Score 9; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQNILPL 9  
 |||||  
 Db 1 SLPQNILPL 9

RESULT 8  
 AAR03864  
 ID AAR03864 standard; Protein; 7 AA.  
 XX AC AAR03864;  
 XX DT 17-FEB-1993 (first entry)  
 XX DE Hypotensive peptide (3).  
 XX KW Hypotensor; salt.  
 XX OS Synthetic.  
 XX PN JP02062828-A.  
 XX PD 02-MAR-1990.  
 XX PF 26-AUG-1988; 88JP-0211696.  
 XX PR 26-AUG-1988; 88JP-0211696.  
 XX PA (AJIN ) AJINOMOTO KK.  
 XX DR WPI; 1990-111933/15.  
 XX PT New peptide used as active ingredient of hypotensive agent -  
 PT which may be prepd. e.g. as tablets, capsules, powder, syrup,  
 PT injection prepn. etc.  
 XX PS Claim; Page ?; 9pp; Japanese.  
 XX CC The peptides given in AAR03862-76 and their salts can be used as  
 CC components of hypotensive agents.  
 CC CC The hypotensor may be in the form of tablets, capsules, powder,  
 CC syrup or injection prepn. contg. 0.001-1000 mg, esp. 0.01-10 mg of  
 CC the peptide.

SQ Sequence 7 AA;  
 Query Match 77.8%; Score 7; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPQNILP 8  
 |||||  
 Db 1 LPQNILP 7

RESULT 9  
 AAY69542  
 ID AAY69542 standard; peptide; 19 AA.  
 XX AC AAY69542;  
 XX DT 19-APR-2000 (first entry)  
 XX

DE Bioactive peptide #8 from whey protein hydrolysate.  
 XX Whey protein hydrolysate; bioactive peptide; non bitter flavour;  
 KW food product; digestible; hypotensive.  
 XX OS Unidentified.  
 XX PN WO9965326-A1.  
 XX PD 23-DEC-1999.  
 XX PF 14-JUN-1999; 99WO-NZ00084.  
 XX PR 17-JUN-1998; 98NZ-0330710.  
 XX PA (NZDA-) NEW ZEALAND DAIRY BOARD.  
 XX PI Schlothauer R, Schollum LM, Singh AM, Reid JR;  
 XX DR WPI; 2000-116705/10.  
 XX PT Preparation of whey protein hydrolysate containing bioactive peptides  
 PT but does not have bitter flavor -  
 XX PS Claim 19; Page 21; 32pp; English.

XX CC Sequences AAY69535-V69536 represent bioactive peptides which are  
 CC components of whey protein hydrolysate. The invention relates to the  
 CC preparation of whey protein hydrolysate containing such bioactive  
 CC peptides by treating a whey protein containing substrate with one or more  
 CC enzymes capable of hydrolysing whey proteins to produce the whey protein  
 CC hydrolysate containing bioactive peptides, and terminating the hydrolysis  
 CC before substantial production of unacceptable bitter flavours. The  
 CC invention also encompasses a non bitter product produced by partial  
 CC hydrolysis of a substrate containing whey proteins, where the product  
 CC comprises bioactive peptides and has a degree of hydrolysis of the whey  
 CC proteins of below 10%, a food product containing the non bitter product,  
 CC any one or a combination of two or more of the bioactive peptides of the  
 CC invention, and a method for reducing systolic blood pressure in a patient  
 CC which comprises administering the non bitter product to the patient. The  
 CC peptides, products and food products are useful in a method for the  
 CC reduction of systolic blood pressure. The whey protein products are free  
 CC from bitter flavours and contain bioactive peptides. The products of the  
 CC process have high digestibility and good organoleptic properties. The  
 CC products may have bland or slightly sweet taste and are free of soapy  
 CC and/or brothy flavours.

SQ Sequence 19 AA;  
 Query Match 66.7%; Score 6; DB 21; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.8;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQNI 6  
 |||||  
 Db 12 SLPQNI 17

RESULT 10  
 AAY45198  
 ID AAY45198 standard; peptide; 11 AA.  
 XX AC AAY45198;  
 XX DT 05-JAN-2000 (first entry)  
 XX DE STAT4 receptor peptide #6.  
 KW STAT4; STAT6; receptor peptide; binding; screening; modulator;  
 KW identification; cellular promoter; phosphotyrosine; autoimmune disease;  
 KW immune response; signal transduction; gene expression; allergy; asthma;  
 KW anaphylaxis; atopic dermatitis; multiple sclerosis; diabetes mellitus;  
 KW rheumatoid arthritis; cellular response; growth factor; cytokine;

KW hormone.  
 XX Synthetic.  
 OS WO950283-A1.  
 XX PD 07-OCT-1999.  
 XX PF 30-MAR-1999; 99WO-US07052.  
 XX PR 31-MAR-1998; 98US-0053003.  
 XX PA (TULA-) TULARIK INC.  
 XX PI Wu P, McKinney J;  
 XX DR WPI; 1999-610835/52.  
 XX PT New peptides containing phosphotyrosine that bind with high affinity to  
 PT STAT 4 or 6, used to identify modulators of binding between STAT and  
 PT its receptor, e.g. for treating autoimmune disease -  
 XX Claim 11; Page 40; 53pp; English.  
 XX The present invention describes peptides (A) that bind to STAT (signal  
 CC transducer and activator of transcription)-4 or -6 when they contain a  
 CC phosphorylated tyrosine residue. Peptides that bind to STAT6 include  
 CC sequence (I) and those that bind to STAT4 contain sequences (II) or  
 CC (III): YK 1X 2X 3 (I); YDP2 3 (II); GYDMPHVL (III); where X<sub>1</sub> = K, V,  
 CC R, I, M or a first non-natural amino acid (Z<sub>1</sub>); X<sub>2</sub> = P, A or S;  
 CC X<sub>3</sub> = W, Y, F, H, L or a second non-natural amino acid (Z<sub>2</sub>); (I) does  
 CC not include the sequence YKPF. Z<sub>3</sub> = Q, H, N or W. STAT4/6 are involved  
 CC in activation and differentiation of lymphocytes and in the transmission  
 CC of signals (generated by binding of cytokines to their receptors) to the  
 CC nucleus, so that modulation of these activities allows control over the  
 CC immune response. (A) are used to identify specific modulators of the  
 CC binding of STAT4 or 6 to their receptors. The modulators are used to  
 CC study mechanisms of signal transduction, for control of gene expression  
 CC for production of recombinant proteins and particularly as lead  
 CC compounds for developing drugs for treatment and prevention of  
 CC autoimmune diseases, allergy, asthma, anaphylaxis, atopic dermatitis,  
 CC multiple sclerosis, diabetes mellitus, rheumatoid arthritis or other  
 CC conditions involving cellular responses to growth factors, cytokines or  
 CC hormones. AAY45189 to AAY45201 represent specifically claimed examples of  
 CC (A).  
 XX SQ Sequence 11 AA;  
 Query Match 55.6%; Score 5; DB 20; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPQNI 6  
 |||||  
 Db 6 LPQNI 10  
 RESULT 11  
 ABB83390  
 ID ABB83390 standard; Peptide; 15 AA.  
 XX AC ABB83390;  
 XX DT 06-SEP-2002 (first entry)  
 XX Human cell death related protein 11.99 peptide fragment.  
 DE Human; cell death related protein 11.99; embryonic development deformity;  
 KW autoimmune disease; tumour; cytostatic; anti-senility.  
 KW Homo sapiens.  
 OS CN1333266-A.  
 XX PN

XX 30-JAN-2002.  
 XX 07-JUL-2000; 2000CN-0117073.  
 XX 07-JUL-2000; 2000CN-0117073.  
 XX (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.  
 XX Mao Y, Xie Y;  
 XX WPI; 2002-305586/35.  
 XX New human cell death related protein 11.99 and encoding polynucleotide,  
 PT useful for treating autoimmune disease and tumor -  
 XX Example 5; Page 20 (Disclosure); 34pp; Chinese.  
 XX The present invention relates to human cell death related protein 11.99  
 CC (see ABB83389). The protein is useful for treating embryonic development  
 CC deformity, autoimmune disease, tumour and for research of anti-senility.  
 CC The present sequence is an N-terminal peptide fragment of the protein,  
 CC which was used in an example from the invention.  
 XX SQ Sequence 15 AA;  
 Query Match 55.6%; Score 5; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 NILPL 9  
 |||||  
 Db 2 NILPL 6  
 RESULT 12  
 ABBG32207  
 ID ABBG32207 standard; peptide; 16 AA.  
 XX AC ABBG32207;  
 XX DT 05-NOV-2002 (first entry)  
 XX Sheep colostrinin derived peptide #1.  
 DE Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia;  
 KW central nervous system disorder; neurological disorder; neurosis;  
 KW mental disorder; psychosis; neurodegenerative disorder;  
 KW Alzheimer's disease; motor neuron disease; immune system disorder;  
 KW acquired immunological deficiency; bacterial infection; viral infection;  
 KW amyloid plaque; dietary supplement; cachexia; weight loss;  
 KW senile dementia; Parkinson's disease; emotional disturbance; depression;  
 KW drug addiction; drug withdrawal.  
 XX OS Ovis aries.  
 XX WO200246211-A2.  
 XX PD 13-JUN-2002.  
 XX 05-DEC-2001; 2001WO-GB05376.  
 XX 06-DEC-2000; 2000GB-0029777.  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 XX Georgiades JA;  
 XX WPI; 2002-619016/66.  
 XX Novel peptides isolated from colostrinin polypeptide, useful for  
 PT treating viral and bacterial infections, disorders of immune system and  
 PT central nervous system e.g., Alzheimer's disease, dementia, and as food

PT additive -  
 XX  
 PS Claim 1; Page 8; 16pp; English.  
 XX  
 CC The invention relates to a peptide derived from colostrinin (a colostrum  
 CC protein known to be a cytokine inducer) substantially entirely consists  
 CC of the peptide sequences appearing as ABG32207-ABG32223. Also included  
 CC are a composition comprising two or more of the peptides in combination  
 CC with a carrier, a dietary supplement comprising an orally ingestible  
 CC combination of the peptide in combination with a carrier and an antibody  
 CC which binds to the peptide, and which is obtainable by using peptide as  
 CC an antigen. The peptide is useful as a medicament for treating chronic  
 CC disorders of central nervous system e.g., neurological disorders and/or  
 CC mental disorders such as psychosis and/or neurosis, dementia,  
 CC neurodegenerative disorders such as Alzheimer's disease, motor  
 CC neuron disease, chronic disorders of immune system, diseases  
 CC with bacterial and viral etiology, acquired immunological deficiencies,  
 CC chronic bacterial, viral infections. The peptide is also useful for  
 CC treating diseases characterised by presence of amyloid plaque. The  
 CC peptide is also useful as a dietary supplement for babies, small  
 CC children, adults who have been subjected to chemotherapy and/or  
 CC adults who have suffered from cachexia or weight loss due to chronic  
 CC disease. The peptide is also useful for treating senile dementia,  
 CC Parkinson's disease, emotional disturbances and depression. The peptides  
 CC may also be used as an auxiliary withdrawal treatment for drug addicts,  
 CC after a period of detoxification, and in persons dependent on stimulants.  
 CC The present sequence is a colostrinin derived peptide of the invention.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 55.6%; Score 5; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQN 5  
 Db 12 SLPQN 16  
 RESULT 13  
 AAY24449  
 ID AAY24449 standard; peptide; 6 AA.  
 AC AAY24449;  
 XX  
 DT 27-SEP-1999 (first entry)  
 XX  
 DE Monoclonal antibody MAB 384 epitope SEQ ID NO:2.  
 XX  
 KW Monoclonal antibody; epitope; multiplexed analysis; diagnosis;  
 KW genetic analysis; flow cytometry; human myelin basic protein; MBP;  
 KW microbial antigen; viral antigen; pathological condition.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 OS Homo sapiens.  
 XX  
 PN WO9936564-A1.  
 XX  
 PD 22-JUL-1999.  
 XX  
 PF 15-JAN-1999; 99WO-US000918.  
 XX  
 PR 16-JAN-1998; 98US-0008387.  
 XX  
 PA (LUMI-) LUMINEX CORP.  
 XX  
 PI Chandler MB, Chandler VS, Fulton JR;  
 XX  
 DR WPI; 1999-444409/37.  
 XX  
 PT Beadset for simultaneous detection of many analytes by flow  
 PT cytometry, e.g. for detecting antigens, antibodies, or nucleic acid

PT mutations  
 XX  
 PS Example; Page 56; 301pp; English.  
 XX  
 CC The present invention describes a beadset (A), able to detect many  
 CC analytes (I) in a single sample by flow cytometry (FC). (A) is produced  
 CC by: (i) providing many subsets of beads which, within each subset, are  
 CC homogeneous as regards at least 3 selected class parameters (C) but  
 CC sufficiently different in at least one C from beads in other subsets to  
 CC provide a profile of C values unique for each subset in FC; (ii)  
 CC coupling the beads in each subset with a reactant (R), specific for a  
 CC given (I) and (iii) mixing the subsets to form an (A) in which subsets  
 CC (and thus bound R) are identifiable in FC from the unique profile of C.  
 CC A method of flow cytometry analysis using (A) is used to detect a very  
 CC wide range of (I), e.g. microbial or viral antigens (particularly from  
 CC pathogens that cause venereal, pulmonary or gastrointestinal disease);  
 CC therapeutic or illicit drugs; antigens or antibodies associated with  
 CC particular pathological conditions (malignancy, allergy, autoimmune  
 CC disease, blood-borne viruses or cardiovascular disease); hormones,  
 CC including those indicative of pregnancy; enzymes; immunoglobulins (Ig),  
 CC particularly of different subclasses; Ig that form part of a  
 CC particular epitope (specifically an epitope of human immune deficiency  
 CC virus) or nucleic acids (particularly for detecting a wide variety of  
 CC mutations, e.g. those present in the ret proto-oncogene, the low density  
 CC lipoprotein receptor, the Duchenne muscular dystrophy, angiotensin p53,  
 CC and Rb genes. The process is particularly used for diagnosis of disease  
 CC and for genetic analysis. The present sequence represents a monoclonal  
 CC antibody MAB 384 epitope used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 44.4%; Score 4; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 Db 3 SLPQ 6  
 RESULT 14  
 AAE09148  
 ID AAE09148 standard; peptide; 6 AA.  
 AC AAE09148;  
 XX  
 DT 15-NOV-2001 (first entry)  
 XX  
 DE Bacteriophage peptide #19, used in the invention.  
 XX  
 KW Vaccine; therapy; autoimmune disorder; Epstein-Barr virus; EBV; anaemia;  
 KW polymyositis; systemic lupus erythematosus; SLE; rheumatoid arthritis;  
 KW Sjogren's syndrome; diabetes mellitus; adenitis; multiple sclerosis;  
 KW demyelinating disease; Hashimoto's thyroiditis; autoimmune infertility;  
 KW hypoparathyroidism; primary biliary cirrhosis; ankylosing spondylitis;  
 KW inflammatory bowel disease; Addison's disease; thyroiditis; filariasis;  
 KW Graves' disease; ulcerative colitis; dermatomyositis; myasthenia gravis;  
 KW Crohn's disease; CREST syndrome; autoimmune cystitis; glomerulonephritis;  
 KW polyarteritis nodosa; hepatitis; atopic rhinitis; Goodpasture's syndrome;  
 KW sarcoidosis; rheumatic fever; anti-phospholipid syndrome; farmer's lung;  
 KW Cushing's syndrome; bird-fancier's lung; alveolitis; erythema nodosum;  
 KW pyoderma gangrenosum; fibromyalgia; Kawasaki's disease; cardiomyopathy;  
 KW Sampter's syndrome; asthma; polymyalgia rheumatica; psoriasis; arteritis;  
 KW erythroblastosis foetalis; cycloitis; IGA nephropathy; Hodgkin's lymphoma;  
 KW renal cell carcinoma; eosinophilia; immunosuppressive; ophthalmological;  
 KW thymimetic; neuroprotective; cytostatic; nephrotropic; antiallergic;  
 KW dengue; antiulcer; vasotropic; antipyretic; hepatotropic.  
 XX  
 OS Bacteriophage.  
 XX  
 PN WO200159481-A2.  
 XX

PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US04191.  
 XX  
 PR 09-FEB-2000; 2000US-0500904.  
 XX  
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX  
 PI Harley JB, James JA, Kaufman KM;  
 XX  
 XX WPI; 2001-522437/57.  
 DR  
 XX Novel vaccine for alleviating or preventing autoimmune disorders  
 PT induced Epstein-Barr virus (EBV) infection e.g. systemic lupus  
 PT erythematosus, juvenile onset diabetes mellitus, comprises EBV virus or  
 PT its component -  
 XX  
 XX Example 10; Page 56; 114pp; English.  
 XX  
 XX The present invention relates to a vaccine for alleviating or preventing  
 CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV),  
 CC comprising EBV or its component in a carrier. The vaccine is useful for  
 CC preventing or alleviating autoimmune disorders induced by EBV, e.g.  
 CC systemic lupus erythematosus (SLE), Sjogren's syndrome, juvenile onset  
 CC diabetes mellitus, rheumatoid arthritis, Wegener's granulomatosis,  
 CC inflammatory bowel disease, polymyositis, dermatomyositis, multiple  
 CC endocrine failure, Schmidt's syndrome, autoimmune uveitis, Addison's  
 CC disease, adrenalitis, primary biliary cirrhosis, Graves' disease,  
 CC thyroiditis, Hashimoto's thyroiditis, autoimmune thyroid disease,  
 CC pernicious and haemolytic anaemia, lupoid hepatitis, demyelinating  
 CC disease, multiple sclerosis, subacute cutaneous lupus erythematosus,  
 CC hypoparathyroidism, Dressler's syndrome, myasthenia gravis, autoimmune  
 CC idiopathic thrombocytopenic purpura, autoimmune pemphigus vulgaris,  
 CC pemphigus, bullous pemphigoid, dermatitis herpetiformis, alopecia  
 CC areata, autoimmune cyatitis, pemphigoid, scleroderma, progressive  
 CC systemic sclerosis, CREST syndrome (calcinosis, Raynaud's oesophageal  
 CC dysmotility, sclerodactyly and telangiectasia), adult onset diabetes  
 CC mellitus (Type II diabetes), male or female autoimmune infertility,  
 CC ankylosing spondylitis, ulcerative colitis, Crohn's disease, mixed  
 CC connective tissue disease, polyarthritis nodosa, systemic necrotising  
 CC vasculitis, glomerulonephritis, atopic dermatitis, atopic rhinitis,  
 CC Goodpasture's syndrome, Chagas' disease, sarcoidosis, rheumatic fever,  
 CC asthma, recurrent abortion, anti-phospholipid syndrome, farmer's lung,  
 CC erythema multiforme, postcardotomy syndrome, Cushing's syndrome,  
 CC autoimmune chronic active hepatitis, bird-fancier's lung, allergic  
 CC encephalomyelitis, toxic necrodermal lysis, alopecia, Alport's syndrome,  
 CC allergic alveolitis, fibrosing alveolitis, interstitial lung disease,  
 CC erythema nodosum, pyoderma gangrenosum, transfusion reaction, chronic  
 CC fatigue syndrome, fibromyalgia, Takayasu's arteritis, Kawasaki's disease,  
 CC polymyalgia rheumatica, temporal arteritis, giant cell arteritis, dengue,  
 CC Sampter's syndrome (triaditis, nasal polyps, eosinophilia) and Behcet's  
 CC disease, Caplan's syndrome, encephalomyositis, erythema elevatum et  
 CC dutinum, psoriasis, erythroblastosis foetalis, Shulman's syndrome, IGA  
 CC nephropathy, Felty's syndrome, fascitis with eosinophilia, filariasis,  
 CC chronic cyclophos, heterochromic cyclophos, Fuch's cyclophos, Hodgkin's and  
 CC non-Hodgkin's lymphoma, cardiomyopathy, Henoch-Schönlein purpura, post  
 CC vaccination syndromes, renal cell carcinoma, Eaton-Lambert syndrome or  
 CC relapsing polychondritis. The present sequence is Bacteriophage  
 CC peptide used in the invention.  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 44.4%; Score 4; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ILPL 9  
 DB 1 ILPL 4  
 RESULT 15  
 AAY31341

ID AAY31341 standard; peptide; 7 AA.  
 XX  
 AC AAY31341;  
 XX  
 DT 01-NOV-1999 (first entry)  
 XX  
 DE Amino acid sequence from B. subtilis spore-binding phage (isolate 10).  
 XX  
 KW Bacterial spore; biopanning; phage-display library; Bacillus; vaccine;  
 KW pathogen detection; biological warfare agent; B. anthracis.  
 XX  
 OS Bacillus subtilis.  
 XX  
 PN W09936081-A1.  
 XX  
 PD 22-JUL-1999.  
 XX  
 PF 14-JAN-1999; 99WO-US00771.  
 XX  
 PR 14-JAN-1998; 98US-0071411.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 XX  
 PI Turnbough CL;  
 XX  
 DR WPI; 1999-468943/39.  
 DR N-PSDB; AAX99276.  
 XX  
 XX Identifying peptides that bind to the surface of bacterial spores by  
 PT biopanning phage-display library, useful as vaccines and diagnostic  
 PT agents  
 XX  
 XX Disclosure; Page 6; 23pp; English.  
 PS  
 XX The invention provides peptides that bind to the surface of bacterial  
 CC spores. These peptides are identified by biopanning a phage-display  
 CC library with the spores. The library is incubated with spores and any  
 CC phage-spore complexes formed recovered by centrifuging. They are washed  
 CC thoroughly, then phage eluted with buffer, the eluate neutralised and  
 CC eluted phage amplified. The procedure is repeated, for 3 or 4 rounds of  
 CC panning, then individual clones purified, amplified and genomic DNA  
 CC extracted for determination of peptide-encoding sequences. Peptides  
 CC encoded by these sequences are then tested for ability to bind to target  
 CC spores. The peptides are used for capture and identification of  
 CC bacterial spores, particularly of the genus Bacillus, particularly for  
 CC detecting pathogens, or otherwise harmful species, in the environment  
 CC (e.g. air, water or food) or in clinical samples. They are also used to  
 CC protect against disease-causing spores (e.g. by incorporation in  
 CC protective masks), and in vaccines to generate a protective antibody  
 CC response. The peptides-specific antibodies are useful as detection  
 CC reagents, e.g. in enzyme-linked immunosorbent assay. The peptides are  
 CC species specific, i.e. they can differentiate between the possible  
 CC biological warfare agent B. anthracis and related species, widely present  
 CC in the environment and likely to give rise to false positive results.  
 CC Sequences AAY31332-344 represent amino acid sequences from B. subtilis  
 CC spore binding phage.  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 44.4%; Score 4; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPQN 5  
 DB 4 LPQN 7  
 RESULT 16  
 AAY84175  
 ID AAY84175 standard; peptide; 7 AA.  
 XX  
 AC AAY84175;



XX 03-JUL-2000 (first entry)  
 XX Amino acid sequence of a peptide derived from mouse leptin.  
 DE Mouse; leptin; blood brain barrier; homeostasis; body mass; anorexia;  
 KW obesity; hyperglycemia; hyperinsulinemia; hyperphagia;  
 KW thyroid dysfunction; infertility; type II diabetes mellitus;  
 KW non-insulin-dependent diabetes mellitus; hematopoiesis dysfunction;  
 KW tumour suppression; weight loss; diet.  
 XX Mus sp.  
 OS WO200011173-A1.  
 XX 02-MAR-2000.  
 XX 20-AUG-1999; 99WO-US19021.  
 XX 21-AUG-1998; 98US-0097457.  
 PR 19-AUG-1999; 99US-0377081.  
 XX (ALBA-) ALBANY MEDICAL COLLEGE.  
 XX Grasso P, Lee DW, Leinung MC;  
 XX WPI; 2000-237652/20.  
 XX Leptin peptides useful for treating pathophysiology relating to  
 PT homeostasis of body mass such as obesity, anorexia, and hematopoiesis  
 PT dysfunction and tumor suppression -  
 XX Claim 7; Page 79; 121pp; English.  
 XX The present sequence represents a peptide derived from mouse leptin.  
 CC The specification describes leptin-derived peptides which have  
 CC increased ability to cross the blood brain barrier and improved  
 CC bio-availability. Peptides derived from leptin are useful for treating  
 CC and preventing pathophysiology relating to homeostasis of body mass  
 CC such as anorexia, obesity comprising hyperglycemia, hyperinsulinemia,  
 CC hyperphagia, thyroid dysfunction, infertility, type II diabetes mellitus  
 CC and non-insulin-dependent diabetes mellitus (NIDDM), and hematopoiesis  
 CC dysfunction and tumor suppression. The peptides are also useful for  
 CC identifying drugs useful in weight loss diet regimen.  
 XX SQ Sequence 7 AA;  
 Query Match 44.4%; Score 4; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 DB 3 SLPQ 6  
 RESULT 17  
 AAW33806  
 ID AAW33806 standard; peptide; 8 AA.  
 XX AAW33806;  
 XX 22-JUN-1998 (first entry)  
 DE Uteroglobin inter helical loop 3 peptide.  
 XX Uteroglobin; immunisation; contraception; antibody; fertility; detection;  
 KW diagnosis; vaccine.  
 XX Synthetic.  
 OS WO9800536-A1.  
 XX

PD 08-JAN-1998.  
 XX 26-JUN-1997; 97WO-CB01740.  
 XX 29-JUN-1996; 96GB-0013705.  
 XX (UKAG-) UK MIN AGRIC FISHERIES & FOOD.  
 XX Symons DBA, Taussig MJ;  
 XX WPI; 1998-086962/08.  
 XX Controlling fertility in female mammals - by immunisation against  
 PT uteroglobin, particularly for oral administration to wild animals  
 XX Example 3; Page 11; 40pp; English.  
 XX This peptide is based on inter-helical loop 3 of Uteroglobin.  
 CC It can be used to promote an immunocontraceptive response in female  
 CC mammals when coupled to a carrier protein. The antibodies raised  
 CC against the peptide and carrier protein bind Uteroglobin resulting in a  
 CC reduction of fertility. Antibodies raised can also be used for detection  
 CC and diagnostic purposes. Peptides AAW33802-W33806 can be used for oral  
 CC administration of viral vaccine vectors for contraceptive purposes in  
 CC e.g. rabbits.  
 XX SQ Sequence 8 AA;  
 Query Match 44.4%; Score 4; DB 19; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 DB 3 SLPQ 6  
 RESULT 18  
 AAY24448  
 ID AAY24448 standard; peptide; 8 AA.  
 XX AAY24448;  
 XX 27-SEP-1999 (first entry)  
 DE Monoclonal antibody MAB 384 epitope SEQ ID NO:1.  
 XX Monoclonal antibody; epitope; multiplexed analysis; diagnosis;  
 KW genetic analysis; flow cytometry; human myelin basic protein; MBP;  
 KW microbial antigen; viral antigen; pathological condition.  
 XX Synthetic.  
 OS Mus sp.  
 OS Homo sapiens.  
 XX WO9936564-A1.  
 XX 22-JUL-1999.  
 XX 15-JAN-1999; 99WO-US00918.  
 XX 16-JAN-1998; 98US-0008387.  
 XX (LUMI-) LUMINEX CORP.  
 XX Chandler WB, Chandler VS, Fulton JR;  
 XX WPI; 1999-444409/37.  
 XX Beadset for simultaneous detection of many analytes by flow  
 PT cytometry, e.g. for detecting antigens, antibodies, or nucleic acid  
 PT mutations  
 XX

PS Example; Page 56; 301pp; English.

XX The present invention describes a beadset (A), able to detect many  
 CC analytes (I) in a single sample by flow cytometry (FC). (A) is produced  
 CC by: (i) providing many subsets of beads which, within each subset, are  
 CC homogeneous as regards at least 3 selected class parameters (C) but  
 CC sufficiently different in at least one C from beads in other subsets to  
 CC provide a profile of C values unique for each subset in FC; (ii)  
 CC coupling the beads in each subset with a reactant (R), specific for a  
 CC given (I) and (iii) mixing the subsets to form an (A) in which subsets  
 CC (and thus bound R) are identifiable in FC from the unique profile of C.  
 CC A method of flow cytometry analysis using (A) is used to detect a very  
 CC wide range of (I), e.g. microbial or viral antigens (particularly from  
 CC pathogens that cause venereal, pulmonary or gastrointestinal disease);  
 CC therapeutic or illicit drugs; antigens or antibodies associated with  
 CC particular pathological conditions (malignancy, allergy, autoimmune  
 CC disease, blood-borne viruses or cardiovascular disease); hormones,  
 CC including those indicative of pregnancy; enzymes; immunoglobulins (Ig),  
 CC particularly of different (sub)classes; Ig that form part of a  
 CC particular epitope (specifically an epitope of human immune deficiency  
 CC virus) or nucleic acids (particularly for detecting a wide variety of  
 CC mutations, e.g. those present in the rat proto-oncogene, the low density  
 CC lipoprotein receptor, the Duchenne muscular dystrophy, angiotensin p53,  
 CC and Rb genes. The process is particularly used for diagnosis of disease  
 CC and for genetic analysis. The present sequence represents a monoclonal  
 CC antibody MAB 384 epitope used in the exemplification of the present  
 CC invention.

SQ Sequence 8 AA;

Query Match 44.4%; Score 4; DB 20; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4

DB 4 SLPQ 7

RESULT 19

AAW98813

ID AAW98813 standard; Peptide; 8 AA.

AC AAW98813;

DT 24-JAN-2002 (first entry)

DE Human peptide #2088 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.

OS Homo sapiens.

PN WO200147944-A2..

XX 05-JUL-2001.

PD 28-DEC-2000; 2000WO-US35498.

PF 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach M;

XX

DR WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -  
 XX Disclosure; Page 4126; 4143pp; English.

PS The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms.

SQ Sequence 8 AA;

Query Match 44.4%; Score 4; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4

DB 5 SLPQ 8

RESULT 20

AAW49282

ID AAW49282 standard; peptide; 9 AA.

AC AAW49282;

XX 05-JUN-1998 (first entry)

DT Human leucocyte antigen DQ4 binding peptide #173.

DE Human leucocyte antigen; HLA-DQ4; combinatorial library;

KW autoimmune disease; chronic articular rheumatism.

OS Synthetic.

XX JP08151396-A.

PD 11-JUN-1996.

XX 28-NOV-1994; 94JP-0292657.

PR 28-NOV-1994; 94JP-0292657.

XX (TEIJ ) TEIJIN LTD.

XX WPI; 1996-329479/33.

PT HLA-binding oligopeptide and an immuno:regulator contg it - used in  
 the treatment of autoimmune disease

PS Claim 4; Page 26; 61pp; Japanese.

XX This peptide is an example of a peptide which binds to a human leucocyte  
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
 CC combinatorial library comprising the sequence AAV05953, by screening  
 CC with an HLA-DQ4 molecule. The peptide is used for the treatment of  
 CC autoimmune disease, or especially for treatment of viral diseases.

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XX SQ Sequence 9 AA;
Query Match 44.4%; Score 4; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLPQ 4
Db 3 SLPQ 6

RESULT 21
AAY5419
ID AAY5419 standard; peptide; 9 AA.
XX
AC AAY5419;
XX
DT 17-JAN-2000 (first entry)
XX
DE HLA binding plu-1 peptide.
XX
KW Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;
KW breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;
KW therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9949034-A1.
XX
PD 30-SEP-1999.
XX
PF 19-MAR-1999; 99WO-GB00866.
XX
PR 20-MAR-1998; 98GB-0005877.
XX
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI Taylor-papadimitriou J;
XX
DR WPI; 1999-591090/50.
XX
PT New nucleic acid encoding the cancer-associated polypeptide plu-1, for
PT diagnosis, treatment and prevention of cancer, especially of breast and
PT ovary -
XX
PS Example 2; Fig 12; 173pp; English.
XX
CC The invention relates to a human cancer-associated polypeptide plu-1.
CC The plu-1 polypeptide can be recombinantly expressed by standard
CC recombinant methodology. Detection of the plu-1 nucleic acid or the
CC polypeptide is used for the following: (i) diagnosis (including imaging)
CC and prognosis of, and determination of susceptibility to, cancer,
CC specifically ovarian or breast cancer; and ii) treating cancer (by
CC inducing an immune response against cancer cells, e.g. as a vaccine, or
CC by antisense inhibition). Antigens derived from the polypeptide are used
CC to generate activated cytotoxic T lymphocytes, or dendritic cells, for
CC subsequent return to the patient for treatment of cancer. The polypeptide
CC may also be used to identify inhibitors of plu-1 activity. Fragments of
CC the polypeptide, and antibodies raised against plu-1, are useful as assay
CC and imaging agents, also therapeutically (to induce an anti-idiotypic
CC response or where conjugated to cytotoxic agents). The plu-1 antigen is
CC expressed more commonly in breast tumors than some known tumor antigens.
CC Sequences AAY5320-629 represent predicted peptides from the plu-1
CC polypeptide which may bind to the human class I alleles B27, A2, A3 and
CC A11.
XX
SQ Sequence 9 AA;
Query Match 44.4%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 6 ILPL 9
Db 5 ILPL 8

RESULT 22
AAY5430
ID AAY5430 standard; peptide; 9 AA.
XX
AC AAY5430;
XX
DT 17-JAN-2000 (first entry)
XX
DE HLA binding plu-1 peptide.
XX
KW Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;
KW breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;
KW therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9949034-A1.
XX
PD 30-SEP-1999.
XX
PF 19-MAR-1999; 99WO-GB00866.
XX
PR 20-MAR-1998; 98GB-0005877.
XX
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI Taylor-papadimitriou J;
XX
DR WPI; 1999-591090/50.
XX
PT New nucleic acid encoding the cancer-associated polypeptide plu-1, for
PT diagnosis, treatment and prevention of cancer, especially of breast and
PT ovary -
XX
PS Example 2; Fig 12; 173pp; English.
XX
CC The invention relates to a human cancer-associated polypeptide plu-1.
CC The plu-1 polypeptide can be recombinantly expressed by standard
CC recombinant methodology. Detection of the plu-1 nucleic acid or the
CC polypeptide is used for the following: (i) diagnosis (including imaging)
CC and prognosis of, and determination of susceptibility to, cancer,
CC specifically ovarian or breast cancer; and ii) treating cancer (by
CC inducing an immune response against cancer cells, e.g. as a vaccine, or
CC by antisense inhibition). Antigens derived from the polypeptide are used
CC to generate activated cytotoxic T lymphocytes, or dendritic cells, for
CC subsequent return to the patient for treatment of cancer. The polypeptide
CC may also be used to identify inhibitors of plu-1 activity. Fragments of
CC the polypeptide, and antibodies raised against plu-1, are useful as assay
CC and imaging agents, also therapeutically (to induce an anti-idiotypic
CC response or where conjugated to cytotoxic agents). The plu-1 antigen is
CC expressed more commonly in breast tumors than some known tumor antigens.
CC Sequences AAY5320-629 represent predicted peptides from the plu-1
CC polypeptide which may bind to the human class I alleles B27, A2, A3 and
CC A11.
XX
SQ Sequence 9 AA;
Query Match 44.4%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 6 ILPL 9
Db 2 ILPL 5

Query Match 44.4%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

## RESULT 23

AA46572  
ID AAY46572 standard; Peptide; 9 AA.

XX  
AC AAY46572;

XX  
DT 01-DEC-1999 (first entry)

XX  
DE Immunogenic peptide having a human leukocyte antigen binding motif #1183.

XX  
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
KW immune response; T cell activation; major histocompatibility complex;  
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
KW vaccine; immunisation.

XX  
OS Synthetic.

XX  
OS Homo sapiens.

XX  
PN WO945954-A1.

XX  
PD 16-SEP-1999.

XX  
PF 13-MAR-1998; 98WO-US05039.

XX  
PR 13-MAR-1998; 98WO-US05039.

XX  
PA (EPIM-) EPIMMUNE INC.

XX  
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX  
DR WPI; 1999-551214/46.

XX  
PT New immunogenic peptides with HLA binding motif, useful in treatment  
PT and diagnosis of cancers and viral diseases -

XX  
PS Claim 1; Page 77; 150pp; English.

XX  
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
CC having a human major histocompatibility complex (MHC) Class I (also  
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
CC response against the antigen from which the peptide is derived.  
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
CC normally induced by an antigen in the form of a peptide fragment bound  
CC to a HLA molecule, rather than the intact foreign antigen itself, and  
CC are particularly important in tumour rejection and in fighting viral  
CC infections. The peptides are therefore useful therapeutically to treat  
CC or prevent viral infections and cancers in mammals (especially humans)  
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
CC They can be administered as vaccines to elicit an immune response in  
CC individuals susceptible or otherwise at risk of viral infection or  
CC cancer, or used to treat chronic or acute conditions. They are also  
CC useful diagnostically, and can be used to induce a cytotoxic T cell  
CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
CC produce CTLs ex vivo for infusion back into a patient. The  
CC polynucleotides encoding the immunogenic peptides are also useful  
CC therapeutically and for immunisation as above.

XX  
SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 20; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4

DB 3 SLPQ 6

## RESULT 24

AA45575

ID AAB45575 standard; Protein; 9 AA.

XX  
AC AAB45575;

XX  
DT 02-MAR-2001 (first entry)

XX  
DE Human B99-2 HLA A1, A3 immunogenic peptide SEQ ID NO 152.

XX  
KW Tumor-associated antigen; B99; immunogenic; humoral immune response;  
KW cellular immune response; immunotherapy; cancer; kidney; lung; colon;  
KW pancreas; breast; stomach; vaccine; diagnosis; treatment.

XX  
OS Homo sapiens.

XX  
PN WO200066727-A1.

XX  
PD 09-NOV-2000.

XX  
PF 19-APR-2000; 2000WO-EP03552.

XX  
PR 28-APR-1999; 99DE-1019225.

XX  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.

XX  
PI Adolf G, Heider K, Sommergruber W;

XX  
DR WPI; 2000-679759/66.

XX  
PT New tumor-associated antigen B99, useful in immunotherapy of cancer,  
PT and related nucleic acid and antibodies -

XX  
PS Example 7; Page 49; 75pp; German.

XX  
CC This invention describes a novel tumor-associated antigen, designated  
CC B99 which has anticancer activity. B99, or its immunogenic fragments or  
CC peptides, induces a humoral and/or cellular immune response against  
CC tumor cells that express B99. B99 (or its immunogenic fragments or  
CC peptides) and also the nucleic acid that encodes them, are useful for  
CC immunotherapy of cancer, in vivo or in vitro, especially cancers of  
CC kidney, lung, colon, pancreas, breast or stomach. Cells that express B99  
CC are useful in cancer vaccines and antibodies (Ab) directed against B99  
CC are used for diagnosis and treatment of cancers that express B99,  
CC optionally when coupled to a cytotoxin or radioisotope. Peptides from  
CC B99 can also be used diagnostically to monitor a patient's response to  
CC treatment and B99, or its DNA, are used to identify specific modulators,  
CC particularly inhibitors, of B99 activity.

XX  
SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQNI 6

DB 5 PQNI 8

## RESULT 25

AA45576

ID AAB45576 standard; Protein; 9 AA.

XX  
AC AAB45576;

XX  
DT 02-MAR-2001 (first entry)

XX  
DE Human B99-2 HLA A\*0201 immunogenic peptide SEQ ID NO 154.

XX  
KW Tumor-associated antigen; B99; immunogenic; humoral immune response;  
KW cellular immune response; immunotherapy; cancer; kidney; lung; colon;  
KW pancreas; breast; stomach; vaccine; diagnosis; treatment.

XX  
OS Homo sapiens.

```

XX PN WO200066727-A1.
XX PD 09-NOV-2000.
XX PF 19-APR-2000; 2000WO-EP03552.
XX PR 28-APR-1999; 99DE-1019225.
XX PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX PI Adolf G, Heider K, Sommergruber W;
XX WPI; 2000-679759/66.
XX PT New tumor-associated antigen B99, useful in immunotherapy of cancer,
XX PT and related nucleic acid and antibodies -
XX PR Example 7; Page 49; 75pp; German.
XX PS This invention describes a novel tumor-associated antigen, designated
CC B99 which has anticancer activity. B99, or its immunogenic fragments or
CC peptides, induces a humoral and/or cellular immune response against
CC tumor cells that express B99. B99 (or its immunogenic fragments or
CC peptides) and also the nucleic acid that encodes them, are useful for
CC immunotherapy of cancer, in vivo or in vitro, especially cancers of
CC kidney, lung, colon, pancreas, breast or stomach. Cells that express B99
CC are useful in cancer vaccines and antibodies (Ab) directed against B99
CC are used for diagnosis and treatment of cancers that express B99,
CC optionally when coupled to a cytotoxin or radioisotope. Peptides from
CC B99 can also be used diagnostically to monitor a patient's response to
CC treatment and B99, or its DNA, are used to identify specific modulators,
CC particularly inhibitors, of B99 activity.
XX SQ Sequence 9 AA;
XX
Query Match 44.4%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PQNI 6
DB 3 PQNI 6
XX
RESULT 26
ABP13308
ID ABP13308 standard; Peptide; 9 AA.
XX AC ABP13308;
XX 15-JUL-2002 (first entry)
XX DE HIV A02 super motif pol peptide #223.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.
XX
WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1 -
XX Claim 32; Page 141; 448pp; English.
XX
The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX SQ Sequence 9 AA;
XX
Query Match 44.4%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLPQ 4
DB 5 SLPQ 8
XX
RESULT 27
ABP15936
ID ABP15936 standard; Peptide; 9 AA.
XX AC ABP15936;
XX 15-JUL-2002 (first entry)
XX DE HIV A24 super motif pol peptide #116.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.
XX

```

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 PS Claim 32; Page 195; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 Db ||||  
 5 SLPQ 8  
 RESULT 28  
 ABP18996  
 ID ABP18996 standard; Peptide; 9 AA.  
 AC  
 XX  
 AC ABP18996;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV B62 super motif pol peptide #2.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 OS  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX

PS Claim 32; Page 258; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 Db ||||  
 5 SLPQ 8  
 RESULT 29  
 AAM22210  
 ID AAM22210 standard; Peptide; 9 AA.  
 XX  
 AC AAM22210;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE HIV peptide SEQ ID NO 95.  
 XX  
 KW Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;  
 KW human immunodeficiency virus; vaccine.  
 XX  
 OS Human immunodeficiency virus.  
 OS Synthetic.  
 XX  
 PN WO200155177-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 29-JAN-2001; 2001WO-DK00059.  
 XX  
 PR 28-JAN-2000; 2000EP-0610017.  
 PR 31-JAN-2000; 2000US-0179333.  
 XX  
 PA (STAT-) STATENS SERUM INST.  
 XX  
 PI Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;  
 XX WPI; 2001-476184/51.  
 DR  
 XX The generation of cytotoxic T cell lymphocytes epitopes for use in  
 PT anti-HIV vaccines -  
 PT  
 XX Claim 13; Page 51; 383pp; English.  
 XX The invention relates to identification of cytotoxic T cell lymphocyte  
 CC

CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or prevent infection of cells in the host, but CTL will limit viral production by killing the cell. The CTL epitopes are useful in medicine, CC in the manufacture of vaccines or diagnostic agents.

XX Sequence 9 AA;

Query Match 44.4%; Score 4; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||  
DB 3 SLPQ 6

RESULT 30

AAO19008  
ID AAO19008 standard; Peptide; 9 AA.

XX AC AAO19008;

XX DT 07-NOV-2002 (first entry)

XX DE Porcine endogenous retrovirus protease substrate peptide #2.

XX KW PERV; protease; virucide; infection; xenotransplant; substrate.

XX OS Unidentified.

XX PN DE10138528-A1.

XX PD 04-JUL-2002.

XX PF 06-AUG-2001; 2001DE-1038528.

XX PR 23-DEC-2000; 2000DE-1064897.

XX PA (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.

XX PI Von Der Helm K, Blusch JH, Seelmeir S;

XX DR WPI; 2002-609974/66.

XX PT New nucleic acid, useful for identifying specific inhibitors for controlling infection following xenotransplantation, encodes porcine endogenous retrovirus protease -

XX PS Claim 8; Page 12; 30pp; German.

XX CC The present invention relates to proteases and their coding sequences from porcine endogenous retroviruses (PERVs) type A, B and C. The coding sequences are useful in screening for inhibitors of proteases, particularly where retroviral. The inhibitors are potentially useful for treating or preventing PERV infections in humans, specifically those who have received a pig organ transplant. The present sequence is a protease substrate of the invention.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILPL 9  
|||  
DB 4 ILPL 7

RESULT 31

ABP47492

ID ABP47492 standard; Peptide; 9 AA.

XX AC ABP47492;

XX DT 19-AUG-2002 (first entry)

XX DE N. meningitidis LOS peptidic mimotope related peptide SEQ ID NO:68.

XX KW Neisseria meningitidis; meningococcus; meningococcal; vaccine; LOS; lipooligosaccharide; monoclonal antibody; antibacterial; infection; antiinflammatory; meningococcal disease.

XX OS Neisseria meningitidis.

XX PN WO200228888-A2.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-EP11409.

XX PR 03-OCT-2000; 2000GB-0024200.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI De Bolle XT, Letesson J, Lobet Y, Mertens PY, Poolman J, Voet P;

XX DR WPI; 2002-479596/51.

XX PT Novel mimotope of Neisseria meningitidis surface, for treating meningococcal disease, comprising a peptide epitope obtainable by screening peptide library with a specific monoclonal antibody -

XX PS Claim 3; Page 41; 55pp; English.

XX CC The present invention describes mimotopes (I) of a surface L3, 7, 9, of meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis comprising a peptide epitope obtained by screening a peptide library with a monoclonal antibody (MAB) like 4B212C10, H44/24, H44/58, H44/70 or H44/78. (I) is antigenically cross-reactive with MAB. (I) have antibacterial and antiinflammatory activities, and can be used in vaccines. MAB is useful in the identification of (I). (I) or MAB are useful as a medicament, and also in the manufacture of a medicament for treating or preventing meningococcal disease. (I) and MAB are useful for treating a patient suffering from or susceptible to meningococcal disease by administering (I) or MAB to the patient. (I) is useful in a diagnostic assay for meningococcal infection to detect antibodies against L3, 7, 9, LOS and to detect the presence of L3, 7, 9 immunotype meningococcus in a sample from a patient. ABN88464 to ABN88487 and ABP47336 to ABP47754 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||  
DB 6 SLPQ 9

RESULT 32

AAE20459

ID AAE20459 standard; peptide; 9 AA.

XX AC AAE20459;

XX DT 01-JUL-2002 (first entry)

XX XX Phosphopeptide #2 used in the exemplification of the invention.

KW Labelling phosphate group; carboxylic acid group; phosphoprotein;  
 XX phosphopeptide.  
 XX  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 XX FH Modified-site 3  
 XX FT /note= "Phosphorylation site"  
 XX  
 XX WO200196869-A1.  
 XX  
 XX 20-DEC-2001.  
 XX  
 XX 12-JUN-2001; 2001WO-US18988.  
 XX  
 XX 12-JUN-2000; 2000US-210972P.  
 XX  
 XX (UNIW ) UNIV WASHINGTON.  
 XX  
 XX Aebersold R, Zhou H;  
 XX  
 XX WPI; 2002-122223/16.  
 XX  
 XX Selective labelling of phosphate groups in peptides and proteins for  
 PT separation, isolation and detection of phosphoproteins and  
 PT phosphopeptides, comprises the presence of carboxylic acids -  
 XX  
 XX Example 4; Page 32; 59pp; English.  
 XX  
 XX The invention relates to a method for selective labelling phosphate  
 CC groups in peptides or proteins in the presence of carboxylic acid groups.  
 CC The new method is used for selectively labelling phosphate groups in  
 CC peptides or proteins in the presence of carboxylic acid groups. It is  
 CC useful in separation, isolation and detection of phosphoproteins and  
 CC phosphopeptides. The present sequence is a phosphopeptide used in the  
 CC exemplification of the invention.  
 XX  
 XX Sequence 9 AA; ~  
 SQ  
 Query Match 44.4%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 Db 5 SLPQ 8  
 ||||  
 RESULT 33  
 ABJ20132  
 ID ABJ20132 standard; Peptide; 9 AA.  
 XX  
 XX AC ABJ20132;  
 XX  
 XX 10-APR-2003 (first entry)  
 XX  
 XX MHC binding peptide SEQ ID No 297.  
 DE  
 XX  
 XX Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;  
 KW antiinflammatory; major histocompatibility complex; MHC;  
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;  
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;  
 KW inflammation; gene therapy; MHC binding peptide.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200294981-A2.  
 XX  
 XX 28-NOV-2002.  
 PD  
 XX  
 XX 16-MAY-2002; 2002WO-IL00383.  
 PF  
 XX 16-MAY-2001; 2001US-290958P.  
 PR

PR 29-MAY-2001; 2001US-0865548.  
 XX  
 XX (TECR ) TECHNION RES & DEV FOUND LTD.  
 XX  
 XX Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchebaum S;  
 XX  
 XX WPI; 2003-210043/20.  
 XX  
 XX Identifying peptides that are capable of binding to major  
 PT histocompatibility complex (MHC) molecules of a particular haplotype by  
 PT analyzing peptides bound to the soluble and secreted form of the MHC  
 PT molecules of the particular haplotype -  
 XX  
 XX Claim 58; Page 219; 238pp; English.  
 XX  
 XX The invention relates to a novel method for identifying peptides  
 CC originating from a particular cell type, which are capable of binding to  
 CC major histocompatibility complex (MHC) molecules of a particular  
 CC haplotype. The method comprises analysing peptides bound to the soluble  
 CC and secreted form of the MHC molecules of the particular haplotype. The  
 CC method is useful for identifying peptides for treating an autoimmune  
 CC disease, such as T or B cell and/or allergic disease or condition,  
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,  
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The  
 CC sequences of the invention may be used in a gene therapy application.  
 CC This sequence represents a peptide relating to the method for identifying  
 CC MHC binding peptides of the invention.  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PQNI 6  
 Db 6 PQNI 9  
 ||||  
 RESULT 34  
 ABP83653  
 ID ABP83653 standard; peptide; 9 AA.  
 XX  
 XX AC ABP83653;  
 XX  
 XX 28-MAR-2003 (first entry)  
 DT  
 XX  
 XX HLA protein 121P2A3 peptide #8.  
 DE  
 XX  
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200283068-A2.  
 XX  
 XX 24-OCT-2002.  
 PD  
 XX  
 XX 09-APR-2002; 2002WO-US11359.  
 PF  
 XX  
 XX 10-APR-2001; 2001US-282739P.  
 PR  
 XX 25-APR-2001; 2001US-286630P.  
 PR  
 XX 22-JUN-2001; 2001US-300373P.  
 PR  
 XX  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX  
 XX WPI; 2003-092956/08.  
 DR  
 XX  
 XX New composition comprising a substance that modulates the status of  
 PT



PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues -

PS Claim 13; Page 129; 362pp; English.

XX The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of the invention.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
Db ||||  
2 SLPQ 5

RESULT 35

ABP83703  
ID ABP83703 standard; peptide; 9 AA.

AC ABP83703;

XX 28-MAR-2003 (first entry)

DT HLA protein 121P2A3 peptide #58.

DE Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

KW humoral immune response; cellular immune response;

KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

OS WO200283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002WO-US11359.

XX 10-APR-2001; 2001US-282739P.

PR 25-APR-2001; 2001US-286630P.

XX 22-JUN-2001; 2001US-300373P.

XX (AGEN-) AGENSYS INC.

XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues -

XX Claim 13; Page 129; 362pp; English.

PS The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of the invention.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
Db ||||  
6 SLPQ 9

RESULT 36

ABP84035  
ID ABP84035 standard; peptide; 9 AA.

XX AC ABP84035;

XX 28-MAR-2003 (first entry)

DE HLA protein 121P2A3 peptide #390.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

KW humoral immune response; cellular immune response;

KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

OS WO200283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002WO-US11359.

XX 10-APR-2001; 2001US-282739P.

PR 25-APR-2001; 2001US-286630P.

XX 22-JUN-2001; 2001US-300373P.

XX (AGEN-) AGENSYS INC.

XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues -

XX Claim 13; Page 135; 362pp; English.

CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4

Db 4 SLPQ 7

RESULT 37

ABP84289

ID ABP84289 standard; peptide; 9 AA.

AC

AC ABP84289;

DT 28-MAR-2003 (first entry)

DE HLA protein 121P2A3 peptide #644.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

KW humoral immune response; cellular immune response;

KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX WO200283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002WO-US11359.

XX 10-APR-2001; 2001US-282739P.

XX 25-APR-2001; 2001US-286630P.

XX 22-JUN-2001; 2001US-300373P.

XX (AGEN-) AGENSYS INC.

XX Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;

XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of

PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune

PT responses or in assessing the status of 121P2A3 gene products in normal

PT versus cancerous tissues -

XX Claim 13; Page 141; 362pp; English.

XX The invention relates to a novel composition comprising a substance that

CC modulates the status of a protein, 121P2A3. The composition of the

CC invention has cytostatic and immunostimulant activity, and is useful as a

CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4

Db 2 SLPQ 5

RESULT 38

ABP84573

ID ABP84573 standard; peptide; 9 AA.

AC

AC ABP84573;

XX 28-MAR-2003 (first entry)

DE HLA protein 121P2A3 peptide #928.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

KW humoral immune response; cellular immune response;

KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX WO200283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002WO-US11359.

XX 10-APR-2001; 2001US-282739P.

XX 25-APR-2001; 2001US-286630P.

XX 22-JUN-2001; 2001US-300373P.

XX (AGEN-) AGENSYS INC.

XX Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;

XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of

PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune

PT responses or in assessing the status of 121P2A3 gene products in normal

PT versus cancerous tissues -

XX Claim 13; Page 146; 362pp; English.

XX The invention relates to a novel composition comprising a substance that

CC modulates the status of a protein, 121P2A3. The composition of the

CC invention has cytostatic and immunostimulant activity, and is useful as a

CC vaccine. The 121P2A3 proteins and polynucleotides are useful for

CC eliciting humoral or cellular immune response. The polynucleotides are

CC useful for characterising cytogenetic abnormalities of this chromosomal

CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX  
 SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLFQ 4  
 ||||  
 Db 2 SLFQ 5

RESULT 39  
 ABP84587  
 ID ABP84587 standard; peptide; 9 AA.

XX AC ABP84587;

XX DT 28-MAR-2003 (first entry)

XX DE HLA protein 121P2A3 peptide #942.

XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

XX KW humoral immune response; cellular immune response;

XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283068-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US11359.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 25-APR-2001; 2001US-286630P.

XX PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.

XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

XX PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX DR WPI; 2003-092956/08.

XX PT New composition comprising a substance that modulates the status of  
 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -

XX PS Claim 13; Page 146; 362pp; English.

XX CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene

CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLFQ 4  
 ||||  
 Db 3 SLFQ 6

RESULT 40

ABP85175

ID ABP85175 standard; peptide; 9 AA.

XX AC ABP85175;

XX DT 28-MAR-2003 (first entry)

XX DE HLA protein 121P2A3 peptide #1530.

XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

XX KW humoral immune response; cellular immune response;

XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283068-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US11359.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 25-APR-2001; 2001US-286630P.

XX PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.

XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

XX PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX DR WPI; 2003-092956/08.

XX PT New composition comprising a substance that modulates the status of  
 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -

XX PS Claim 13; Page 158; 362pp; English.

XX CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a

CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX Sequence 9 AA;  
 SQ

Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLPQ 4  
 Db 4 SLPQ 7

## RESULT 41

ABP85517  
 ID ABP85517 standard; peptide; 9 AA.

XX AC  
 XX ABP85517;  
 DT 28-MAR-2003 (first entry)

XX DE HLA protein 121P2A3 peptide #1872.

XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.  
 XX WO200283068-A2.  
 XX 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US11359.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.  
 XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison K, Ge W, Jakobovits A;

XX DR WPI; 2003-092956/08.  
 XX

XX New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -

XX PS Claim 13; Page 164; 362pp; English.

XX The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in

CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX Sequence 9 AA;  
 SQ

Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLPQ 4  
 Db 4 SLPQ 7

## RESULT 42

ABP85775  
 ID ABP85775 standard; peptide; 9 AA.

XX AC  
 XX ABP85775;  
 XX DT 28-MAR-2003 (first entry)

XX DE HLA protein 121P2A3 peptide #2130.

XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.  
 XX WO200283068-A2.  
 XX 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US11359.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.  
 XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison K, Ge W, Jakobovits A;

XX DR WPI; 2003-092956/08.  
 XX

XX New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -

XX PS Claim 13; Page 174; 362pp; English.

XX The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
 Db 6 SLPQ 9  
 |||||

RESULT 43  
 ABP85776  
 ID ABP85776 standard; peptide; 9 AA.  
 XX  
 AC ABP85776;  
 XX  
 DT 28-MAR-2003 (first entry)  
 XX  
 DE HLA protein 121P2A3 peptide #2131.  
 XX  
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283068-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 09-APR-2002; 2002WO-US11359.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX  
 WPI; 2003-092956/08.  
 XX  
 DR New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX  
 PS Claim 13; Page 174; 362pp; English.  
 XX  
 CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX  
 SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
 Db 2 SLPQ 5  
 |||||

RESULT 44  
 ABP85857  
 ID ABP85857 standard; peptide; 9 AA.  
 XX  
 AC ABP85857;  
 XX  
 DT 28-MAR-2003 (first entry)  
 XX  
 DE HLA protein 121P2A3 peptide #2212.  
 XX  
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283068-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 09-APR-2002; 2002WO-US11359.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX  
 WPI; 2003-092956/08.  
 XX  
 DR New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX  
 PS Claim 13; Page 175; 362pp; English.  
 XX  
 CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX  
 SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
 DB 1 SLPQ 4

RESULT 45  
 ABP86000  
 ID ABP86000 standard; peptide; 9 AA.  
 XX  
 AC ABP86000;  
 XX  
 DT 28-MAR-2003 (first entry)  
 XX  
 DE HLA protein 121P2A3 peptide #2355.  
 XX  
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283068-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 09-APR-2002; 2002WO-US11359.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX  
 DR WPI; 2003-092956/08.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX  
 PS Claim 13; Page 176; 362pp; English.  
 XX  
 CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP8646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
 DB 1 SLPQ 4

RESULT 46  
 ABP86064  
 ID ABP86064 standard; peptide; 9 AA.  
 XX  
 AC ABP86064;  
 XX  
 DT 28-MAR-2003 (first entry)  
 XX  
 DE HLA protein 121P2A3 peptide #2419.  
 XX  
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283068-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 09-APR-2002; 2002WO-US11359.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX  
 DR WPI; 2003-092956/08.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX  
 PS Claim 13; Page 177; 362pp; English.  
 XX  
 CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP8646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 47  
 ABP86202  
 ID ABP86202 standard; peptide; 9 AA.  
 XX AC  
 XX DT 28-MAR-2003 (first entry)  
 XX AC ABP86202;  
 XX DT 28-MAR-2003 (first entry)  
 XX DE HLA protein 121P2A3 peptide #2557.  
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 XX KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283068-A2.  
 XX PD 24-OCT-2002.  
 XX PF 09-APR-2002; 2002WO-US11359.  
 XX PR 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.  
 XX DR New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX Claim 13; Page 178; 362pp; English.  
 XX CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 DB 1 SLPQ 4  
 RESULT 48  
 ABP86278  
 ID ABP86278 standard; peptide; 9 AA.

XX AC ABP86278;  
 XX DT 28-MAR-2003 (first entry)  
 XX DE HLA protein 121P2A3 peptide #2633.  
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283068-A2.  
 XX PD 24-OCT-2002.  
 XX PF 09-APR-2002; 2002WO-US11359.  
 XX PR 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.  
 XX DR New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX Claim 13; Page 179; 362pp; English.  
 XX CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 DB 5 SLPQ 8  
 RESULT 49  
 ABP86279  
 ID ABP86279 standard; peptide; 9 AA.  
 XX AC ABP86279;  
 XX

DT 28-MAR-2003 (first entry)  
 XX HLA protein 121P2A3 peptide #2634.  
 DE Human, 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 XX humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 KW Homo sapiens.  
 OS WO200283068-A2.  
 XX 24-OCT-2002.  
 XX 09-APR-2002; 2002WO-US11359.  
 PN 10-APR-2001; 2001US-282739P.  
 XX 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX (AGEN-) AGENSYS INC.  
 PA Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 PI WPI; 2003-092956/08.  
 DR New composition comprising a substance that modulates the status of  
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 PT Claim 13; Page 179; 362pp; English.  
 PS The invention relates to a novel composition comprising a substance that  
 XX modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 DB 4 SLPQ 7  
 RESULT 50  
 ABP86394  
 ID ABP86394 standard; peptide; 9 AA.  
 XX  
 AC ABP86394;  
 XX 28-MAR-2003 (first entry)  
 DT HLA protein 121P2A3 peptide #2749.  
 XX Human, 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 DE suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Human, 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 OS Homo sapiens.  
 XX WO200283068-A2.  
 XX 24-OCT-2002.  
 XX 09-APR-2002; 2002WO-US11359.  
 PF 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX (AGEN-) AGENSYS INC.  
 PA Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 PI WPI; 2003-092956/08.  
 DR New composition comprising a substance that modulates the status of  
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 PT Claim 13; Page 180; 362pp; English.  
 PS The invention relates to a novel composition comprising a substance that  
 XX modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 DB 2 SLPQ 5  
 RESULT 51  
 ABP86425  
 ID ABP86425 standard; peptide; 9 AA.  
 XX  
 AC ABP86425;  
 XX 28-MAR-2003 (first entry)  
 DT HLA protein 121P2A3 peptide #2780.  
 DE Human, 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.





PD 24-OCT-2002.  
 XX 09-APR-2002; 2002WO-US11359.  
 PF 10-APR-2001; 2001US-282739P.  
 XX 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX (AGEN-) AGENSYS INC.  
 PA Challita-eid PM, Raitano AB, Farris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.  
 DR New composition comprising a substance that modulates the status of  
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX Claim 13; Page 182; 362pp; English.  
 PS The invention relates to a novel composition comprising a substance that  
 XX modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX Sequence 9 AA;  
 SQ Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 DB 3 SLPQ 6  
 RESULT 54  
 ABP86679  
 ID ABP86679 standard; peptide; 9 AA.  
 XX AC ABP86679;  
 XX 28-MAR-2003 (first entry)  
 DT HLA protein 121P2A3 peptide #3034.  
 DE Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 XX humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX Homo sapiens.  
 OS WO200283068-A2.  
 PN 24-OCT-2002.  
 XX 09-APR-2002; 2002WO-US11359.  
 PF 10-APR-2001; 2001US-282739P.  
 XX 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX (AGEN-) AGENSYS INC.  
 PA Challita-eid PM, Raitano AB, Farris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.  
 DR New composition comprising a substance that modulates the status of  
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX Claim 13; Page 182; 362pp; English.  
 PS The invention relates to a novel composition comprising a substance that  
 XX modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX Sequence 9 AA;  
 SQ Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX (AGEN-) AGENSYS INC.  
 XX Challita-eid PM, Raitano AB, Farris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.  
 DR New composition comprising a substance that modulates the status of  
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX Claim 13; Page 183; 362pp; English.  
 PS The invention relates to a novel composition comprising a substance that  
 XX modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX Sequence 9 AA;  
 SQ Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 DB 2 SLPQ 5  
 RESULT 55  
 ABP86764  
 ID ABP86764 standard; peptide; 9 AA.  
 XX AC ABP86764;  
 XX 28-MAR-2003 (first entry)  
 DT HLA protein 121P2A3 peptide #3119.  
 DE Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 XX suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 OS Homo sapiens.  
 OS WO200283068-A2.  
 PN 24-OCT-2002.  
 XX 09-APR-2002; 2002WO-US11359.  
 PF 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 PA Challita-eid PM, Raitano AB, Farris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.  
 DR New composition comprising a substance that modulates the status of  
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX Claim 13; Page 183; 362pp; English.  
 PS The invention relates to a novel composition comprising a substance that  
 XX modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX Sequence 9 AA;  
 SQ Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of

PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune

PT responses or in assessing the status of 121P2A3 gene products in normal

PT versus cancerous tissues -

XX Claim 13; Page 185; 362pp; English.

XX The invention relates to a novel composition comprising a substance that

CC modulates the status of a protein, 121P2A3. The composition of the

CC invention has cytostatic and immunostimulant activity, and is useful as a

CC vaccine. The 121P2A3 proteins and polynucleotides are useful for

CC eliciting humoral or cellular immune response. The polynucleotides are

CC useful for characterising cytogenetic abnormalities of this chromosomal

CC locus, as tools that can be used to delineate cytogenetic abnormalities

CC in the chromosomal region that encodes 121P2A3 that may contribute to

CC malignant phenotype, and in assessing the status of 121P2A3 gene

CC products in normal versus cancerous tissues. The proteins are useful

CC for generating and characterising domain-specific antibodies, for

CC identifying agents or cellular factors that bind to 121P2A3 or a

CC particular structure domain, and in various therapeutic and diagnostic

CC contexts, including cancer vaccines. The antibodies or T cells reactive

CC with the product are useful in passive or active immunisation, and in

CC imaging methodologies for the management of cancer. The sequences shown

CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of

CC the invention.

XX Sequence 9 AA;

SQ

Query Match 44.4%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4

Db 6 SLPQ 9

|||||

RESULT 58

ABP86978

ID ABP86978 standard; peptide; 9 AA.

AC ABP86978;

XX

XX 28-MAR-2003 (first entry)

DT

DE HLA protein 121P2A3 peptide #3333.

XX

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

KW humoral immune response; cellular immune response;

KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

OS

XX WO200283068-A2.

PN

XX

XX 24-OCT-2002.

PD

XX

XX 09-APR-2002; 2002WO-US11359.

PF

XX

XX 10-APR-2001; 2001US-282739P.

PR

XX 25-APR-2001; 2001US-286630P.

PR

XX 22-JUN-2001; 2001US-300373P.

PR

XX (AGEN-) AGENSYS INC.

PA

XX

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PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

PI

XX WPI; 2003-092956/08.

DR

XX

PT New composition comprising a substance that modulates the status of

PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune

PT responses or in assessing the status of 121P2A3 gene products in normal

PT versus cancerous tissues -

XX Claim 13; Page 185; 362pp; English.

XX The invention relates to a novel composition comprising a substance that

CC modulates the status of a protein, 121P2A3. The composition of the

CC invention has cytostatic and immunostimulant activity, and is useful as a

CC vaccine. The 121P2A3 proteins and polynucleotides are useful for

CC eliciting humoral or cellular immune response. The polynucleotides are

CC useful for characterising cytogenetic abnormalities of this chromosomal

CC locus, as tools that can be used to delineate cytogenetic abnormalities

CC in the chromosomal region that encodes 121P2A3 that may contribute to

CC malignant phenotype, and in assessing the status of 121P2A3 gene

CC products in normal versus cancerous tissues. The proteins are useful

CC for generating and characterising domain-specific antibodies, for

CC identifying agents or cellular factors that bind to 121P2A3 or a

CC particular structure domain, and in various therapeutic and diagnostic

CC contexts, including cancer vaccines. The antibodies or T cells reactive

CC with the product are useful in passive or active immunisation, and in

CC imaging methodologies for the management of cancer. The sequences shown

CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of

CC the invention.

XX Sequence 9 AA;

SQ

Query Match 44.4%; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4

Db 5 SLPQ 8

|||||

RESULT 59

ABP87159

ID ABP87159 standard; peptide; 9 AA.

AC ABP87159;

XX

XX 28-MAR-2003 (first entry)

DT

DE HLA protein 121P2A3 peptide #3514.

XX

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

KW humoral immune response; cellular immune response;

KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

OS

XX WO200283068-A2.

PN

XX

XX 24-OCT-2002.

PD

XX

XX 09-APR-2002; 2002WO-US11359.

PF

XX

XX 10-APR-2001; 2001US-282739P.

PR

XX 25-APR-2001; 2001US-286630P.

PR

XX 22-JUN-2001; 2001US-300373P.

PR

XX (AGEN-) AGENSYS INC.

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XX

XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

PI

XX WPI; 2003-092956/08.

DR

XX

XX New composition comprising a substance that modulates the status of

PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune

PT responses or in assessing the status of 121P2A3 gene products in normal

PT

PT versus cancerous tissues -

XX Claim 13; Page 187; 362pp; English.

CC The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of the invention.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
DB 6 SLPQ 9  
|||||

RESULT 60

ABP87242

ID ABP87242 standard; peptide; 9 AA.

XX AC ABP87242;

XX DT 28-MAR-2003 (first entry)

XX DE HLA protein 121P2A3 peptide #3597.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
KW humoral immune response; cellular immune response;  
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283068-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US11359.

XX PR 10-APR-2001; 2001US-282739P.

PR 25-APR-2001; 2001US-286630P.

PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.

XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues -

XX Claim 13; Page 188; 362pp; English.

XX The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of the invention.

XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
DB 1 SLPQ 4  
|||||

RESULT 61

ABP87320

ID ABP87320 standard; peptide; 9 AA.

XX AC ABP87320;

XX DT 28-MAR-2003 (first entry)

XX DE HLA protein 121P2A3 peptide #3675.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
KW humoral immune response; cellular immune response;  
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283068-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US11359.

XX PR 10-APR-2001; 2001US-282739P.

PR 25-APR-2001; 2001US-286630P.

PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.

XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues -

XX Claim 13; Page 189; 362pp; English.

XX The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the

CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating agents or cellular factors that bind to 121P2A3 or a  
 CC identifying agents or characterising domain-specific antibodies, for  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX  
 SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
 Db 5 SLPQ 8  
 ||||  
 ||||

RESULT 62  
 ABP87402  
 ID ABP87402 standard; peptide; 9 AA.

AC ABP87402;  
 DT 28-MAR-2003 (first entry)

XX HLA protein 121P2A3 peptide #3757.  
 DE Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

XX humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX Homo sapiens.

OS WO200283068-A2.  
 PN 24-OCT-2002.

XX 09-APR-2002; 2002WO-US11359.  
 XX 10-APR-2001; 2001US-282739P.

PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.

XX (AGEN-) AGENSYS INC.  
 PA Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;

PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -

XX Claim 13; Page 189; 362pp; English.

XX The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC eliciting humoral or cellular immune response. The polynucleotides are

CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating agents or cellular factors that bind to 121P2A3 or a  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
 Db 4 SLPQ 7  
 ||||  
 ||||

RESULT 63  
 ABP87403  
 ID ABP87403 standard; peptide; 9 AA.

AC ABP87403;  
 DT 28-MAR-2003 (first entry)

XX HLA protein 121P2A3 peptide #3758.  
 DE Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

XX humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX Homo sapiens.

OS WO200283068-A2.  
 PN 24-OCT-2002.

XX 09-APR-2002; 2002WO-US11359.  
 XX 10-APR-2001; 2001US-282739P.

PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.

XX (AGEN-) AGENSYS INC.  
 PA Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;

PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -

XX Claim 13; Page 189; 362pp; English.

XX The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC eliciting humoral or cellular immune response. The polynucleotides are

CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX  
 SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQP 4  
 ||||  
 Db 2 SLQP 5

RESULT 64  
 ABP87537  
 ID ABP87537 standard; peptide; 9 AA.  
 XX AC ABP87537;  
 XX DT 28-MAR-2003 (first entry)  
 XX DE HLA protein 121P2A3 peptide #3892.  
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response; SSH;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283068-A2.  
 XX PD 24-OCT-2002.  
 XX PF 09-APR-2002; 2002WO-US11359.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PR 22-JUN-2001; 2001US-300373P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.  
 XX PT New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX Claim 13; Page 191; 362pp; English.

CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies are useful

CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX  
 SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLQP 4  
 ||||  
 Db 3 SLQP 6

RESULT 65  
 ABP87705  
 ID ABP87705 standard; peptide; 9 AA.  
 XX AC ABP87705;  
 XX DT 28-MAR-2003 (first entry)  
 XX DE HLA protein 121P2A3 peptide #4060.  
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283068-A2.  
 XX PD 24-OCT-2002.  
 XX PF 09-APR-2002; 2002WO-US11359.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PR 22-JUN-2001; 2001US-300373P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.  
 XX PT New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX Claim 13; Page 192; 362pp; English.

CC The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive

CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX SQ Sequence '9 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPO 4  
 ||||  
 Db 4 SLPO 7

RESULT 66  
 ABP87729  
 ID ABP87729 standard; peptide; 9 AA.

XX AC ABP87729;  
 XX DT 28-MAR-2003 (first entry)  
 XX DE HLA protein 121P2A3 peptide #4084.  
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX OS Homo sapiens.

XX PN WO200283068-A2.  
 XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US11359.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.

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 XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -

XX Claim 13; Page 193; 362pp; English.

XX The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of

CC the invention.  
 XX SQ Sequence 9 AA;

Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPO 4  
 ||||  
 Db 3 SLPO 6

RESULT 67

ABP87761  
 ID ABP87761 standard; peptide; 9 AA.

XX AC ABP87761;  
 XX DT 28-MAR-2003 (first entry)  
 XX DE HLA protein 121P2A3 peptide #4116.  
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX OS Homo sapiens.

XX PN WO200283068-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US11359.  
 XX PR 10-APR-2001; 2001US-282739P.  
 XX PR 25-APR-2001; 2001US-286630P.  
 XX PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.

XX PI Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -

XX Claim 13; Page 193; 362pp; English.

XX The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.

XX SQ Sequence 9 AA;



Query Match		44.4%;	Score 4;	DB 24;	Length 9;												
Best Local Similarity		100.0%;	Pred. No. 9.3e+05;														
Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;										
		Gaps	0;														
QY	1 SLPQ 4																
DB	6 SLPQ 9																
RESULT 68																	
ABP87883	ID ABP87883 standard; peptide; 9 AA.																
XX	AC	ABP87883;															
XX	DT	28-MAR-2003 (first entry)															
XX	DE	HLA protein 121P2A3 peptide #4238.															
XX	KW	Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;															
KW	humoral immune response; cellular immune response;																
KW	suppression subtractive hybridisation; HLA; human leukocyte antigen.																
XX	OS	Homo sapiens.															
XX	PN	WO200283068-A2.															
XX	PD	24-OCT-2002.															
XX	PF	09-APR-2002; 2002WO-US11359.															
XX	PR	10-APR-2001; 2001US-282739P.															
PR	25-APR-2001; 2001US-286630P.																
PR	22-JUN-2001; 2001US-300373P.																
XX	PA	(AGEN-) AGENSYS INC.															
XX	PI	Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;															
PI	Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;																
XX	WPI; 2003-092956/08.																
XX	New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues -																
PS	Claim 13; Page 194; 362pp; English.																
XX	The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of the invention.																
XX	Sequence	9 AA;															
Query Match		44.4%;	Score 4;	DB 24;	Length 9;												
Best Local Similarity		100.0%;	Pred. No. 9.3e+05;														
Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;										
		Gaps	0;														
QY	1 SLPQ 4																
DB	6 SLPQ 9																

Query Match		44.4%;	Score 4;	DB 24;	Length 9;												
Best Local Similarity		100.0%;	Pred. No. 9.3e+05;														
Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;										
		Gaps	0;														
QY	1 SLPQ 4																
DB	5 SLPQ 8																
RESULT 69																	
ABP87884	ID ABP87884 standard; peptide; 9 AA.																
XX	AC	ABP87884;															
XX	DT	28-MAR-2003 (first entry)															
XX	DE	HLA protein 121P2A3 peptide #4239.															
XX	KW	Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;															
KW	humoral immune response; cellular immune response;																
KW	suppression subtractive hybridisation; HLA; human leukocyte antigen.																
XX	OS	Homo sapiens.															
XX	PN	WO200283068-A2.															
XX	PD	24-OCT-2002.															
XX	PF	09-APR-2002; 2002WO-US11359.															
XX	PR	10-APR-2001; 2001US-282739P.															
PR	25-APR-2001; 2001US-286630P.																
PR	22-JUN-2001; 2001US-300373P.																
XX	PA	(AGEN-) AGENSYS INC.															
XX	PI	Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;															
PI	Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;																
XX	WPI; 2003-092956/08.																
XX	New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues -																
PS	Claim 13; Page 194; 362pp; English.																
XX	The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune response. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of the invention.																
XX	Sequence	9 AA;															
Query Match		44.4%;	Score 4;	DB 24;	Length 9;												
Best Local Similarity		100.0%;	Pred. No. 9.3e+05;														
Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;										
		Gaps	0;														
QY	1 SLPQ 4																
DB	5 SLPQ 8																

Db 2 SLPQ 5  
|||||

RESULT 70  
ABP87956  
ID ABP87956 standard; peptide; 9 AA.  
XX AC ABP87956;  
XX AC  
XX DT 28-MAR-2003 (first entry)  
XX DE  
XX DE HLA protein 121P2A3 peptide #4311.  
XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
KW humoral immune response; cellular immune response;  
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
XX OS Homo sapiens.  
XX PN WO200283068-A2.  
XX PD 24-OCT-2002.  
XX PF 09-APR-2002; 2002WO-US11359.  
XX PR 10-APR-2001; 2001US-282739P.  
XX PR 25-APR-2001; 2001US-286630P.  
XX PR 22-JUN-2001; 2001US-300373P.  
XX PA (AGEN-) AGENSYS INC.  
XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
XX WPI; 2003-092956/08.  
XX DR New composition comprising a substance that modulates the status of  
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
PT responses or in assessing the status of 121P2A3 gene products in normal  
PT versus cancerous tissues -  
XX Claim 13; Page 195; 362pp; English.  
XX CC The invention relates to a novel composition comprising a substance that  
CC modulates the status of a protein, 121P2A3. The composition of the  
CC invention has cytostatic and immunostimulant activity, and is useful as a  
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
CC eliciting humoral or cellular immune response. The polynucleotides are  
CC useful for characterising cytogenetic abnormalities of this chromosomal  
CC locus, as tools that can be used to delineate cytogenetic abnormalities  
CC in the chromosomal region that encodes 121P2A3 that may contribute to  
CC malignant phenotype, and in assessing the status of 121P2A3 gene  
CC products in normal versus cancerous tissues. The proteins are useful  
CC for generating and characterising domain-specific antibodies, for  
CC identifying agents or cellular factors that bind to 121P2A3 or a  
CC particular structure domain, and in various therapeutic and diagnostic  
CC contexts, including cancer vaccines. The antibodies or T cells reactive  
CC with the product are useful in passive or active immunisation, and in  
CC imaging methodologies for the management of cancer. The sequences shown  
CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
CC the invention.  
XX SQ Sequence 9 AA;  
Query Match 44.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||||  
Db 1 SLPQ 4

RESULT 71

ABP88213  
ID ABP88213 standard; peptide; 9 AA.  
XX AC ABP88213;  
XX DT 28-MAR-2003 (first entry)  
XX DE HLA protein 121P2A3 peptide #4568.  
XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
KW humoral immune response; cellular immune response;  
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
XX OS Homo sapiens.  
XX PN WO200283068-A2.  
XX PD 24-OCT-2002.  
XX PF 09-APR-2002; 2002WO-US11359.  
XX PR 10-APR-2001; 2001US-282739P.  
XX PR 25-APR-2001; 2001US-286630P.  
XX PR 22-JUN-2001; 2001US-300373P.  
XX PA (AGEN-) AGENSYS INC.  
XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
XX WPI; 2003-092956/08.  
XX DR New composition comprising a substance that modulates the status of  
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
PT responses or in assessing the status of 121P2A3 gene products in normal  
PT versus cancerous tissues -  
XX Claim 13; Page 197; 362pp; English.  
XX CC The invention relates to a novel composition comprising a substance that  
CC modulates the status of a protein, 121P2A3. The composition of the  
CC invention has cytostatic and immunostimulant activity, and is useful as a  
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
CC eliciting humoral or cellular immune response. The polynucleotides are  
CC useful for characterising cytogenetic abnormalities of this chromosomal  
CC locus, as tools that can be used to delineate cytogenetic abnormalities  
CC in the chromosomal region that encodes 121P2A3 that may contribute to  
CC malignant phenotype, and in assessing the status of 121P2A3 gene  
CC products in normal versus cancerous tissues. The proteins are useful  
CC for generating and characterising domain-specific antibodies, for  
CC identifying agents or cellular factors that bind to 121P2A3 or a  
CC particular structure domain, and in various therapeutic and diagnostic  
CC contexts, including cancer vaccines. The antibodies or T cells reactive  
CC with the product are useful in passive or active immunisation, and in  
CC imaging methodologies for the management of cancer. The sequences shown  
CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
CC the invention.  
XX SQ Sequence 9 AA;  
Query Match 44.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||||  
Db 1 SLPQ 4

RESULT 72  
ABP88298

ID ABP88298 standard; peptide; 9 AA.  
 AC ABP88298;  
 XX  
 XX  
 XX 28-MAR-2003 (first entry)  
 XX  
 DE HLA protein 121P2A3 peptide #4653.  
 XX  
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283068-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 09-APR-2002; 2002WO-US11359.  
 XX  
 PF 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX  
 XX (AGEN-) AGENSYS INC.  
 XX  
 PA Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 PI WPI; 2003-092956/08.  
 XX  
 DR New composition comprising a substance that modulates the status of  
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX  
 PS Claim 13; Page 198; 362pp; English.  
 XX  
 XX The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 SLPQ 4  
 DB 5 SLPQ 8  
 XX  
 RESULT 73  
 ABP88299  
 ID ABP88299 standard; peptide; 9 AA.  
 XX  
 AC ABP88299;

XX  
 DT 28-MAR-2003 (first entry)  
 XX  
 DE HLA protein 121P2A3 peptide #4654.  
 XX  
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283068-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 09-APR-2002; 2002WO-US11359.  
 XX  
 PF 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX  
 XX (AGEN-) AGENSYS INC.  
 XX  
 PA Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;  
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 PI WPI; 2003-092956/08.  
 XX  
 DR New composition comprising a substance that modulates the status of  
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 XX  
 PS Claim 13; Page 198; 362pp; English.  
 XX  
 XX The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 SLPQ 4  
 DB 4 SLPQ 7  
 XX  
 RESULT 74  
 ABP88346  
 ID ABP88346 standard; peptide; 9 AA.  
 XX  
 AC ABP88346;  
 XX  
 XX 28-MAR-2003 (first entry)  
 XX

DE HLA protein 121P2A3 peptide #4701.  
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX Homo sapiens.  
 OS  
 XX WO200283068-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX  
 XX 09-APR-2002; 2002WO-US11359.  
 PF  
 XX 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DBH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 PI WPI; 2003-092956/08.  
 DR  
 XX New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 PT  
 XX Claim 13; Page 198; 362pp; English.  
 PS  
 XX The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 |||||  
 Db 6 SLPQ 9  
 |||||  
 RESULT 75  
 ABP88410  
 ID ABP88410 standard; peptide; 9 AA.  
 XX  
 XX AC ABP88410;  
 XX  
 DT 28-MAR-2003 (first entry)  
 XX  
 DE HLA protein 121P2A3 peptide #4765.  
 XX  
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
 KW

KW humoral immune response; cellular immune response;  
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
 XX Homo sapiens.  
 OS  
 XX WO200283068-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX  
 XX 09-APR-2002; 2002WO-US11359.  
 PF  
 XX 10-APR-2001; 2001US-282739P.  
 PR 25-APR-2001; 2001US-286630P.  
 PR 22-JUN-2001; 2001US-300373P.  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
 PI Afar DBH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
 PI WPI; 2003-092956/08.  
 DR  
 XX New composition comprising a substance that modulates the status of  
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
 PT responses or in assessing the status of 121P2A3 gene products in normal  
 PT versus cancerous tissues -  
 PT  
 XX Claim 13; Page 199; 362pp; English.  
 PS  
 XX The invention relates to a novel composition comprising a substance that  
 CC modulates the status of a protein, 121P2A3. The composition of the  
 CC invention has cytostatic and immunostimulant activity, and is useful as a  
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
 CC eliciting humoral or cellular immune response. The polynucleotides are  
 CC useful for characterising cytogenetic abnormalities of this chromosomal  
 CC locus, as tools that can be used to delineate cytogenetic abnormalities  
 CC in the chromosomal region that encodes 121P2A3 that may contribute to  
 CC malignant phenotype, and in assessing the status of 121P2A3 gene  
 CC products in normal versus cancerous tissues. The proteins are useful  
 CC for generating and characterising domain-specific antibodies, for  
 CC identifying agents or cellular factors that bind to 121P2A3 or a  
 CC particular structure domain, and in various therapeutic and diagnostic  
 CC contexts, including cancer vaccines. The antibodies or T cells reactive  
 CC with the product are useful in passive or active immunisation, and in  
 CC imaging methodologies for the management of cancer. The sequences shown  
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of  
 CC the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 44.4%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLPQ 4  
 |||||  
 Db 3 SLPQ 6  
 |||||

Search completed: November 25, 2003, 18:16:06  
 Job time : 31.1543 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 17.9043 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-19  
Perfect score: 9  
Sequence: 1 SLPQNILPL 9

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications\_AA.\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pcp.\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pcp.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pcp.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pcp.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	15	US-10-281-652-19
2	4	44.4	7	11	US-09-229-751A-28
3	4	44.4	9	9	US-09-880-713A-1
4	4	44.4	10	12	US-09-573-822C-655
5	4	44.4	11	14	US-10-101-487-94
6	4	44.4	11	14	US-10-101-487-98
7	4	44.4	12	12	US-09-990-832C-82
8	4	44.4	12	12	US-10-189-437-539
9	4	44.4	13	9	US-09-848-164-9
10	4	44.4	13	9	US-09-847-185-41
11	4	44.4	13	10	US-09-900-379-9
12	4	44.4	13	12	US-09-824-200-10
13	4	44.4	13	15	US-10-224-286-41
14	4	44.4	14	10	US-09-966-955A-39
15	4	44.4	14	15	US-10-028-075B-101
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Sequence 21, Appl  
Sequence 23, Appl

89 Sequence 28, Appl  
90 Sequence 208, App  
91 Sequence 335, App  
92 Sequence 25, Appl  
93 Sequence 62, Appl  
94 Sequence 25, Appl  
95 Sequence 14, Appl  
96 Sequence 28, Appl  
97 Sequence 150, App  
98 Sequence 436, App  
99 Sequence 67, Appl  
100 Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-10-281-652-19  
; Sequence 19, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-19

Query Match 100.0%; Score 9; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQNILPL 9  
Db 1 SLPQNILPL 9

RESULT 2  
US-09-229-751A-28  
; Sequence 28, Application US/09229751A  
; Publication No. US20030044838A1  
; GENERAL INFORMATION:  
; APPLICANT: Turnbough, Charles K  
; TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glenna Hendricks  
; STREET: P.O. Box 2509  
; CITY: Fairfax  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22031  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/229,751A  
; FILING DATE: 14-Jan-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hendricks, Glenna M  
; REGISTRATION NUMBER: 32,535  
; REFERENCE/DOCKET NUMBER: turn  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 425-8405  
; TELEFAX: (703) 425-8406  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-09-229-751A-28

Query Match 44.4%; Score 4; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 2 LPQN 5  
Db 4 LPQN 7

RESULT 3  
US-09-880-713A-1  
; Sequence 1, Application US/09880713A  
; Patent No. US20030049307A1  
; GENERAL INFORMATION:  
; APPLICANT: Abersold, Ruedi  
; APPLICANT: Zhou, Huilin  
; TITLE OF INVENTION: Selective Labeling and Isolation of Phosphopeptides and  
; TITLE OF INVENTION: Applications to Proteome Analysis  
; FILE REFERENCE: 39-00  
; CURRENT APPLICATION NUMBER: US/09/880,713A  
; CURRENT FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: US 60/210,972  
; PRIOR FILING DATE: 2000-06-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: bovine  
US-09-880-713A-1

Query Match 44.4%; Score 4; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
Db 5 SLPQ 8

RESULT 4  
US-09-573-822C-655  
; Sequence 655, Application US/09573822C  
; Publication No. US20030199011A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome se  
; FILE REFERENCE: Microbe patent

; CURRENT APPLICATION NUMBER: US/09/573,822C  
; CURRENT FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 804  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 655  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: mycoplasma genitalium  
; FEATURE:  
; OTHER INFORMATION: Sequence located in MG301 at 66-75 and may interact with Sequence  
; OTHER INFORMATION: this patent.  
US-09-573-822C-655

Query Match 44.4%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
Db 2 QNIL 5

RESULT 5  
US-10-101-487-94  
; Sequence 94, Application US/10101487  
; Publication No. US20020169125A1  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, DAVID W.  
; APPLICANT: BERGMAN, PHILIP A.  
; APPLICANT: LOFQUIST, ALAN  
; APPLICANT: PIETZ, GREGORY E.  
; APPLICANT: TOMPKINS, CHRISTOPHER K.  
; APPLICANT: WAGGONER JR., DAVID W.  
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 077319/0329  
; CURRENT APPLICATION NUMBER: US/10/101,487  
; CURRENT FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: 60/277,705  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-101-487-94

Query Match 44.4%; Score 4; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0

QY 1 SLPQ 4  
Db 8 SLPQ 11

RESULT 6  
US-10-101-487-98  
; Sequence 98, Application US/10101487  
; Publication No. US20020169125A1  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, DAVID W.  
; APPLICANT: BERGMAN, PHILIP A.  
; APPLICANT: LOFQUIST, ALAN  
; APPLICANT: PIETZ, GREGORY E.  
; APPLICANT: TOMPKINS, CHRISTOPHER K.  
; APPLICANT: WAGGONER JR., DAVID W.  
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 077319/0329

; CURRENT APPLICATION NUMBER: US/10/101,487  
; CURRENT FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: 60/277,705  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 98  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-101-487-98

Query Match 44.4%; Score 4; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
Db 8 SLPQ 11

RESULT 7  
US-09-990-832C-82  
; Sequence 82, Application US/09990832C  
; Publication No. US20030149235A1  
; GENERAL INFORMATION:  
; APPLICANT: University Court of the University of Glasgow  
; TITLE OF INVENTION: Targeting peptides  
; FILE REFERENCE: PC/MC/JM/P11910US  
; CURRENT APPLICATION NUMBER: US/09/990,832C  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 82  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Targeting peptide sequence  
US-09-990-832C-82

Query Match 44.4%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
Db 9 SLPQ 12

RESULT 8  
US-10-189-437-539  
; Sequence 539, Application US/10189437  
; Publication No. US20030194414A1  
; GENERAL INFORMATION:  
; APPLICANT: BOGOCH, SAMUEL  
; APPLICANT: BOGOCH, ELENORE S.  
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE  
; FILE REFERENCE: 09425/46905  
; CURRENT APPLICATION NUMBER: US/10/189,437  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: 10/105,232  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: 09/984,057  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 729  
; SOFTWARE: PatentIn 2.1

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; SEQ ID NO 539
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-437-539
Query Match      44.4%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 NILP 8
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Db      2 NILP 5

RESULT 9
US-09-848-164-9
; Sequence 9, Application US/09848164
; Patent No. US20020034513A1
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; Jiao, Jin-An
; Burkhardt, Martin
; Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/848,164
; FILING DATE: 03-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,615
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-848-164-9
Query Match      44.4%; Score 4; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLFQ 4
        |||||
Db      4 SLFQ 7

US-09-847-185-41
; Sequence 41, Application US/09847185
; Patent No. US20020076392A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: COMBINING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-847-185-41
Query Match      44.4%; Score 4; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 QNIL 7
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Db      1 QNIL 4

RESULT 11
US-09-900-379-9
; Sequence 9, Application US/09900379
; Publication No. US20020198144A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; Rhode, Peter R.
; Widanz, Jon A.
; Grammer, Susan
; Edwards, Ana C.
; Chavallaz, Pierre-Andre
; Jiao, Jin-An
; TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
```



STATE: Illinois  
COUNTRY: USA  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICANT: S. Pearson, Louise S.  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/776,084  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/US95/09816  
FILING DATE: 31-JUL-1995  
APPLICATION NUMBER: US 08/382,454  
FILING DATE: 01-FEB-1995  
APPLICATION NUMBER: US 08/283,302  
FILING DATE: 29-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match 44.4%; Score 4; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
DB 4 SLPQ 7

RESULT 12  
US-09-824-200-10  
Sequence 10, Application US/09824200  
Publication No. US20030167531A1  
GENERAL INFORMATION:  
APPLICANT: RUSSELL, DOUGLAS A.  
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF BIOACTIVE, AUTHENTIC  
FILE OF INVENTION: POLYPEPTIDES FROM PLANTS  
FILE REFERENCE: 16712.0031  
CURRENT APPLICATION NUMBER: US/09/824,200  
CURRENT FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/194,217  
PRIOR FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (4)  
OTHER INFORMATION: hydroxyproline

Query Match 44.4%; Score 4; DB 12; Length 13;

Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLPQ 4  
DB 10 SLPQ 13  
RESULT 13  
US-10-224-286-41  
Sequence 41, Application US/10224286  
Publication No. US20030108517A1  
GENERAL INFORMATION:  
APPLICANT: Soo Hoo, William  
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
RESPONSE USING SAME  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL & FLORES, LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 19-Aug-2002  
APPLICATION NUMBER: US/10/224,286  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/902,516  
FILING DATE: 29-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IM 2442  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)535-9001  
TELEFAX: (619)535-8949  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-10-224-286-41

Query Match 44.4%; Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
DB 1 QNIL 4

RESULT 14  
US-09-966-955A-39  
Sequence 39, Application US/09966955A  
Patent No. US2002015563A1  
GENERAL INFORMATION:  
APPLICANT: Perez-Villar, Juan J.  
APPLICANT: Chang, Han  
APPLICANT: Yang, Wen-Pin  
APPLICANT: Wu, Yuli  
APPLICANT: Whitney, Gena S.  
APPLICANT: Kanner, Steven B.

; TITLE OF INVENTION: Identification and Cloning of a Full-length Human  
; TITLE OF INVENTION: Clink-related Gene, MIST (Mast Cell Immunoreceptor  
; TITLE OF INVENTION: Signal Transducer)  
; FILE REFERENCE: 3053-4113US1  
; CURRENT APPLICATION NUMBER: US/09/966,955A  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: 60/237030  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-966-955A-39

Query Match 44.4%; Score 4; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 NILP 8  
Db 10 NILP 13

RESULT 15  
US-10-028-075B-101  
; Sequence 101, Application US/10028075B  
; Publication No. US20030113733A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisrar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Gene regulator  
; FILE REFERENCE: 2183-5223US  
; CURRENT APPLICATION NUMBER: US/10/028,075B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: EP 01203748.7  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 101  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence  
US-10-028-075B-101

Query Match 44.4%; Score 4; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLPQ 4  
Db 9 SLPQ 12

RESULT 16  
US-10-029-206A-101  
; Sequence 101, Application US/10029206A  
; Publication No. US20030119720A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisrar A.  
; APPLICANT: Benner, Robert  
; TITLE OF INVENTION: Oligopeptide treatment of anthrax  
; FILE REFERENCE: 2183-5222US  
; CURRENT APPLICATION NUMBER: US/10/029,206A  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/821,380  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 101

; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Mm.42246.3  
US-10-029-206A-101

Query Match 44.4%; Score 4; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLPQ 4  
Db 9 SLPQ 12

RESULT 17  
US-09-813-383-4  
; Sequence 4, Application US/09813383  
; Patent No. US20020111312A1  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, KENNETH G.  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS  
; FILE REFERENCE: 098810/027 8741  
; CURRENT APPLICATION NUMBER: US/09/813,383  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-813-383-4

Query Match 44.4%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLPQ 4  
Db 8 SLPQ 11

RESULT 18  
US-09-813-383-5  
; Sequence 5, Application US/09813383  
; Patent No. US20020111312A1  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, KENNETH G.  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS  
; FILE REFERENCE: 098810/027 8741  
; CURRENT APPLICATION NUMBER: US/09/813,383  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-813-383-5

Query Match 44.4%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
|||  
Db 11 SLPQ 14

## RESULT 19

US-09-813-383-6  
; Sequence 6, Application US/09813383  
; Patent No. US20020111312A1  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, KENNETH G.  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS  
; FILE REFERENCE: 098810/027 8741  
; CURRENT APPLICATION NUMBER: US/09/813,383  
; CURRENT FILING DATE: 2001-10-12  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-813-383-6

Query Match 44.4%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
|||  
Db 3 SLPQ 6

## RESULT 20

US-09-923-831-25  
; Sequence 25, Application US/09923831  
; Patent No. US20020115142A1  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Val'rie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/923,831  
; CURRENT FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 09/183,706  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-831-25

Query Match 44.4%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QNIL 7  
|||  
Db 1 QNIL 4

## RESULT 21

US-09-813-463A-4  
; Sequence 4, Application US/09813463A  
; Patent No. US20020147303A1

; GENERAL INFORMATION:  
; APPLICANT: WARREN, KENNETH G.  
; APPLICANT: CATZ, INGRID  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS  
; FILE REFERENCE: 098810/027 8740  
; CURRENT APPLICATION NUMBER: US/09/813,463A  
; CURRENT FILING DATE: 2002-01-11  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-813-463A-4

Query Match 44.4%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
|||  
Db 8 SLPQ 11

## RESULT 22

US-09-813-463A-5  
; Sequence 5, Application US/09813463A  
; Patent No. US20020147303A1  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, KENNETH G.  
; APPLICANT: CATZ, INGRID  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS  
; FILE REFERENCE: 098810/027 8740  
; CURRENT APPLICATION NUMBER: US/09/813,463A  
; CURRENT FILING DATE: 2002-01-11  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-813-463A-5

Query Match 44.4%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
|||  
Db 11 SLPQ 14

## RESULT 23

US-09-813-463A-6  
; Sequence 6, Application US/09813463A  
; Patent No. US20020147303A1  
; GENERAL INFORMATION:  
; APPLICANT: WARREN, KENNETH G.  
; APPLICANT: CATZ, INGRID  
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND  
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO  
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS  
; FILE REFERENCE: 098810/027 8740

; CURRENT APPLICATION NUMBER: US/09/813,463A  
 ; CURRENT FILING DATE: 2002-01-11  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: peptide  
 US-09-813-463A-6

Query Match 44.4%; Score 4; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
 ||||  
 Db 3 SLPQ 6

## RESULT 24

US-09-766-889A-37  
 ; Sequence 37, Application US/09766889A  
 ; Patent No. US20020164654A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Luiten, Rosalie  
 ; APPLICANT: Boon-Falleur, Thierry  
 ; APPLICANT: van der Bruggen, Pierre  
 ; APPLICANT: Stroobant, Vincent  
 ; APPLICANT: Demotte, Nathalie  
 ; APPLICANT: Schultz, Erwin  
 ; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
 ; FILE REFERENCE: L0461/7104  
 ; CURRENT APPLICATION NUMBER: US/09/766,889A  
 ; CURRENT FILING DATE: 2001-01-19  
 ; PRIOR APPLICATION NUMBER: US 60/177,242  
 ; PRIOR FILING DATE: 2000-01-20  
 ; PRIOR APPLICATION NUMBER: US 60/243,212  
 ; PRIOR FILING DATE: 2000-10-25  
 ; NUMBER OF SEQ ID NOS: 59  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 37  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-766-889A-37

Query Match 44.4%; Score 4; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
 ||||  
 Db 1 QNIL 4

## RESULT 25

US-09-895-814-964  
 ; Sequence 964, Application US/09895814  
 ; Publication No. US20020193296A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqiu  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel X.  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William T.  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Hural, John  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Houghton, Raymond L.  
 ; APPLICANT: Vinals de Bassols, Carlota  
 ; APPLICANT: Foy, Teresa  
 ; APPLICANT: Fanger, Gary R.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 ; FILE REFERENCE: 210121.427C26  
 ; CURRENT APPLICATION NUMBER: US/09/895,814  
 ; CURRENT FILING DATE: 2001-06-29  
 ; NUMBER OF SEQ ID NOS: 990  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 964  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-895-814-964

Query Match 44.4%; Score 4; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
 ||||  
 Db 2 SLPQ 5

## RESULT 26

US-10-009-792A-23  
 ; Sequence 23, Application US/10009792A  
 ; Publication No. US20030153049A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LEE, Sang-Yup  
 ; APPLICANT: JEONG, Ki-Jun  
 ; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN  
 ; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)  
 ; FILE REFERENCE: HYLEE60.001APC  
 ; CURRENT APPLICATION NUMBER: US/10/009,792A  
 ; CURRENT FILING DATE: 2002-10-29  
 ; PRIOR APPLICATION NUMBER: PCT/KR01/00549  
 ; PRIOR FILING DATE: 2001-03-31  
 ; PRIOR APPLICATION NUMBER: KR 10-2000-0017052  
 ; PRIOR FILING DATE: 2000-03-31  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 23  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-009-792A-23

Query Match 44.4%; Score 4; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
 ||||  
 Db 9 SLPQ 12

## RESULT 27

US-10-144-678A-964  
 ; Sequence 964, Application US/10144678A  
 ; Publication No. US20030157089A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun

```

; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Basols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 964
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-964

Query Match 44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4
Db 2 SLPQ 5

RESULT 28
US-10-170-832-66
; Sequence 66, Application US/10170832
; Publication No. US20030170792A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-66

Query Match 44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-494

Query Match 44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7
Db 1 QNIL 4

RESULT 30
US-10-239-313A-495
; Sequence 495, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 495
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-495

Query Match 44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 495
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-495

Query Match 44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 4 QNIL 7  
|||||  
Db 1 QNIL 4

## RESULT 31

US-10-239-313A-496  
; Sequence 496, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 496  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-496

Query Match 44.4%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
|||||  
Db 1 QNIL 4

## RESULT 32

US-10-239-313A-497  
; Sequence 497, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 497  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-497

Query Match 44.4%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
|||||  
Db 1 QNIL 4

## RESULT 33

US-10-239-313A-498  
; Sequence 498, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 498  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-498

Query Match 44.4%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
|||||  
Db 1 QNIL 4

## RESULT 34

US-10-239-313A-499  
; Sequence 499, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 499  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-239-313A-499

Query Match 44.4%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7

```
Db      1 QNIL 4

RESULT 35
US-10-239-313A-500
; Sequence 500, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 500
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-500

Query Match      44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 QNIL 7
      ||||
      1 QNIL 4

RESULT 36
US-10-239-313A-502
; Sequence 502, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 502
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-502

Query Match      44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 QNIL 7
      ||||
      1 QNIL 4

RESULT 37
US-10-239-313A-503
; Sequence 503, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 503
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-503

Query Match      44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 QNIL 7
      ||||
      1 QNIL 4

RESULT 38
US-10-294-025-964
; Sequence 964, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 964
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-964

Query Match      44.4%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
      ||||
      2 SLPQ 5

RESULT 39
US-10-012-896-964
; Sequence 964, Application US/10012896
; Publication No. US20020183251A1
```

; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals de Bassols, Carlota  
; APPLICANT: Foy, Teresa  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Wantanabe, Yoshihiro  
; APPLICANT: Meagher, Madeleine Joy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C27  
; CURRENT APPLICATION NUMBER: US/10/012,896  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 1011  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 964  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-012-896-964

Query Match 44.4%; Score 4; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLFQ 4  
Db 2 SLFQ 5

RESULT 40  
US-10-161-097-24  
; Sequence 24, Application US/10161097  
; Publication No. US20030096404A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSENZWEIG, Michael  
; APPLICANT: PYKEIT, Mark J.  
; APPLICANT: SCADEN, David T.  
; APPLICANT: POZNANSKY, Mark C.  
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
; TITLE OF INVENTION: DEVICES  
; FILE REFERENCE: C1005/7012/KA/ERG  
; CURRENT APPLICATION NUMBER: US/10/161,097  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US/09/574,749  
; PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 60/107,972  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: PCT/US99/26795  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/524,749  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24

; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Homo Sapiens source  
US-10-161-097-24

Query Match 44.4%; Score 4; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
Db 1 QNIL 4

RESULT 41  
US-08-736-019-187  
; Sequence 187, Application US/08736019  
; Publication No. US20030207799A1  
; GENERAL INFORMATION:  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Stroobant, Paul  
; APPLICANT: Minghetti, Luisa  
; APPLICANT: Waterfield, Michael  
; APPLICANT: Marchionni, Mark  
; APPLICANT: Chen, Mario  
; APPLICANT: Hiles, Ian  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 189  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM Compatible Pentium  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/736,019  
; FILING DATE: 22-OCT-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/471,833  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/036,555  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,173  
; FILING DATE: 23-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/907,138  
; FILING DATE: 30-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/940,389  
; FILING DATE: 03-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/863,703  
; FILING DATE: 03-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 91 07566.3  
; FILING DATE: 10-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bieker-Brady, Kristina  
; REGISTRATION NUMBER: 39,109  
; REFERENCE/DOCKET NUMBER: 04585/00200Q  
; TELECOMMUNICATION INFORMATION:



TELEPHONE: (617) 428-0200  
TELEFAX: (617) 428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 187:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-736-019-187

Query Match 44.4%; Score 4; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 PQNI 6  
DB 8 PQNI 11

RESULT 42  
US-09-841-132-40  
; Sequence 40, Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; FILE REFERENCE: 210121.469C8  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
; SEQ ID NO 40  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: made in the lab  
US-09-841-132-40

Query Match 44.4%; Score 4; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 NILP 8  
DB 3 NILP 6

RESULT 43  
US-09-841-132-99  
; Sequence 99, Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; FILE REFERENCE: 210121.469C8  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
; SEQ ID NO 99  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab

US-09-841-132-99

Query Match 44.4%; Score 4; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 NILP 8  
DB 4 NILP 7

RESULT 44  
US-10-189-437-538  
; Sequence 538, Application US/10189437  
; Publication No. US20030194414A1  
; GENERAL INFORMATION:  
; APPLICANT: BOGOCH, SAMUEL  
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE  
; FILE REFERENCE: 09425/46905  
; CURRENT APPLICATION NUMBER: US/10/189,437  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: 10/105,232  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: 09/984,057  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 729  
; SOFTWARE: PatentIn 2.1  
; SEQ ID NO 538  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-189-437-538

Query Match 44.4%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 NILP 8  
DB 2 NILP 5

RESULT 45  
US-09-864-761-40780  
; Sequence 40780, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 40780  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC015842.4  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.91  
; US-09-864-761-40780

Query Match 44.4%; Score 4; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9,9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NILP 8  
|||  
Db 10 NILP 13

RESULT 46  
US-09-864-761-46244  
; Sequence 46244, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 46244  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL157826.2  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4  
; US-09-864-761-46244

Query Match 44.4%; Score 4; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9,9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILPL 9  
|||  
Db 11 ILPL 14

RESULT 47  
US-09-984-056-40  
; Sequence 40, Application US/09984056  
; Patent No. US20020120106A1  
; GENERAL INFORMATION:  
; APPLICANT: BOGOCH, SAMUEL  
; APPLICANT: BOGOCH, ELENORE S.  
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICONS AND METHODS OF USE  
; FILE REFERENCE: 09425-46903  
; CURRENT APPLICATION NUMBER: US/09/984,056  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 09/146,755  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: 09/817,144  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 08/198,139  
; PRIOR FILING DATE: 1994-02-17  
; NUMBER OF SEQ ID NOS: 103

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; SOFTWARE: PatentIn 2.1
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Ophiostoma novo-ulmi
US-09-984-056-40

Query Match      44.4%; Score 4; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ILPL 9
      |||||
Db      3 ILPL 6

RESULT 48
US-09-984-057-40
; Sequence 40, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN-CONTAINING SEQUENCES
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Ophiostoma novo-ulmi
US-09-984-057-40

Query Match      44.4%; Score 4; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ILPL 9
      |||||
Db      3 ILPL 6

RESULT 49
US-09-873-415-1
; Sequence 1, Application US/09873415
; Publication No. US20030166589A1
; GENERAL INFORMATION:
; APPLICANT: Wildbaum, Gizi
; APPLICANT: Netzer, Nir
; APPLICANT: Karin, Nathan
; TITLE OF INVENTION: METHOD AND PHARMACEUTICAL COMPOSITION FOR THE TREATMENT
; FILE REFERENCE: 01/21982
; CURRENT APPLICATION NUMBER: US/09/873,415
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-873-415-1

Query Match      44.4%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
      |||||
Db      3 SLPQ 6

RESULT 50
US-10-105-232-40
; Sequence 40, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Ophiostoma novo-ulmi
US-10-105-232-40

Query Match      44.4%; Score 4; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ILPL 9
      |||||
Db      3 ILPL 6

RESULT 51
US-10-189-437-40
; Sequence 40, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
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; SOFTWARE: PatentIn 2.1
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Ophiostoma novo-ulmi
US-10-189-437-40

Query Match
Best Local Similarity 44.4%; Score 4; DB 12; Length 17;
Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILPL 9
   ||||
Db 3 ILPL 6

RESULT 52
US-10-189-437-537
; Sequence 537, Application US/10189437
; Publication No. US2003019441A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 537
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-437-537

Query Match
Best Local Similarity 44.4%; Score 4; DB 12; Length 17;
Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NILP 8
   ||||
Db 3 NILP 6

RESULT 53
US-09-836-433-28
; Sequence 28, Application US/09836433
; Publication No. US2003004979A1
; GENERAL INFORMATION:
; APPLICANT: Ueda, Shigeru
; TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
; FILE REFERENCE: NO. US2003004979A1 Assigned
; CURRENT APPLICATION NUMBER: US/09/836,433
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Bacillus brevis
US-09-836-433-28

Query Match
Best Local Similarity 44.4%; Score 4; DB 11; Length 18;
Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4
   ||||
Db 11 SLPQ 14

RESULT 54
US-10-084-813-238
; Sequence 238, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-238

Query Match
Best Local Similarity 44.4%; Score 4; DB 15; Length 18;
Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4
   ||||
Db 15 SLPQ 18

RESULT 55
US-10-084-813-239
; Sequence 239, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 239
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-239

Query Match
Best Local Similarity 44.4%; Score 4; DB 15; Length 18;
Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4
   ||||
Db 11 SLPQ 14
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; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR.
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 967
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-967

Query Match      44.4%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ILPL 9
Db      12 ILPL 15

RESULT 59
US-09-736-084-20
; Sequence 20, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/736,084
; FILING DATE: 13-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. US20020107211A1, September 30, 1994
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
;

; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
; US-10-084-813-240

Query Match      44.4%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
Db      7 SLPQ 10

RESULT 57
US-10-084-813-241
; Sequence 241, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
; US-10-084-813-241

Query Match      44.4%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
Db      3 SLPQ 6

RESULT 58
US-10-225-567A-967
; Sequence 967, Application US/10225567A
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```

; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR.
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 967
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-967

Query Match      44.4%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ILPL 9
Db      12 ILPL 15

RESULT 59
US-09-736-084-20
; Sequence 20, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
; NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/736,084
; FILING DATE: 13-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. US20020107211A1, September 30, 1994
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
;

; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
; US-10-084-813-240

Query Match      44.4%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
Db      7 SLPQ 10

RESULT 57
US-10-084-813-241
; Sequence 241, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
; US-10-084-813-241

Query Match      44.4%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
Db      3 SLPQ 6

RESULT 58
US-10-225-567A-967
; Sequence 967, Application US/10225567A
```

;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; DESCRIPTION: ob peptide fragment  
;; FRAGMENT TYPE: Internal  
;; ORIGINAL SOURCE:  
;; ORGANISM: Murine  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-736-084-20

Query Match 44.4%; Score 4; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
Db 5 SLPQ 8

## RESULT 60

US-09-858-580-25  
; Sequence 25, Application US/09858580  
; Patent No. US20020176864A1  
; GENERAL INFORMATION:  
; APPLICANT: Burrows et al.  
; TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of  
; antigen-specific T-Cells  
; FILE REFERENCE: 48823  
; CURRENT APPLICATION NUMBER: US/09/858,580  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/153,586  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/064,552  
; PRIOR FILING DATE: 1997-09-16  
; PRIOR APPLICATION NUMBER: 60/064,555  
; PRIOR FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: artificial  
; OTHER INFORMATION: peptide  
US-09-858-580-25

Query Match 44.4%; Score 4; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
Db 2 SLPQ 5

## RESULT 61

US-09-858-580-30  
; Sequence 30, Application US/09858580  
; Patent No. US20020176864A1  
; GENERAL INFORMATION:  
; APPLICANT: Burrows et al.  
; TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of  
; antigen-specific T-Cells  
; FILE REFERENCE: 48823  
; CURRENT APPLICATION NUMBER: US/09/858,580  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/153,586  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/064,552  
; PRIOR FILING DATE: 1997-09-16  
; PRIOR APPLICATION NUMBER: 60/064,555  
; PRIOR FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 30

;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 30  
;; LENGTH: 19  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: artificial  
;; OTHER INFORMATION: peptide  
US-09-858-580-30

Query Match 44.4%; Score 4; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
Db 2 SLPQ 5

## RESULT 62

US-09-847-172-25  
; Sequence 25, Application US/09847172  
; Publication No. US20030007978A1  
; GENERAL INFORMATION:  
; APPLICANT: BURROWS, GREGORY G.  
; APPLICANT: VANDENBARK, ARTHUR A.  
; TITLE OF INVENTION: RECOMBINANT MHC MOLECULES USEFUL FOR MANIPULATION OF ANTIGEN-SPE  
; CIFIC T-CELLS  
; FILE REFERENCE: 899-58137  
; CURRENT APPLICATION NUMBER: US/09/847,172  
; PRIOR FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: US 60/200,942  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 09/153,586  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: US 60/064,555  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/064,552  
; PRIOR FILING DATE: 1997-09-16  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-847-172-25

Query Match 44.4%; Score 4; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
Db 2 SLPQ 5

## RESULT 63

US-09-847-172-30  
; Sequence 30, Application US/09847172  
; Publication No. US20030007978A1  
; GENERAL INFORMATION:  
; APPLICANT: BURROWS, GREGORY G.  
; APPLICANT: VANDENBARK, ARTHUR A.  
; TITLE OF INVENTION: RECOMBINANT MHC MOLECULES USEFUL FOR MANIPULATION OF ANTIGEN-SPE  
; CIFIC T-CELLS  
; FILE REFERENCE: 899-58137  
; CURRENT APPLICATION NUMBER: US/09/847,172  
; CURRENT FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: US 60/200,942

; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 09/153,586  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: US 60/064,555  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/064,552  
; PRIOR FILING DATE: 1997-09-16  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-847-172-30

Query Match 44.4%; Score 4; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
|||  
Db 2 SLPQ 5

## RESULT 64

US-09-316-393-20  
; Sequence 20, Application US/09316393  
; Publication No. US20030040039A1  
; GENERAL INFORMATION:  
; APPLICANT: THE ROCKEFELLER UNIVERSITY  
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/316.393  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/292,345  
; FILING DATE: August 17, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-087  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; DESCRIPTION: ob peptide  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: Murine  
US-09-316-393-20

Query Match 44.4%; Score 4; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4  
|||  
Db 5 SLPQ 8

## RESULT 65

US-09-841-132-230  
; Sequence 230, Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
; FILE REFERENCE: 210121.469C8  
; CURRENT APPLICATION NUMBER: US/09/841,132  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
; SEQ ID NO 230  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-841-132-230

Query Match 44.4%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NILP 8  
|||  
Db 14 NILP 17

## RESULT 66

US-09-841-132-231  
; Sequence 231, Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
; FILE REFERENCE: 210121.469C8  
; CURRENT APPLICATION NUMBER: US/09/841,132  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
; SEQ ID NO 231  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-841-132-231

Query Match 44.4%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NILP 8  
|||  
Db 10 NILP 13

## RESULT 67

US-09-841-132-232

; Sequence 232, Application US/09841132

; Patent No. US20020061848A1

; GENERAL INFORMATION:

; APPLICANT: Bhatia, Ajay

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Probst, Peter

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

; FILE REFERENCE: 210121.469C8

; CURRENT APPLICATION NUMBER: US/09/841.132

; CURRENT FILING DATE: 2001-04-23

; NUMBER OF SEQ ID NOS: 599

; SOFTWARE: FastSeq for Windows Version 3.0/4.0

; SEQ ID NO 232

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

US-09-841-132-232

Query Match

44.4%; Score 4; DB 9; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NILP 8

Db 5 NILP 8

## RESULT 68

US-09-999-220B-60

; Sequence 60, Application US/09999220B

; Publication No. US2003005923A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB

; TITLE OF INVENTION: K-alpha1, AND VARIANTS THEREOF

; FILE REFERENCE: D0050NP

; CURRENT APPLICATION NUMBER: US/09/999,220B

; CURRENT FILING DATE: 2002-06-04

; PRIOR APPLICATION NUMBER: US 60/245,383

; PRIOR FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: US 60/257,780

; PRIOR FILING DATE: 2000-12-21

; PRIOR APPLICATION NUMBER: US 60/269,854

; PRIOR FILING DATE: 2001-02-20

; NUMBER OF SEQ ID NOS: 143

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 60

; LENGTH: 20

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-999-220B-60

Query Match

44.4%; Score 4; DB 11; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILPL 9

Db 11 ILPL 14

## RESULT 69

US-10-029-386-34147

; Sequence 34147, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 34147  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC009290.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6  
US-10-029-386-34147

Query Match

44.4%; Score 4; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QNIL 7

Db 8 QNIL 11

## RESULT 70

US-10-189-437-536

; Sequence 536, Application US/10189437

; Publication No. US20030194414A1

; GENERAL INFORMATION:

; APPLICANT: BOGOCH, SAMUEL

; APPLICANT: BOGOCH, ELENORE S.

; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE

; FILE REFERENCE: 09425/46905

; CURRENT APPLICATION NUMBER: US/10/189,437

; CURRENT FILING DATE: 2002-07-08

; PRIOR APPLICATION NUMBER: 10/105,232

; PRIOR FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: 09/984,057

; PRIOR FILING DATE: 2001-10-26

; PRIOR APPLICATION NUMBER: 60/303,396

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: 60/278,761

; PRIOR FILING DATE: 2001-03-27

; NUMBER OF SEQ ID NOS: 729

; SOFTWARE: PatentIn 2.1

; SEQ ID NO 536

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-189-437-536

Query Match

44.4%; Score 4; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NILP 8

Db 4 NILP 7

## RESULT 71

US-10-043-487-457

; Sequence 457, Application US/10043487

; Publication No. US20030055220A1

; GENERAL INFORMATION:

; APPLICANT: HYBRIGENICS

; APPLICANT: PIERRE, LEGRAIN

; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptides

; TITLE OF INVENTION: mammalian polypeptides

; FILE REFERENCE: B4778A



```
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 457
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Shigella Flexneri
US-10-043-487-457

Query Match      44.4%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 NILP 8
Db      8 NILP 11

RESULT 72
US-09-834-765-737
; Sequence 737, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.6USUL
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 737
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-737

Query Match      33.3%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLP 3
Db      1 SLP 3

RESULT 73
US-09-852-910-9
; Sequence 9, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S
; FILE REFERENCE: 2861-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 4
```

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; TYPE: PRT
; ORGANISM: mammal
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(4)
; OTHER INFORMATION: PAR-34
US-09-852-910-9

Query Match      33.3%; Score 3; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LPQ 4
Db      1 LPQ 3

RESULT 74
US-10-137-867-60
; Sequence 60, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 60
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-60

Query Match      33.3%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLP 3
Db      2 SLP 4

RESULT 75
US-10-122-822-12
; Sequence 12, Application US/10122822
; Publication No. US20030084477A1
; GENERAL INFORMATION:
; APPLICANT: Purdue Research Foundation
; TITLE OF INVENTION: GENES ENHANCING DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: 7024-511
; CURRENT APPLICATION NUMBER: US/10/122,822
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/202,161
; PRIOR FILING DATE: 1999-06-14
```

; PRIOR APPLICATION NUMBER: PCT/US97/10382  
; PRIOR FILING DATE: 1997-06-12  
; PRIOR APPLICATION NUMBER: 60/046,494  
; PRIOR FILING DATE: 1997-05-14  
; PRIOR APPLICATION NUMBER: 60/019,633  
; PRIOR FILING DATE: 1996-06-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: ASCII  
; SEQ ID NO 12  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Lycopersicon esculentum  
; FEATURE:  
; OTHER INFORMATION: Amino Acids 36-39 of SEQ ID NO:1 and SEQ ID NO:4; amino acids 8-1  
; OTHER INFORMATION: ID NO:2.  
US-10-122-822-12

Query Match 33.3%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 LPL 9  
|||  
Db 2 LPL 4

Search completed: November 25, 2003, 20:25:45  
Job time : 18.9043 secs



ALIGNMENTS

RESULT 1  
US-09-641-803-19  
; Sequence 19, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265-00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-641-803-19

Query Match 100.0%; Score 9; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQNILPL 9  
| | | | | | | |  
Db 1 SLPQNILPL 9

RESULT 2  
US-09-053-003-18  
; Sequence 18, Application US/09053003  
; Patent No. 6207391  
; GENERAL INFORMATION:  
; APPLICANT: Wu, Pengguang  
; APPLICANT: McKinney, Judi  
; TITLE OF INVENTION: High-Throughput Screening Assays for  
; TITLE OF INVENTION: Modulators of STAT4 and STAT6 Activity  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/053,003  
; FILING DATE: 31-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Timothy L.  
; REGISTRATION NUMBER: 35,367  
; REFERENCE/DOCKET NUMBER: 018781-0008000US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 5  
; OTHER INFORMATION: /product= "OTHER"  
; OTHER INFORMATION: /note= "Xaa = Tyr or phosphotyrosine"  
US-09-053-003-18

Query Match 55.6%; Score 5; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPQNI 6  
| | | | |  
Db 6 LPQNI 10

RESULT 3  
US-09-053-003-23  
; Sequence 23, Application US/09053003  
; Patent No. 6207391  
; GENERAL INFORMATION:  
; APPLICANT: Wu, Pengguang  
; APPLICANT: McKinney, Judi  
; TITLE OF INVENTION: High-Throughput Screening Assays for  
; TITLE OF INVENTION: Modulators of STAT4 and STAT6 Activity  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/053,003  
; FILING DATE: 31-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Timothy L.  
; REGISTRATION NUMBER: 35,367  
; REFERENCE/DOCKET NUMBER: 018781-0008000US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 5  
; OTHER INFORMATION: /product= "OTHER"  
; OTHER INFORMATION: /note= "Xaa = phosphotyrosine"  
US-09-053-003-23

Query Match 55.6%; Score 5; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LPQNI 6  
|  
|  
|  
|  
|  
|  
Db 6 LPQNI 10

RESULT 4  
US-09-000-286A-2  
; Sequence 2, Application US/09000286A  
; Patent No. 6449562  
; GENERAL INFORMATION:  
; APPLICANT: Luminex Corporation  
; APPLICANT: Chandler, Van S.  
; APPLICANT: Fulton, Jerrold R.  
; APPLICANT: Chandler, Mark B.  
; TITLE OF INVENTION: Multiplexed Analysis of Clinical Specimens Apparatus and Method  
; FILE REFERENCE: 112802.500  
; CURRENT APPLICATION NUMBER: US/09/000,286A  
; CURRENT FILING DATE: 1998-08-18  
; PRIOR APPLICATION NUMBER: PCT/US96/16198  
; PRIOR FILING DATE: 1996-10-10  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-000-286A-2

Query Match 44.4%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLPQ 4  
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|  
|  
|  
|  
|  
Db 3 SLPQ 6

RESULT 5  
US-09-000-286A-1  
; Sequence 1, Application US/09000286A  
; Patent No. 6449562  
; GENERAL INFORMATION:  
; APPLICANT: Luminex Corporation  
; APPLICANT: Chandler, Van S.  
; APPLICANT: Fulton, Jerrold R.  
; APPLICANT: Chandler, Mark B.  
; TITLE OF INVENTION: Multiplexed Analysis of Clinical Specimens Apparatus and Method  
; FILE REFERENCE: 112802.500  
; CURRENT APPLICATION NUMBER: US/09/000,286A  
; CURRENT FILING DATE: 1998-08-18  
; PRIOR APPLICATION NUMBER: PCT/US96/16198  
; PRIOR FILING DATE: 1996-10-10  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-000-286A-1

Query Match 44.4%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLPQ 4  
|  
|  
|  
|  
|  
|  
Db 4 SLPQ 7

RESULT 6  
5194592-46  
; Patent No. 5194592

; APPLICANT: YOSHIDA, HAJIME  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL  
; POLYPEPTIDES DERIVATIVES OF HUMAN GRANULOCYTE COLONY  
; STIMULATING FACTOR  
; NUMBER OF SEQUENCES: 83  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/318,527  
; FILING DATE: 3-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 136,647  
; FILING DATE: 22-DEC-1987  
; SEQ ID NO:46:  
; LENGTH: 8  
5194592-46

Query Match 44.4%; Score 4; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLPQ 4  
|  
|  
|  
|  
|  
|  
Db 2 SLPQ 5

RESULT 7  
US-08-318-856A-42  
; Sequence 42, Application US/08318856A  
; Patent No. 5972351  
; GENERAL INFORMATION:  
; APPLICANT: Adrian V.S. Hill, et al.  
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-  
; TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE  
; TITLE OF INVENTION: ANTIGENS (AS AMENDED)  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., Suite 800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1+  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,856A  
; FILING DATE: October 3, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 92 08 068.8  
; FILING DATE: April 3, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 92 17 704.7  
; FILING DATE: August 20, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/GB93/00711  
; FILING DATE: April 5, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee Cheng  
; REGISTRATION NUMBER: 40,949  
; REFERENCE/DOCKET NUMBER: 263-PP1R1577US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 721-8200  
; TELEFAX: (202) 721-8250  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-318-856A-42

Query Match 44.4%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||  
Db 6 SLPQ 9

## RESULT 8

US-08-159-339A-1079  
; Sequence 1079, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; TITLE OF INVENTION: Uses  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1079:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-159-339A-1079

Query Match 44.4%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||  
Db 1 SLPQ 4

## RESULT 9

US-08-159-339A-371

; Sequence 371, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; TITLE OF INVENTION: Uses  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 371:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-159-339A-371

Query Match 44.4%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||  
Db 1 SLPQ 4

## RESULT 10

US-08-159-339A-1096  
; Sequence 1096, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; TITLE OF INVENTION: Uses  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP

```

, STREET: Two Embarcadero Center, Eighth Floor
, CITY: San Francisco
, STATE: CA
, COUNTRY: USA
, ZIP: 94111-3834
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Diskette
, COMPUTER: IBM Compatible
, OPERATING SYSTEM: DOS
, SOFTWARE: FastSeq for Windows Version 2.0
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/159,339A
, FILING DATE: 29-NOV-1993
, CLASSIFICATION: 424
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/926,666
, FILING DATE: 07-AUG-1992
, APPLICATION NUMBER: US 08/027,746
, FILING DATE: 05-MAR-1993
, APPLICATION NUMBER: US 08/103,396
, FILING DATE: 06-AUG-1993
, ATTORNEY/AGENT INFORMATION:
, NAME: Weber, Ellen Lauver
, REGISTRATION NUMBER: 32,762
, REFERENCE/DOCKET NUMBER: 018623-005030US
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (415) 576-0200
, TELEFAX: (415) 576-0300
, TELEX:
, INFORMATION FOR SEQ ID NO: 1096:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 10 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: peptide
US-08-159-339A-1096

```

```
Query Match      44.4%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
```

Qy	1	4
	SLPQ	
D <sub>b</sub>	6	9
	SLPO	

```

RESULT 11
5194592-21
; Patent NO. 5194592
; APPLICANT: YOSHIDA, HAJIME
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL
; POLYPEPTIDES DERIVATIVES OF HUMAN GRANULOCYTE COLONY
; STIMULATING FACTOR
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/318,527
; FILING DATE: 3-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 136,647
; FILING DATE: 22-DEC-1987
; SEQ ID NO:21:
; LENGTH: 10
5194592-21

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Query Match      44.4%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Qy	1	4
	SLPQ	

  

Db	2	5
	SLPQ	

RESULT 12  
 US-08-934-222-40  
 ; Sequence 40, Application US/08934222  
 ; Patent No. 5928896  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EVANS, Herbert J.  
 ; APPLICANT: KINI, R. Manjunatha  
 ; TITLE OF INVENTION: Polypeptides That Include Conformation-  
 ; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
 ; TITLE OF INVENTION: Site  
 ; NUMBER OF SEQUENCES: 153  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: Suite 500, 3000 K Street NW  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20007  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/934,222  
 ; FILING DATE: 19-SEPT-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/532,818  
 ; FILING DATE: 03-MAY-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: U.S. 08/143,364  
 ; FILING DATE: 29-OCT-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: U.S. 08/051,741  
 ; FILING DATE: 23-APR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Isaacson, John P.  
 ; REGISTRATION NUMBER: 33,751  
 ; REFERENCE/DOCKET NUMBER: 040433/0148  
 ; INFORMATION FOR SEQ ID NO: 40:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 12 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 US-08-934-222-40

```
Query Match      44.4%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 SLPQ 4  
|||  
Db 8 SLPQ 11

RESULT 13  
US-08-933-402-40  
; Sequence 40, Application US/08933402  
; Patent No. 5948887  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINL, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Prote  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA

ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,402  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-402-40

Query Match 44.4%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||  
DB 8 SLPQ 11

RESULT 14  
US-09-207-621-40  
Sequence 40, Application US/09207621  
Patent No. 5952465  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/207,621  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-207-621-40

Query Match 44.4%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||  
DB 8 SLPQ 11

RESULT 15  
US-08-532-818-40  
Sequence 40, Application US/08532818  
Patent No. 5965698  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-532-818-40

Query Match 44.4%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||



Db 8 SLPQ 11

## RESULT 16

US-09-231-797-40  
; Sequence 40, Application US/09231797  
; Patent No. 6084066  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,797  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-231-797-40

Query Match 44.4%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4

Db 8 SLPQ 11

## RESULT 17

US-08-934-224-40  
; Sequence 40, Application US/08934224  
; Patent No. 6100044  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,843  
; FILING DATE: 19-SEPT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:

; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,224  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-934-224-40

Query Match 44.4%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4

Db 8 SLPQ 11

## RESULT 18

US-08-933-843-40  
; Sequence 40, Application US/08933843  
; Patent No. 611069  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,843  
; FILING DATE: 19-SEPT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-933-843-40

Query Match          44.4%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
        ||||
Db      8 SLPQ 11

RESULT 19
US-09-306-756-4
; Sequence 4, Application US/09306756
; Patent No. 6136542
; GENERAL INFORMATION:
; APPLICANT: Demers, Brigitte
; APPLICANT: Sansonetti, Philippe J.
; APPLICANT: Parsot, Claude
; TITLE OF INVENTION: METHOD FOR SCREENING FOR INHIBITORS AND ACTIVATORS OF
; TYPE OF INVENTION: TYPE III SECRETION MACHINERY IN GRAM-NEGATIVE BACTERIA
; FILE REFERENCE: 03495.0171
; CURRENT APPLICATION NUMBER: US/09/306,756
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: 60/085,234
; EARLIER FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Shigella flexneri
; US-09-306-756-4

Query Match          44.4%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
        ||||
Db      9 SLPQ 12

RESULT 20
US-08-934-223-40
; Sequence 40, Application US/08934223
; Patent No. 6147189
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TYPE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
```

```
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-934-223-40

Query Match          44.4%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
        ||||
Db      8 SLPQ 11

RESULT 21
US-09-413-492-40
; Sequence 40, Application US/09413492
; Patent No. 6258550
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TYPE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-413-492-40

Query Match 44.4%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
|||  
DB 8 SLPQ 11

RESULT 22  
US-09-199-242E-10  
Sequence 10, Application US/09199242E  
Patent No. 6280991

GENERAL INFORMATION:  
APPLICANT: Raines, Ronald T

TITLE OF INVENTION: Engineered Cytotoxic Ribonuclease  
FILE REFERENCE: Engineered Cytotoxic Ribonuclease  
CURRENT APPLICATION NUMBER: US/09/199,242E

CURRENT FILING DATE: 1998-11-24  
PRIOR APPLICATION NUMBER: 08/950,866

PRIOR FILING DATE: 1997-10-15

PRIOR APPLICATION NUMBER: 60/097,797

PRIOR FILING DATE: 1998-09-28

NUMBER OF SEQ ID NOS: 11

SOFTWARE: WordPerfect

SEQ ID NO 10

LENGTH: 12

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Partial sequence from human eosinophil derived neurotoxin

US-09-199-242E-10

Query Match 44.4%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQNI 6  
|||  
DB 7 PQNI 10

RESULT 23

US-07-977-672-7

Sequence 7, Application US/07977672

Patent No. 5651993

GENERAL INFORMATION:

APPLICANT: Edelson, Richard L.

APPLICANT: Gasparro, Francis P.

APPLICANT: Tigelaar, Robert E.

TITLE OF INVENTION: Specific Immune System Modulation

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Ave.

CITY: Boston

STATE: MA

COUNTRY: U.S.A.  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,672  
FILING DATE: 19921118  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: Y0060/7001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/720-3500

TELEFAX: 617/720-2441

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: mouse

US-07-977-672-7

Query Match 44.4%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILPL 9  
|||  
DB 2 ILPL 5

RESULT 24

US-07-977-672-8

Sequence 8, Application US/07977672

Patent No. 5651993

GENERAL INFORMATION:

APPLICANT: Edelson, Richard L.

APPLICANT: Gasparro, Francis P.

APPLICANT: Tigelaar, Robert E.

TITLE OF INVENTION: Specific Immune System Modulation

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Ave.

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/977,672

FILING DATE: 19921118

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: Y0060/7001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/720-3500

TELEFAX: 617/720-2441

INFORMATION FOR SEQ ID NO: 8:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: mouse
US-07-977-672-8

Query Match 44.4%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILPL 9
Db 2 ILPL 5

RESULT 25
US-08-596-387B-9
; Sequence 9, Application US/08596387B
; Patent No. 5869270
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Jiso, Jin-An
; APPLICANT: Burkhardt, Martin
; APPLICANT: Wong, Hing
; TITLE OF INVENTION: MHC COMPLEXES AND USSES THEREOF
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bade International, Inc.
; STREET: 1717 Deerfield Road
; CITY: Deerfield
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60015
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,387B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09816
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/382,454
; FILING DATE: 01-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,302
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pearson, Louise S.
; REGISTRATION NUMBER: 32,369
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 267-5300
; TELEFAX: (708) 267-5376
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-596-387B-9

Query Match 44.4%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4
Db 4 SLPQ 7

RESULT 26
US-08-902-516-41
; Sequence 41, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-902-516-41

Query Match 44.4%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7
Db 1 QNIL 4

RESULT 27
US-08-964-725-16
; Sequence 16, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLASS, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
```

NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,725  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5997.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5939265e  
US-08-964-725-16

Query Match 44.4%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NILP 8  
DB 2 NILP 5

RESULT 28  
US-09-067-615-9  
Sequence 9, Application US/09067615  
Patent No. 6309645  
GENERAL INFORMATION:  
APPLICANT: Rhode, Peter R.  
APPLICANT: Jiao, Jin-An  
APPLICANT: Burkhardt, Martin  
APPLICANT: Wong, Hing  
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bade International, Inc.  
STREET: 1717 Deerfield Road  
CITY: Deerfield  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60015  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/067,615  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/596,387  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/382,454  
FILING DATE: 01-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/283,302  
FILING DATE: 29-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pearson, Louise S.  
REGISTRATION NUMBER: 32,369  
REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708) 267-5300  
TELEFAX: (708) 267-5376  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
US-09-067-615-9  
Query Match 44.4%; Score 4; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
DB 4 SLPQ 7

RESULT 29  
US-08-822-940-7  
Sequence 7, Application US/08822940  
Patent No. 6355238  
GENERAL INFORMATION:  
APPLICANT: Edelson, Richard L.  
Gasparro, Francis P.  
Tigelaar, Robert E.  
TITLE OF INVENTION: Specific Immune System Modulation  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Ave.  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/822,940  
FILING DATE: 21-Mar-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,672  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: Y0060/7001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid



; CITY: Deerfield  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60015  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/09816A  
; FILING DATE: 31-JUL-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/382,454  
; FILING DATE: 01-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/283,302  
; FILING DATE: 29-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pearson, Louise S.  
; REGISTRATION NUMBER: 32,369  
; REFERENCE/DOCKET NUMBER: STR-4665-CIP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (708) 267-5300  
; TELEFAX: (708) 267-5376  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; PCT-US95-09816A-9

Query Match 44.4%; Score 4; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
Db 4 SLPQ 7

RESULT 33  
US-08-082-849B-19  
; Sequence 19, Application US/08082849B  
; Patent No. 5677274  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Klimpel, Kurt R.  
; APPLICANT: Arora, Naveen  
; APPLICANT: Singh, Yogendra  
; APPLICANT: Nichols, Peter J.  
; TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and  
; TITLE OF INVENTION: Related Methods  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082,849B  
; FILING DATE: 25-JUN-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/021,601  
; FILING DATE: 12-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 15280-161-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-082-849B-19

Query Match 44.4%; Score 4; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
Db 10 QNIL 13

RESULT 34  
US-08-950-866-7  
; Sequence 7, Application US/08950866  
; Patent No. 5840296  
; GENERAL INFORMATION:  
; APPLICANT: Raines, Ronald T  
; TITLE OF INVENTION: Engineered Cytotoxic Ribonuclease A  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/950,866  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seay, Nicholas J.  
; REGISTRATION NUMBER: 27386  
; REFERENCE/DOCKET NUMBER: 960296.94592  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608-251-5000  
; TELEFAX: 608-251-9166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-950-866-7

Query Match 44.4%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQNI 6  
Db 8 PQNI 11

```
RESULT 35
PCT-US94-01624-19
; Sequence 19, Application PC/TUS9401624
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Atora, Naveen
; APPLICANT: Singh, Yogendra
; APPLICANT: Nicholas, Peter J.
; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
; TITLE OF INVENTION: RELATED METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
; STREET: Steuart Street Tower, 20th Floor, One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01624
; FILING DATE: June 25, 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-01624-19

Query Match 44.4%; Score 4; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7
DB 10 QNIL 13

RESULT 36
US-08-268-251-9
; Sequence 9, Application US/08268251
; Patent No. 5585475
; GENERAL INFORMATION:
; APPLICANT: Jamieson, Gordon A
; APPLICANT: Dedman, John R
; APPLICANT: Kaezel, Marcia A
; TITLE OF INVENTION: Calmodulin-Binding Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,251
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/831,219
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 272.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-268-251-9

Query Match 44.4%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4
DB 2 SLPQ 5

RESULT 37
US-08-210-880B-7
; Sequence 7, Application US/08210880B
; Patent No. 5641486
; GENERAL INFORMATION:
; APPLICANT: HINRICH, STEVEN H.
; APPLICANT: ORTEN, DANA J.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR INHIBITING
; TITLE OF INVENTION: CRIB/ATF1 FAMILY DETERMINED TRANSCRIPTION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HENDERSON & STURM
; STREET: 1125 S. 103RD ST., #330
; CITY: OMAHA
; STATE: NE
; COUNTRY: US
; ZIP: 68124
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,880B
; FILING DATE: 18-MAR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JONDLE, ROBERT J.
; REGISTRATION NUMBER: 33,915
; REFERENCE/DOCKET NUMBER: 63066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 402-398-9000
; TELEFAX: 402-398-9005
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
```



STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-210-880B-7

Query Match 44.4%; Score 4; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
 ||||  
 Db 7 SLPQ 10

## RESULT 38

US-08-771-411-7  
 ; Sequence 7, Application US/08771411  
 ; Patent No. 5844096  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HINRICHS, STEVEN H.  
 ; APPLICANT: ORTEN, DANA J.  
 ; TITLE OF INVENTION: METHOD AND COMPOSITION FOR INHIBITING  
 ; TITLE OF INVENTION: CREB/ATF1 FAMILY DETERMINED TRANSCRIPTION  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HENDERSON & STURM  
 ; STREET: 1125 S. 103RD ST., #330  
 ; CITY: OMAHA  
 ; STATE: NE  
 ; COUNTRY: US  
 ; ZIP: 68124

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/771,411  
 FILING DATE: 20-DEC-1996  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/210,880  
 FILING DATE: 18-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JONDLE, ROBERT J.  
 REGISTRATION NUMBER: 33,915  
 REFERENCE/DOCKET NUMBER: 63066  
 TELEPHONE: 402-398-9000  
 TELEFAX: 402-398-9005  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-771-411-7

Query Match 44.4%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
 ||||  
 Db 7 SLPQ 10

## RESULT 39

US-08-735-253-18  
 ; Sequence 18, Application US/08735253  
 ; Patent No. 5942491  
 ; GENERAL INFORMATION:

APPLICANT: Root-Bernstein, Robert S.  
 TITLE OF INVENTION: Methods and Compositions for Treating  
 TITLE OF INVENTION: Arthritis  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.  
 STREET: 180 N. Stetson  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: U.S.A.  
 ZIP: 60601

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/735,253  
 FILING DATE:  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 5942491thrup, Thomas E.  
 REGISTRATION NUMBER: 33,268  
 REFERENCE/DOCKET NUMBER: MIC3302P0010US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 616-5400  
 TELEFAX: (312) 616-5460  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-735-253-18

Query Match 44.4%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQ 4  
 ||||  
 Db 3 SLPQ 6

## RESULT 40

US-09-036-582-22  
 ; Sequence 22, Application US/09036582A  
 ; Patent No. 5965381  
 ; GENERAL INFORMATION:  
 ; APPLICANT: van der Bruggen, Pierre  
 ; APPLICANT: Cornelis, Guy R.  
 ; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
 ; TITLE OF INVENTION: WITH RECOMBINANT YERSINIA  
 ; FILE REFERENCE: 11154  
 ; CURRENT APPLICATION NUMBER: US/09/036,582A  
 ; CURRENT FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 22  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Human Tyrosinase peptide  
 ; US-09-036-582-22

Query Match 44.4%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
 ||||  
 Db 1 QNIL 4

```
RESULT 41
US-09-183-706-25
; Sequence 25, Application US/09183706
; Patent No. 6245525
; GENERAL INFORMATION:
; APPLICANT: Martelange, Valrie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461/7054
; CURRENT APPLICATION NUMBER: US/09/183,706
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 09/122,989
; EARLIER FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-183-706-25

Query Match      44.4%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 QNIL 7
        ||||
Db      1 QNIL 4

RESULT 42
US-09-166-448-66
; Sequence 66, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Cortbals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-66

Query Match      44.4%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 QNIL 7
        ||||
Db      1 QNIL 4

RESULT 43
US-09-567-995-25
; Sequence 25, Application US/09567995
; Patent No. 6303756
; GENERAL INFORMATION:
; APPLICANT: Martelange, Val,rie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: 11727

Query Match      44.4%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
        ||||
Db      12 SLPQ 15

RESULT 44
US-09-194-062-5
; Sequence 5, Application US/09194062
; Patent No. 6344442
; GENERAL INFORMATION:
; APPLICANT: HABENICHT, URSULA- FRIEDERIKE
; APPLICANT: LOBBIA, ALESSANDRO
; TITLE OF INVENTION: ZONA PELLUCIDA PROTEINS FOR CONTRACEPTION
; FILE REFERENCE: SCH-1660
; CURRENT APPLICATION NUMBER: US/09/194,062
; CURRENT FILING DATE: 1997-05-03
; EARLIER APPLICATION NUMBER: PCT/DE97/01092
; EARLIER FILING DATE: 1997-05-22
; EARLIER APPLICATION NUMBER: DE 196 22 289.3
; EARLIER FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide derived from murine or homo sapiens origin
US-09-194-062-5

Query Match      44.4%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLPQ 4
        ||||
Db      12 SLPQ 15

RESULT 45
US-09-165-863-22
; Sequence 22, Application US/09165863
; Patent No. 6407063
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Demotte, Nathalie
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy
; APPLICANT: Stroobant, Vincent
; APPLICANT: Lurquin, Christophe
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Chauv, Pascal
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; TITLE OF INVENTION: PROCEDURE
; FILE REFERENCE: 11727
```

; CURRENT APPLICATION NUMBER: US/09/165.863  
; CURRENT FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human Tyrosinase peptide  
; US-09-165-863-22

Query Match 44.4%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 4 QNIL 7  
|  
|  
|  
|  
Db 1 QNIL 4

## RESULT 46

US-09-009-953-74  
; Sequence 74, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly  
; Reactive DR Restricted Epitopes

; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA

ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-09-009-953-74

Query Match 44.4%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 SLPO 4  
|  
|  
|  
|

Db 10 SLPO 13

## RESULT 47

US-09-009-953-198  
; Sequence 198, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly  
; Reactive DR Restricted Epitopes

; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA

ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 198:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 198:  
US-09-009-953-198

Query Match 44.4%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 4 QNIL 7  
|  
|  
|  
|  
Db 1 QNIL 4

## RESULT 48

US-09-697-884-66  
; Sequence 66, Application US/09697884  
; Patent No. 6426217  
; GENERAL INFORMATION:  
; APPLICANT: Chau, Pascal  
; APPLICANT: Vantomme, Val,rie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Corthals, Jurgan  
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES

FILE REFERENCE: L0461/7052  
CURRENT APPLICATION NUMBER: US/09/697,884  
CURRENT FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: 09/166,448  
PRIOR FILING DATE: 1998-10-05  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 66  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-697-884-66

Query Match 44.4%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
Db 1 QNIL 4

## RESULT 49

US-09-289-350-22  
Sequence 22, Application US/09289350  
Patent No. 6531451  
GENERAL INFORMATION:  
APPLICANT: Chaux, Pascal  
APPLICANT: Luiten, Rosalie  
APPLICANT: Demotte, Nathalie  
APPLICANT: Delfour, Marie-Therese  
APPLICANT: Lurquin, Christophe  
APPLICANT: Traversari, Catia  
APPLICANT: Stroobant, Vincent  
APPLICANT: Cornelis, Guy R.  
APPLICANT: Boon-Falleur, Thierry  
APPLICANT: Van Der Bruggen, Pierre  
TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
FILE REFERENCE: 117272  
CURRENT APPLICATION NUMBER: US/09/289,350  
CURRENT FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: 09/165,863  
PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Human Tyrosinase peptide  
US-09-289-350-22

Query Match 44.4%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
Db 1 QNIL 4

## RESULT 50

US-09-574-749B-24  
Sequence 24, Application US/09574749B  
Patent No. 6548299  
GENERAL INFORMATION:  
APPLICANT: ROSENZWEIG, Michael  
APPLICANT: PYKETT, Mark J.  
APPLICANT: SCADDEN, David T.  
APPLICANT: POZNANSKY, Mark C.  
TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
TITLE OF INVENTION: DEVICES

FILE REFERENCE: C1005/7012/KA/ERG  
CURRENT APPLICATION NUMBER: US/09/574,749B  
CURRENT FILING DATE: 2002-05-31  
PRIOR APPLICATION NUMBER: US 60/107,972  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: PCT/US99/26795  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: US 09/524,749  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: S8  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 24  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Homo Sapiens source  
US-09-574-749B-24

Query Match 44.4%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QNIL 7  
Db 1 QNIL 4

## RESULT 51

PCT-US93-01112-9  
Sequence 9, Application PC/TUS9301112  
GENERAL INFORMATION:  
APPLICANT: Jamieson, Gordon A  
APPLICANT: Kedman, John R  
APPLICANT: Kaetzel, Marcia A  
TITLE OF INVENTION: Calmodulin-Binding Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/01112  
FILING DATE: 19930208  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/831,219  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Grant D  
REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 272.001  
TELEPHONE: (510) 601-2706  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-01112-9

Query Match 44.4%; Score 4; DB 5; Length 15;

```
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 SLPQ 4
Db 2 SLPQ 5

RESULT 52
US-08-145-006C-17
; Sequence 17, Application US/08145006C
; Patent No. 5656452
; GENERAL INFORMATION:
; APPLICANT: Rao, Anjana
; APPLICANT: Hogan, Patrick Gerald
; APPLICANT: McCaffrey, Patricia
; APPLICANT: Jain, Jugnu
; TITLE OF INVENTION: NF-ATp, A T LYMPHOCYTE
; TITLE OF INVENTION: DNA-BINDING PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,006C
; FILING DATE: October 29, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,052
; FILING DATE: February 11, 1993
; APPLICATION NUMBER: 08/006,067
; FILING DATE: January 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 04590/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-145-006C-17

Query Match 44.4%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QNIL 7
Db 13 QNIL 16

RESULT 53
US-08-307-724B-19
; Sequence 19, Application US/08307724B
; Patent No. 5785974
; GENERAL INFORMATION:
; APPLICANT: Jos Ignacio Casal Alvarez
; APPLICANT: Carmen Vela Olmo

; APPLICANT: Joannes Pieter Maria Langeveld
; APPLICANT: Robert Hans Melloen
; APPLICANT: Kristian Dalsgaard
; TITLE OF INVENTION: "SYNTHETIC PEPTIDES AND
; TITLE OF INVENTION: VACCINES AGAINST PARVOVIRUS"
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HARRISON & EGBERT
; STREET: 1018 Preston Street, Suite 100
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch., 1.2 MB storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS (version 3.30)
; SOFTWARE: WordPerfect5.1 (WP5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,724B
; FILING DATE: September 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/ES94/00006
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: John S. Egbert
; REGISTRATION NUMBER: 30627
; REFERENCE/DOCKET NUMBER: 11523
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 223-4034
; TELEFAX: (713) 223-4873
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: N-terminal end
; ORIGINAL SOURCE:
; ORGANISM: Canine Parvovirus (CPV)
; STRAIN: Type 2
; US-08-307-724B-19

Query Match 44.4%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLPQ 4
Db 12 SLPQ 15

RESULT 54
US-08-469-526A-187
; Sequence 187, Application US/08469526A
; Patent No. 5792849
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Maio Su
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
```

```

;
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,526A
; FILING DATE: 06 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-7045
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 187:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-469-526A-187
;
; Query Match 44.4%; Score 4; DB 1; Length 16;
; Best Local Similarity 100.0%; Pred. No. 1.8e-02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 3 PQNI 6
; Db 8 PQNI 11
;
; RESULT 55
; US-08-734-591A-187
; Sequence 187, Application US/08734591A
; Patent No. 5854220
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Hiles, Ian
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95

```

```

;
; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,591A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,335
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 187:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
; US-08-734-591A-187
;
; Query Match 44.4%; Score 4; DB 2; Length 16;
; Best Local Similarity 100.0%; Pred. No. 1.8e-02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 3 PQNI 6
; Db 8 PQNI 11
;
; RESULT 56
; US-08-470-335-187
; Sequence 187, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; PREPARATION AND USE
; FILE REFERENCE: 04585/00200B
; CURRENT APPLICATION NUMBER: US/08/470,335F
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187

```

;  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Bos taurus  
US-08-470-335-187

Query Match 44.4%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQNI 6  
Db 8 PQNI 11

## RESULT 57

US-08-735-021-187  
; Sequence 187, Application US/08735021B  
; Patent No. 6194377  
; GENERAL INFORMATION:  
; APPLICANT: GOODEARL, ANDREW  
; APPLICANT: STROOBANT, PAUL  
; APPLICANT: MINGHETTI, LUISA  
; APPLICANT: WATERFIELD, MICHAEL  
; APPLICANT: MARCHIONNI, MARK  
; APPLICANT: CHEN, MARIO S.  
; APPLICANT: HILES, IAN  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR

; FILE REFERENCE: 04585/00200L  
; CURRENT APPLICATION NUMBER: US/08/735,021B  
; CURRENT FILING DATE: 1996-10-22  
; EARLIER APPLICATION NUMBER: 08/472,065  
; EARLIER FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 08/036,555  
; EARLIER FILING DATE: 1993-03-24  
; EARLIER APPLICATION NUMBER: 07/965,173  
; EARLIER FILING DATE: 1992-10-23  
; EARLIER APPLICATION NUMBER: 07/940,389  
; EARLIER FILING DATE: 1992-09-03  
; EARLIER APPLICATION NUMBER: 07/907,138  
; EARLIER FILING DATE: 1992-06-30  
; EARLIER APPLICATION NUMBER: 07/863,703  
; EARLIER FILING DATE: 1992-04-03  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 187  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Bos taurus  
US-08-735-021-187

Query Match 44.4%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQNI 6  
Db 8 PQNI 11

## RESULT 58

US-08-734-664A-187  
; Sequence 187, Application US/08734664A  
; Patent No. 6204241  
; GENERAL INFORMATION:  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Stroobant, Paul  
; APPLICANT: Minghetti, Luisa  
; APPLICANT: Waterfield, Michael  
; APPLICANT: Marchionni, Mark  
; APPLICANT: Chen, Mario  
; APPLICANT: Hiles, Ian  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR

; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 187  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM Compatible Pentium  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/734,664A  
; FILING DATE: 22-OCT-1996  
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/249,322  
; FILING DATE: 26-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/036,555  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,173  
; FILING DATE: 23-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/940,389  
; FILING DATE: 03-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/907,138  
; FILING DATE: 30-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/863,703  
; FILING DATE: 03-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 91 07566.3  
; FILING DATE: 10-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bleker-Brady, Kristina  
; REGISTRATION NUMBER: 39,109  
; REFERENCE/DOCKET NUMBER: 04585/00200J  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 428-0200  
; TELEFAX: (617) 428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 187:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-734-664A-187

Query Match 44.4%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQNI 6  
Db 8 PQNI 11

## RESULT 59

US-08-470-339-187  
; Sequence 187, Application US/08470339C  
; Patent No. 6232286  
; GENERAL INFORMATION:  
; APPLICANT: GOODEARL, ANDREW  
; APPLICANT: STROOBANT, PAUL  
; APPLICANT: MINGHETTI, LUISA  
; APPLICANT: WATERFIELD, MICHAEL

APPLICANT: MARCHIONNI, MARK  
APPLICANT: CHEN, MARIO S.  
APPLICANT: HILES, IAN  
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
PREPARATION AND USE  
FILE REFERENCE: 04595/002008  
CURRENT APPLICATION NUMBER: US/08/470,339C  
CURRENT FILING DATE: 1995-06-06  
EARLIER APPLICATION NUMBER: 08/036,555  
EARLIER FILING DATE: 1993-03-24  
EARLIER APPLICATION NUMBER: 07/940,389  
EARLIER FILING DATE: 1992-09-03  
EARLIER APPLICATION NUMBER: 07/907,138  
EARLIER FILING DATE: 1992-06-30  
EARLIER APPLICATION NUMBER: 07/863,703  
EARLIER FILING DATE: 1992-04-03  
EARLIER APPLICATION NUMBER: 91 07566.3 GB  
EARLIER FILING DATE: 1999-04-10  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 187  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Bos taurus  
US-08-470-339-187

Query Match 44.4%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQNI 6  
Db 8 PQNI 11

RESULT 60  
US-09-556-877-40  
Sequence 40, Application US/09556877  
Patent No. 6432916  
GENERAL INFORMATION:  
APPLICANT: Probst, Peter  
APPLICANT: Bhatia, Ajay  
APPLICANT: Skeiky, Yasir  
APPLICANT: Fling, Steve  
APPLICANT: Maisonneuve, Jeff  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
DIAGNOSIS OF CHLAMYDIAL INFECTION  
FILE REFERENCE: 210121.469C5  
CURRENT APPLICATION NUMBER: US/09/556,877  
CURRENT FILING DATE: 2000-04-19  
NUMBER OF SEQ ID NOS: 305  
SOFTWARE: FastSeq for Windows Version 3.0/4.0  
SEQ ID NO 40  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: made in the lab  
US-09-556-877-40

Query Match 44.4%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NILP 8  
Db 3 NILP 6

RESULT 61  
US-09-556-877-99  
Sequence 99, Application US/09556877  
Patent No. 6432916

GENERAL INFORMATION:  
APPLICANT: Probst, Peter  
APPLICANT: Bhatia, Ajay  
APPLICANT: Skeiky, Yasir  
APPLICANT: Fling, Steve  
APPLICANT: Maisonneuve, Jeff  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
DIAGNOSIS OF CHLAMYDIAL INFECTION  
FILE REFERENCE: 210121.469C5  
CURRENT APPLICATION NUMBER: US/09/556,877  
CURRENT FILING DATE: 2000-04-19  
NUMBER OF SEQ ID NOS: 305  
SOFTWARE: FastSeq for Windows Version 3.0/4.0  
SEQ ID NO 99  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Made in a lab  
US-09-556-877-99

Query Match 44.4%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NILP 8  
Db 4 NILP 7

RESULT 62  
US-09-288-594A-40  
Sequence 40, Application US/09288594A  
Patent No. 6447779  
GENERAL INFORMATION:  
APPLICANT: Probst, Peter  
APPLICANT: Bhatia, Ajay  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Fling, Steven P.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE TREATMENT  
AND DIAGNOSIS OF CHLAMYDIAL INFECTION  
FILE REFERENCE: 210121.469C1  
CURRENT APPLICATION NUMBER: US/09/288,594A  
CURRENT FILING DATE: 1999-04-08  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 40  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: made in the lab  
US-09-288-594A-40

Query Match 44.4%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NILP 8  
Db 3 NILP 6

RESULT 63  
US-09-620-412C-40  
Sequence 40, Application US/09620412C  
Patent No. 6448234  
GENERAL INFORMATION:  
APPLICANT: Steven P. Fling  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
DIAGNOSIS OF CHLAMYDIAL INFECTION  
FILE REFERENCE: 210121.469C7  
CURRENT APPLICATION NUMBER: US/09/620,412C



```
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 40
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: made in the lab
US-09-620-412C-40

Query Match      44.4%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 NILP 8
Db      3 NILP 6

RESULT 64
US-09-620-412C-99
; Sequence 99, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 99
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-99

Query Match      44.4%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 NILP 8
Db      4 NILP 7

RESULT 65
US-09-410-568-40
; Sequence 40, Application US/09410568
; Patent No. 6555115
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fang, Hang
; APPLICANT: Jen, Shyian
; APPLICANT: Stromberg, Erica Jean
; APPLICANT: Enghart, Susan E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.469C2
; CURRENT APPLICATION NUMBER: US/09/410,568
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 40
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: made in the lab
US-09-410-568-40

Query Match      44.4%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 NILP 8
Db      4 NILP 7

RESULT 66
US-09-410-568-99
; Sequence 99, Application US/09410568
; Patent No. 6555115
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fang, Hang
; APPLICANT: Jen, Shyian
; APPLICANT: Stromberg, Erica Jean
; APPLICANT: Enghart, Susan E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.469C2
; CURRENT APPLICATION NUMBER: US/09/410,568
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-410-568-99

Query Match      44.4%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 NILP 8
Db      4 NILP 7

RESULT 67
US-09-598-419-40
; Sequence 40, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 40
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: made in the lab
US-09-598-419-40

Query Match      44.4%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NILP 8  
|||  
Db 3 NILP 6

## RESULT 68

US-09-598-419-99  
; Sequence 99, Application US/09598419  
; Patent No. 6565856  
; GENERAL INFORMATION:  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Scholler, John  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
; FILE REFERENCE: 210121.469C6  
; CURRENT APPLICATION NUMBER: US/09/598,419  
; CURRENT FILING DATE: 2000-06-20  
; NUMBER OF SEQ ID NOS: 357  
; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
; SEQ ID NO 99  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-598-419-99

Query Match 44.4%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 NILP 8  
|||  
Db 4 NILP 7

## RESULT 69

PCT-US94-00545-17  
; Sequence 17, Application PC/TUS9400545  
; GENERAL INFORMATION:  
; APPLICANT: Rao, Anjana  
; APPLICANT: Hogan, Patrick Gerald  
; APPLICANT: McCaffrey, Patricia  
; APPLICANT: Jain, Jugnu  
; TITLE OF INVENTION: NF-ATp, A T LYMPHOCYTE  
; TITLE OF INVENTION: DNA-BINDING PROTEIN  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/00545  
; FILING DATE: 18-JAN-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/145,006  
; FILING DATE: October 29, 1993  
; APPLICATION NUMBER: 08/017,052  
; FILING DATE: February 11, 1993  
; APPLICATION NUMBER: 08/006,067  
; FILING DATE: January 15, 1993  
; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 04590/007001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
PCT-US94-00545-17

Query Match 44.4%; Score 4; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 4 QNIL 7  
|||  
Db 13 QNIL 16

## RESULT 70

US-08-637-759B-118  
; Sequence 118, Application US/08637759B  
; Patent No. 5876931  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/637,759B  
; FILING DATE: 03-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 118:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-637-759B-118

Query Match 44.4%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 6 ILPL 9  
 ||||  
 Db 12 ILPL 15

RESULT 71  
 US-08-871-355A-118  
 ; Sequence 118, Application US/08871355A  
 ; Patent No. 6015669  
 ; GENERAL INFORMATION:  
 ; APPLICANT: David William Holden  
 ; TITLE OF INVENTION: Identification of Genes  
 ; NUMBER OF SEQUENCES: 501  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Patrea L. Pabst  
 ; STREET: 2800 One Atlantic Center  
 ; STREET: 1201 West Peachtree Street  
 ; CITY: Atlanta  
 ; STATE: Georgia  
 ; COUNTRY: USA  
 ; ZIP: 30309-3450  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/871,355A  
 ; FILING DATE: 09-JUN-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB95/02875  
 ; FILING DATE: 11-DEC-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pabst, Patrea L.  
 ; REGISTRATION NUMBER: 31,284  
 ; REFERENCE/DOCKET NUMBER: RPMS 101 CON  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (404) 873-8794  
 ; TELEFAX: (404) 873-8795  
 ; INFORMATION FOR SEQ ID NO: 118:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 17 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; US-08-871-355A-118

Query Match 44.4%; Score 4; DB 3; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 6 ILPL 9  
 ||||  
 Db 12 ILPL 15

RESULT 72  
 US-09-123-485-1  
 ; Sequence 1, Application US/09123485  
 ; Patent No. 6316420  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nathan Karin et al.  
 ; TITLE OF INVENTION: DNA VACCINES ENCODING C-C CHEMOKINES AND  
 ; TITLE OF INVENTION: USE OF SAME FOR PROTECTIVE IMMUNITY  
 ; TITLE OF INVENTION: AGAINST MULTIPLE SCLEROSIS  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

STREET: 20001 Jefferson Davis Highway, Suite 207  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: United States of America  
 ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
 ; COMPUTER: Twinhead\* Slimnote-890TX  
 ; OPERATING SYSTEM: MS DOS version 6.2,  
 ; SOFTWARE: Word for Windows version 2.0 converted  
 ; SOFTWARE: to an ASCII file  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/123,485  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Friedmam, Mark M.  
 ; REGISTRATION NUMBER: 33,883  
 ; REFERENCE/DOCKET NUMBER: 910/5  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 972-3-562553  
 ; TELEFAX: 972-3-562554  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 17  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-09-123-485-1

Query Match 44.4%; Score 4; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 SLPQ 4  
 ||||  
 Db 3 SLPQ 6

RESULT 73  
 US-09-201-945-118  
 ; Sequence 118, Application US/09201945  
 ; Patent No. 6342215  
 ; GENERAL INFORMATION:  
 ; APPLICANT: David William Holden  
 ; TITLE OF INVENTION: Identification of Genes  
 ; NUMBER OF SEQUENCES: 501  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Patrea L. Pabst  
 ; STREET: 2800 One Atlantic Center  
 ; STREET: 1201 West Peachtree Street  
 ; CITY: Atlanta  
 ; STATE: Georgia  
 ; COUNTRY: USA  
 ; ZIP: 30309-3450  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/201,945  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/637,759  
 ; FILING DATE:  
 ; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: RMS 101  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-09-201-945-118

Query Match 44.4%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 6 ILPL 9  
Db 12 ILPL 15

RESULT 74  
US-08-468-540B-14  
Sequence 14, Application US/08468540B  
Patent No. 5858980  
GENERAL INFORMATION:  
APPLICANT: Weiner, Howard  
APPLICANT: Hafner, David  
APPLICANT: Miller, Ariel  
APPLICANT: Al-Sabbagh, Ahmad  
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,540B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5858980e  
US-08-468-540B-14

Query Match 44.4%; Score 4; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 SLPQ 4  
Db 1 SLPQ 4

RESULT 75  
US-08-347-563A-20  
Sequence 20, Application US/08347563A  
Patent No. 5935810  
GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY  
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,563A  
FILING DATE: No. 5935810ember 30, 1994  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/292,345  
FILING DATE: August 17, 1994

ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-087 CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521

INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid

TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
DESCRIPTION: ob peptide fragment

FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Murine

US-08-347-563A-20

Query Match 44.4%; Score 4; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 SLPQ 4  
Db 5 SLPQ 8

Search completed: November 25, 2003, 20:16:16  
Job time : 10.8138 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 9.20213 Seconds  
(without alignments)  
104.507 Million cell updates/sec

Title: US-09-641-801-20

Perfect score: 10

Sequence: 1 TQTPVVPPF 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR\_76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	40.0	15	PQ0778	NADH2 dehydrogenas
2	4	40.0	17	PH1340	Ig heavy chain DJ
3	3	30.0	7	PQ0727	H2 class I protein
4	3	30.0	8	PT0298	Ig heavy chain CRD
5	3	30.0	9	A61358	bradykinin-like pe
6	3	30.0	10	XASNPC	angiotensin-conver
7	3	30.0	10	S36849	Ig heavy chain V r
8	3	30.0	11	C61497	seed protein ws-18
9	3	30.0	12	S55629	protoporphyrinogen
10	3	30.0	12	C39109	hypothetical 1.2K
11	3	30.0	12	B44818	extracellular lipa
12	3	30.0	12	S52561	5-enolpyruvylshiki
13	3	30.0	12	A60528	insulin-like growt
14	3	30.0	12	A33520	inhibitory diffusi
15	3	30.0	12	PD0021	muconate cycloisom
16	3	30.0	13	A44818	extracellular lipa
17	3	30.0	13	S70723	lipamide dehydrog
18	3	30.0	13	PT0331	Ig heavy chain CRD
19	3	30.0	13	B20907	Ig kappa-l chain J
20	3	30.0	13	PC4391	cysteine proteinas
21	3	30.0	13	C61576	ribosomal protein
22	3	30.0	14	A33798	D-amino-acid oxida
23	3	30.0	14	A61002	photosystem II oxy
24	3	30.0	14	PN0147	omega-gliadine 1 a
25	3	30.0	14	B60683	malate dehydrogena
26	3	30.0	14	B56884	Pax-QMR, long form
27	3	30.0	15	I52734	gene c-Ki-ras prot
28	3	30.0	15	S26531	T-cell receptor al
29	3	30.0	15	D48648	hypothetical leade

30	3	30.0	15	JN0730	hypothetical 1.7K
31	3	30.0	15	A57003	hypothetical prote
32	3	30.0	15	S59489	steroid monooxygen
33	3	30.0	15	PA0014	seed storage prote
34	3	30.0	15	PN0172	seed storage prote
35	3	30.0	15	PS0276	phosphoribulokinas
36	3	30.0	15	B61457	alpha-glucosidase
37	3	30.0	15	A36527	juvenile-hormone e
38	3	30.0	15	E56978	collagen alpha 2(X
39	3	30.0	15	A42413	Ig heavy chain V r
40	3	30.0	15	I65478	c-Ki-ras - hamster
41	3	30.0	16	S03405	hydrogenase (EC 1.
42	3	30.0	16	S11290	matrix protein M1
43	3	30.0	16	PS0256	22K protein 4208 -
44	3	30.0	16	S09084	proteasome chain 3
45	3	30.0	17	C37520	glutathione transf
46	3	30.0	17	A49237	45/47K antigen - M
47	3	30.0	17	S66213	glucose 1-dehydrog
48	3	30.0	17	S59481	hydroxyproline-ric
49	3	30.0	17	S50742	proteinase inhibit
50	3	30.0	17	I55612	thyroid hormone re
51	3	30.0	17	E23734	insulin-like growt
52	3	30.0	17	I53392	Cu33 antigen homol
53	3	30.0	17	B25348	glycogen(starch) s
54	3	30.0	18	A32220	T-cell receptor de
55	3	30.0	18	B60277	pilin - Vibrio par
56	3	30.0	18	A60277	pilin - Vibrio par
57	3	30.0	18	S70612	alpha-macroglobuli
58	3	30.0	18	S09026	carboxylesterase (
59	3	30.0	19	SI3046	calreticulin - rab
60	3	30.0	19	FC1315	large granule L2 c
61	3	30.0	19	PH1352	Ig heavy chain DJ
62	3	30.0	19	A44356	37K adherens junct
63	3	30.0	20	S04961	malate dehydrogena
64	3	30.0	20	S09022	carboxylesterase (
65	3	30.0	20	S09025	carboxylesterase (
66	3	30.0	20	S09023	carboxylesterase (
67	3	30.0	20	A05313	apolipoprotein A-I
68	3	30.0	20	A60372	pollen allergen Po
69	3	30.0	20	PQ0046	citrate (si)-synth
70	3	30.0	20	B44835	cdmpglucose 4,6-de
71	3	30.0	20	S57286	translation elonga
72	3	30.0	20	PA0022	protein QAL00011 -
73	3	30.0	20	PQ0732	superoxide dismuta
74	3	30.0	20	PS0188	superoxide dismuta
75	3	30.0	20	A38600	trypsin inhibitor
76	3	30.0	20	A61414	chymotrypsin (EC 3
77	3	30.0	20	D56046	urinary tract ston
78	3	30.0	20	A60812	plasma proteinase
79	3	30.0	20	A42267	J-kappa recombinat
80	3	30.0	20	B35473	H+-transporting tw
81	2	20.0	4	I57745	D-mannosate hydrol
82	2	20.0	4	I57255	ribosomal protein
83	2	20.0	4	I54357	schwannomin - mous
84	2	20.0	5	A60521	glycogen phosphory
85	2	20.0	5	JN0862	peptidyl-dipeptida
86	2	20.0	5	B22565	R-phycoerythrin al
87	2	20.0	5	PQ0009	angiotensin-conver
88	2	20.0	5	B37988	acid proteinase li
89	2	20.0	5	JS0319	subesophageal gang
90	2	20.0	5	S11127	phosphoprotein, bo
91	2	20.0	5	JT0870	phytoalbumine alp
92	2	20.0	6	A61049	halo-toxin - pseud
93	2	20.0	6	I51317	bHLH transcription
94	2	20.0	6	I65546	MHC H2-L antigen -
95	2	20.0	7	S19630	ribosomal protein
96	2	20.0	7	A61081	tryptophyllin, bas
97	2	20.0	7	PT0087	ribulose-bisphosph
98	2	20.0	7	E61491	seed protein ws-5
99	2	20.0	7	S71299	ICL2 protein - Par
100	2	20.0	7	PT0283	Ig heavy chain CRD

## ALIGNMENTS

## RESULT 1

PQ0778  
 NADH2 dehydrogenase (EC 1.6.99.3) 46K chain - fava bean mitochondrion (fragment)  
 N;Alternate names: complex I 46K chain; NADH-ubiquinone reductase 46K chain  
 C;Species: mitochondrion Vicia faba (fava bean)  
 C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 03-Jun-2002  
 C;Accession: PQ0778  
 R;Letterme, S.; Boutry, M.  
 Plant Physiol. 102, 435-443, 1993  
 A;Title: Purification and preliminary characterization of mitochondrial complex I (NADH:  
 A;Reference number: PQ0775; MUID:94151437; PMID:8108509  
 A;Accession: PQ0778  
 A;Molecule type: protein  
 A;Residues: 1-15 <LET>  
 C;Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th  
 ranging from 5K to 75K.  
 C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by  
 C;Genetics:  
 A;Genome: mitochondrion  
 C;Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 40.0%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8  
 ||||  
 Db 10 VVVP 13

## RESULT 2

PH1340  
 Ig heavy chain DJ region (clone C252-113) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PH1340  
 R;Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
 A;Reference number: PH1302; MUID:93094761; PMID:1460419  
 A;Accession: PH1340  
 A;Molecule type: DNA  
 A;Residues: 1-17 <WAS>  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 4; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8  
 ||||  
 Db 3 VVVP 6

## RESULT 3

PQ0727  
 H2 class I protein (imported) - rice (fragment)  
 C;Species: Oryza sativa (rice)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C;Accession: PQ0727  
 R;Komatsu, S.; Kajiwara, H.; Hirano, H.  
 Theor. Appl. Genet. 86, 935-942, 1993  
 A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension  
 A;Reference number: PQ0696  
 A;Accession: PQ0727  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-7 <KOM>

Query Match 30.0%; Score 3; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7  
 ||||  
 Db 5 VVW 7

## RESULT 4

PT0298  
 Ig heavy chain CRD3 region (clone 5-103A) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C;Accession: PT0298  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 393-407, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A;Reference number: PT0222; MUID:91108337; PMID:1899102  
 A;Accession: PT0298  
 A;Molecule type: DNA  
 A;Residues: 1-8 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7  
 ||||  
 Db 4 VVW 6

## RESULT 5

A61358  
 bradykinin-like peptide I - Japanese pond frog  
 C;Species: Rana nigromaculata (Japanese pond frog)  
 C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 02-Sep-2000  
 C;Accession: A61358  
 R;Nakajima, T.  
 Chem. Pharm. Bull. 16, 769-770, 1968  
 A;Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin  
 A;Reference number: A61358; MUID:68412013; PMID:5677638  
 A;Accession: A61358  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <NAK>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: skin

Query Match 30.0%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
 ||||  
 Db 1 VPP 3

## RESULT 6

XASNPC  
 angiotensin-converting enzyme inhibitor - aspic viper  
 C;Species: Vipera aspis (aspic viper)  
 C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 08-Dec-1995  
 C;Accession: A60377  
 R;Komori, Y.; Sugihara, H.  
 Int. J. Biochem. 22, 767-771, 1990  
 A;Title: Characterization of a new inhibitor for angiotensin converting enzyme from the  
 A;Reference number: A60377; MUID:90382616; PMID:2169439  
 A;Accession: A60377  
 A;Molecule type: protein  
 A;Residues: 1-10 <KOM>  
 C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid  
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
|||  
Db 8 VPP 10

## RESULT 7

S36849  
Ig heavy chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1994 #sequence\_revision 01-Dec-1995 #text\_change 05-Nov-1999  
C;Accession: S36849  
R;Jacob, J.; Kelsoe, G.  
submitted to the EMBL Data Library, July 1992  
A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)  
A;Reference number: S25024  
A;Accession: S36849  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-10 <JAC>  
A;Cross-references: EMBL:X67382; NID:G50070; PIDN:CAA47794.1; PID:e51590; PID:g1333861  
C;Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVV 7  
|||  
Db 6 VVV 8

## RESULT 8

C61497  
seed protein ws-18 - winged bean (fragment)  
C;Species: Psophocarpus tetragonolobus (winged bean)  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C;Accession: C61497  
R;Hirano, H.  
J. Protein Chem. 8, 115-130, 1989  
A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional polyacrylamide gels  
A;Reference number: A61491; MUID:89351606; PMID:2765119  
A;Accession: C61497  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <HIR>  
C;Keywords: glycoprotein; seed

Query Match 30.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
|||  
Db 5 VPP 7

## RESULT 9

S65629  
protoporphyrinogen oxidase (EC 1.3.3.4) - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 26-May-2000  
C;Accession: S65629  
R;Fukutani, S.; Yoshinaga, T.; Furukawa, T.; Kohn, H.; Tokunaga, R.; Nishimura, K.; Inoue, J. Biochem. 230, 760-765, 1995  
A;Title: Induction of terminal enzymes for heme biosynthesis during differentiation of mouse erythroid cells  
A;Reference number: S65629; MUID:95331315; PMID:7607249

A;Accession: S65629  
A;Molecule type: protein  
A;Residues: 1-12 <TAK>

C;Genetics:

A;Genome: nuclear

C;Function:

A;Pathway: heme biosynthesis; porphyrin biosynthesis

C;Superfamily: phytoene dehydrogenase

C;Keywords: heme biosynthesis; mitochondrion; oxidoreductase; porphyrin biosynthesis

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVV 7  
|||  
Db 4 VVV 6

## RESULT 10

C39109  
hypothetical 1.2K protein - hepatitis C virus  
N;Alternate names: hypothetical protein 3  
C;Species: hepatitis C virus  
C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
C;Accession: C39109; JQ1586  
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-  
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification  
A;Reference number: A39109; MUID:91156678; PMID:1705704  
A;Accession: C39109  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-12 <HAN>  
A;Cross-references: GB:M58406  
R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
J. Gen. Virol. 73, 1521-1525, 1992  
A;Title: Cloning and sequencing of the structural region and expression of putative core  
A;Reference number: JQ1584; MUID:92300349; PMID:1318944  
A;Accession: JQ1586  
A;Molecule type: genomic RNA  
A;Residues: 1-12 <KUM>  
A;Experimental source: strain U.K.

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
|||  
Db 7 VPP 9

## RESULT 11

B44818  
extracellular lipase - Pseudomonas aeruginosa (fragment)  
C;Species: Pseudomonas aeruginosa  
C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Nov-1994  
C;Accession: B44818  
R;Gilbert, B.J.; Cornish, A.; Jones, C.W.  
J. Gen. Microbiol. 137, 2223-2229, 1991  
A;Title: Purification and properties of extracellular lipase from Pseudomonas aeruginosa  
A;Reference number: A44818; MUID:92085040; PMID:1748875  
A;Accession: B44818  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <GIL>  
A;Experimental source: strain EF228  
A;Note: sequence extracted from NCBI backbone (NCBI:70393)

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQT 3  
|||  
Db 3 TOT 5

## RESULT 12

S52561  
5-enolpyruvylshikimate-3-phosphate - Euglena gracilis  
C/Species: Euglena gracilis  
C/Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 01-Sep-1995  
C/Accession: S52561  
R;Reinbothe, C.; Ortel, B.; Parthier, B.; Reinbothe, S.  
Mol. Gen. Genet. 245, 616-622, 1994  
A/Title: Cytosolic and plastid forms of 5-enolpyruvylshikimate-3-phosphate synthase in E.  
A/Reference number: S52561; MUID:95107260; PMID:7808412  
A/Accession: S52561  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <REI>

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVV 7  
|||  
Db 10 VVV 12

## RESULT 13

A60528  
insulin-like growth factor-binding protein, serum - pig (fragment)  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-May-2000  
C/Accession: A60528  
R;Walton, P.E.; Baxter, R.C.; Burleigh, B.D.; Ehterton, T.D.  
Comp. Biochem. Physiol. B 92, 561-567, 1989  
A/Title: Purification of the serum acid-stable insulin-like growth factor binding protein  
A/Reference number: A60528; MUID:89209787; PMID:2468442  
A/Accession: A60528  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <WAL>

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
|||  
Db 9 PVV 11

## RESULT 14

A33520  
inhibitory diffusible factor - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 29-Jan-1990 #sequence\_revision 29-Jan-1990 #text\_change 30-Sep-1993  
C/Accession: A33520  
R;Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.  
J. Biol. Chem. 264, 6021-6024, 1989  
A/Title: Isolation and amino-terminal sequence of a novel cellular growth inhibitor (inh  
A/Reference number: A33520; MUID:89197888; PMID:2703477  
A/Accession: A33520  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <BLA>

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
|||  
Db 9 PVV 11

## RESULT 15

PD0021  
muconate cycloisomerase (EC 5.5.1.1) II - Frateuria sp. ANA-18 (fragment)  
N/Alternate names: MC II  
C/Species: Frateuria sp. ANA-18  
C/Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 18-Jul-2001  
C/Accession: PD0021  
R;Murakami, S.; Takemoto, J.; Takashima, A.; Shinke, R.; Aoki, K.  
Biosci. Biotechnol. Biochem. 62, 1129-1133, 1998  
A/Title: Purification and characterization of two muconate cycloisomerase isozymes from  
A/Reference number: PD0020; MUID:98357223; PMID:9692194  
A/Accession: PD0021  
A/Molecule type: protein  
A/Residues: 1-12 <MUR>

C/Keywords: intramolecular lyase; isomerase

Query Match 30.0%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5  
|||  
Db 4 TPV 6

## RESULT 16

A44818  
extracellular lipase - Pseudomonas aeruginosa (fragment)  
C/Species: Pseudomonas aeruginosa  
C/Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997  
C/Accession: A44818  
R;Gilbert, E.J.; Cornish, A.; Jones, C.W.  
J. Gen. Microbiol. 137, 2223-2229, 1991  
A/Title: Purification and properties of extracellular lipase from Pseudomonas aeruginosa  
A/Reference number: A44818; MUID:92085040; PMID:11748875  
A/Accession: A44818  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: nucleic acid  
A/Residues: 1-13 <GIL>

A/Experimental source: strain TE3285  
A/Note: sequence extracted from NCBI backbone (NCBIP:70395)  
C/Superfamily: Pseudomonas triacylglycerol lipase

Query Match 30.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQT 3  
|||  
Db 4 TOT 6

## RESULT 17

S70723  
lipamide dehydrogenase homolog - Salmonella typhimurium (fragment)  
C/Species: Salmonella typhimurium  
C/Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
C/Accession: S70723  
R;Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.  
Mol. Microbiol. 17, 523-531, 1995  
A/Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophil  
A/Reference number: S70719; MUID:96100451; PMID:8559071  
A/Accession: S70723  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <QIS>

A/Experimental source: strain SL1344



Query Match 30.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPV 5  
 |||  
 DB 6 TPV 8  
 |||

RESULT 18  
 PT0331  
 Ig heavy chain CRD3 region (clone J2-121) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0331  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102  
 A:Accession: PT0331  
 A:Molecule type: DNA  
 A:Residues: 1-13 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPF 10  
 |||  
 DB 10 PPF 12  
 |||

RESULT 19  
 B20907  
 Ig kappa-1 chain.J2 region - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 16-Aug-1996  
 C:Accession: B20907; B53275  
 R;Emorine, L.; Max, E.E.  
 Nucleic Acids Res. 11, 8877-8890, 1983  
 A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple  
 A:Reference number: A20907; MUID:84169523; PMID:6324107  
 C:Accession: B20907  
 A:Molecule type: DNA  
 A:Residues: 1-13 <EMO>  
 R;Ayadi, H.; Marche, P.N.; Cazenave, P.A.  
 Immunogenetics 34, 201-207, 1991  
 A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.  
 A:Reference number: A53275; MUID:91372868; PMID:1905995  
 C:Accession: B53275  
 A:Molecule type: DNA  
 A:Residues: 1-13 <AYA>  
 A:Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBIP:56163)  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVW 7  
 |||  
 DB 10 VVW 12  
 |||

RESULT 20  
 PC4391  
 cysteine proteinase (EC 3.4.22.-) B - Fressia reflacta ssp. 'Golden leader' (fragment)  
 C:Species: Fressia reflacta ssp. 'Golden leader'  
 C:Date: 10-Nov-1997 #sequence\_revision 10-Nov-1997 #text\_change 07-May-1999  
 C:Accession: PC4391  
 R;Kaneda, M.; Yonezawa, H.; Uchikoba, T.

Biosci. Biotechnol. Biochem. 61, 1554-1559, 1997  
 A:Title: Purification and characterization of a cysteine protease from corms of freesia,  
 A:Reference number: PC4391; MUID:97480942; PMID:9339558  
 C:Accession: PC4391  
 A:Molecule type: protein  
 A:Residues: 1-13 <KAN>  
 A:Experimental source: corms  
 C:Comment: This enzyme plays many proteolytic functions in intracellular and extracellular  
 C:Keywords: cysteine proteinase; hydrolase

Query Match 30.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPF 10  
 |||  
 DB 2 PPF 4  
 |||

## RESULT 21

C61576  
 ribosomal protein L30 - Actinomadura malachitica (fragment)

C:Species: Actinomadura malachitica  
 C:Date: 20-Oct-1994 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
 C:Accession: C61576  
 R;Ochi, K.; Miyadoh, S.; Tamura, T.

Int. J. Syst. Bacteriol. 41, 234-239, 1991  
 A:Title: Polyacrylamide gel electrophoresis analysis of ribosomal protein AT-L30 as a no  
 A:Reference number: A61576; MUID:91307971; PMID:1854638  
 C:Accession: C61576

A:Molecule type: protein  
 A:Residues: 1-13 <OCH>  
 C:Keywords: protein biosynthesis; ribosome

Query Match 30.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TOT 3  
 |||  
 DB 6 TOT 8  
 |||

## RESULT 22

A33798  
 D-amino-acid oxidase (EC 1.4.3.3) - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 16-Mar-1990 #sequence\_revision 16-Mar-1990 #text\_change 31-Oct-1997  
 C:Accession: A33798  
 R;Watanabe, F.; Fukui, K.; Momoi, K.; Miyake, Y.

Biochem. Biophys. Res. Commun. 165, 1422-1427, 1989  
 A:Title: Expression of normal and abnormal porcine kidney D-amino acid oxidases in Esche  
 A:Reference number: A33798; MUID:90121258; PMID:2575382  
 C:Accession: A33798

A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <WAT>  
 C:Superfamily: D-amino-acid oxidase  
 C:Keywords: oxidoreductase

Query Match 30.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVW 7  
 |||  
 DB 3 VVW 5  
 |||

## RESULT 23

A61002

photosystem II oxygen-evolving complex protein 1 - common tobacco (fragment)  
 N;Alternate names: thylakoid membrane protein

C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C;Accession: A61002  
R;Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; C  
Electrophoresis 11, 528-536, 1990  
A;Title: Two-dimensional gel electrophoresis, protein electrophoresis and microsequencing  
A;Reference number: A61002; MUID:91031404; PMID:1699755  
C;Accession: A61002  
A;Molecule type: protein  
A;Residues: 1-14 <BAU>  
C;Keywords: chloroplast; membrane protein; photosynthesis; photosystem II; thylakoid

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VPP 9  
|||  
Db 3 VPP 5

RESULT 24  
PN0147  
omega-gliadine 1 and 2 - Aegilops longissima (fragment)  
C;Species: Aegilops longissima  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: PN0147; PN0146  
R;Odintsova, T.I.; Egorov, T.A.  
Biochimica 55, 509-516, 1990  
A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of  
A;Reference number: PN0146; MUID:90283493; PMID:2354218  
A;Accession: PN0147  
A;Molecule type: protein  
A;Residues: 1-14 <ODI>  
A;Experimental source: strain K-202  
A;Note: omega-gliadine 2 (amino-terminal fragment)  
A;Accession: PN0146  
A;Molecule type: protein  
A;Residues: 1-9 <OD2>  
A;Experimental source: strain K-202  
A;Note: omega-gliadine 1 (amino-terminal fragment)

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTP 4  
|||  
Db 12 QTP 14

RESULT 25  
B60683  
malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)  
C;Species: Panicum sp. (millet)  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 24-Feb-1994  
C;Accession: B60683  
R;Murata, T.; Ikeda, J.; Takano, M.; Ohsugi, R.  
Plant Cell Physiol. 30, 429-437, 1989  
A;Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.  
A;Reference number: A60683  
A;Accession: B60683  
A;Molecule type: protein  
A;Residues: 1-14 <MUR>  
C;Keywords: oxido-reductase; photosynthesis

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VPP 8  
|||  
Db 12 VPP 14

## RESULT 26

B56884  
Pax-QNR, long form - quail (fragment)  
C;Species: Coturnix coturnix (quail)  
C;Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 21-Jul-2000  
C;Accession: B56884  
R;Dozier, C.; Carriere, C.; Grevin, D.; Martin, P.; Quatannens, B.; Stehelin, D.; Saule,  
Cell Growth Differ. 4, 281-289, 1993  
A;Title: Structure and DNA-binding properties of Pax-QNR, a paired box- and homeobox-con  
A;Reference number: A56884; MUID:93264300; PMID:8098617  
A;Accession: B56884  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-14 <DOZ>  
A;Cross-references: GB:X68169; NID:g311558; PIDN:CAA48271.1; PID:g311559  
A;Experimental source: neuroretina cells  
C;Keywords: alternative splicing; retina

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPV 5  
|||  
Db 3 TPV 5

## RESULT 27

I52734  
gene C-Ki-ras protein - hamster (fragment)  
C;Species: Cricetinae gen. sp. (hamster)  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 28-May-1999  
C;Accession: I52734  
R;Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian,  
Carcinogenesis 16, 931-939, 1995  
A;Title: Differences in molecular biological, biological and growth characteristics betw  
A;Reference number: I52734; MUID:95246257; PMID:7728976  
A;Accession: I52734  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-15 <RES>  
A;Cross-references: GB:S77068; NID:g914176  
C;Genetics:  
A;Gene: c-Ki-ras  
C;Superfamily: ras transforming protein; translation elongation factor Tu homology  
C;Keywords: GTP binding

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVW 7  
|||  
Db 7 VVW 9

## RESULT 28

S26531  
T-cell receptor alpha chain V region (clone Cw3/701.1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
A;Variety: clone Cw3/701.1  
C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
C;Accession: S26531  
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
J. Exp. Med. 176, 439-447, 1992  
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A;Reference number: S26512; MUID:92364546; PMID:1380061  
A;Accession: S26531  
A;Molecule type: mRNA  
A;Residues: 1-15 <CAS>  
A;Cross-references: EMBL:X67982

A:Experimental source: cytolytic T-lymphocyte, clone Cw3/701.1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: T-cell receptor

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQT 3  
 |||  
 Db 4 TQT 6

## RESULT 29

D48648  
 hypothetical leader peptide (ilvB 5' region) - Corynebacterium glutamicum  
 C:Species: Corynebacterium glutamicum  
 C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 12-Dec-1997  
 C:Accession: D48648

R:Keilhauer, C.; Eggeling, L.; Sahm, H.  
 J. Bacteriol. 175, 5595-5603, 1993

A:Title: Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the  
 A:Reference number: A48648; MUID:93374855; PMID:8366043

A:Accession: D48648

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <KEI>

A:Cross-references: GB:L09232

C:Superfamily: unassigned leader peptides

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVV 7  
 |||  
 Db 7 VVV 9

## RESULT 30

JN0730  
 hypothetical 1.7K protein - phage SPPI  
 N:Alternate names: hypothetical protein 42.1  
 C:Species: phage SPPI

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999  
 C:Accession: JN0730

R:Chai, S.; Szepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.

Gene 129, 41-49, 1993

A:Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPPI 9  
 A:Reference number: JN0729; MUID:93328123; PMID:8335259

A:Accession: JN0730

A:Molecule type: DNA

A:Residues: 1-15 <CHA>

A:Cross-references: EMBL:X65941

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPF 10  
 |||  
 Db 6 PPF 8

## RESULT 31

A57003  
 hypothetical protein - Mycobacterium paratuberculosis (fragment)  
 C:Species: Mycobacterium paratuberculosis

C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 03-Oct-1995  
 C:Accession: A57003

R:Thomas, T.J.; Andrews Jr., R.E.; Thoen, C.O.

Vet. Microbiol. 32, 351-362, 1992

A:Title: Molecular cloning and characterization of Mycobacterium paratuberculosis promob

A:Reference number: A57003; MUID:93088535; PMID:1455629  
 A:Accession: A57003  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-15 <THO>  
 A:Experimental source: ATCC 19598  
 A:Note: sequence extracted from NCBI backbone (NCBIN:120808, NCBIP:120809)

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5  
 |||  
 Db 6 TPV 8

## RESULT 32

S59489  
 steroid monooxygenase - Rhodococcus rhodochrous (fragment)  
 C:Species: Rhodococcus rhodochrous

C:Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

A:Accession: S59489

R:Miyamoto, M.; Matsumoto, J.; Iwaya, T.; Itagaki, E.

Biochim. Biophys. Acta 1251, 115-124, 1995

A:Title: Bacterial steroid monooxygenase catalyzing the Baeyer-Villiger oxidation of C(2

A:Reference number: S59489; MUID:95399430; PMID:7669800

A:Accession: S59489

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <MIY>

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVV 7  
 |||  
 Db 8 VVV 10

## RESULT 33

PA0014  
 seed storage protein 12S 3 - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995

C:Accession: PA0014

R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona

A:Reference number: PA0001

A:Accession: PA0014

A:Molecule type: protein

A:Residues: 1-15 <KAM>

A:Experimental source: seed

C:Keywords: seed; storage protein

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
 |||  
 Db 6 VPP 8

## RESULT 34

PN0173  
 seed storage protein 12S4 - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 22-Dec-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Mar-2001

C:Accession: PN0173

R:Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.

submitted to JIPID, December 1995

A;Description: Two dimensional electrophoresis of plant proteins and standardization of  
A;Reference number: PN0173  
A;Accession: PN0173  
A;Molecule type: protein  
A;Residues: 1-15 <TSU>  
A;Experimental source: seeds

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
|||  
Db 6 VPP 8

#### RESULT 35

PS0276

phosphoribulokinase (EC 2.7.1.19) - rice (strain Nihonbare) (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Mar-1995  
C;Accession: PS0276  
R;Taugita, A.

submitted to JIPID, April 1993

A;Reference number: PS0206

A;Accession: PS0276

A;Molecule type: protein

A;Residues: 1-15 <TSU>

A;Experimental source: leaf, chlorophyll, stem

C;Keywords: phosphotransferase

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
|||  
Db 5 PVV 7

#### RESULT 36

B61457

alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)

C;Species: Tetrahymena pyriformis

C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-Dec-1999

C;Accession: B61457

R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.

J. Protozool. 36, 562-567, 1989

A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification  
A;Reference number: A61457; MUID:90095988; PMID:2689637

A;Accession: B61457

A;Molecule type: protein

A;Residues: 1-15 <BAN>

C;Genetics:

A;Genetic code: SGC5

C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monom

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPF 10  
|||  
Db 3 PPF 5

#### RESULT 37

A36527

juvenile-hormone esterase (EC 3.1.1.59) - tobacco hornworm (fragment)

C;Species: Manduca sexta (tobacco hornworm)

C;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 03-Feb-1994

C;Accession: A36527

R;Venkatesh, K.; Abdel-Aal, Y.A.I.; Armstrong, F.B.; Roe, R.M.  
J. Biol. Chem. 265, 21727-21732, 1990

A;Title: Characterization of affinity-purified juvenile hormone esterase from the plasma

A;Reference number: A36527; MUID:91072375; PMID:2254326

A;Accession: A36527

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <VEN>

C;Keywords: carboxylic ester hydrolase

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVV 7  
|||  
Db 8 VVV 10

#### RESULT 38

E56978

collagen alpha 2(XI) chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 03-Oct-1995

C;Accession: E56978

R;Wu, J.J.; Eyre, D.R.

J. Biol. Chem. 270, 18865-18870, 1995

A;Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ins

A;Reference number: A56978; MUID:95370194; PMID:7642541

A;Accession: E56978

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <WUA>

A;Note: the residue designated 'X' is modified lysine cross-linked to 1(XI) Lys-23 in FS

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
|||  
Db 11 PVV 13

#### RESULT 39

A42413

Ig heavy chain V region (LBL-copurifying) - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 07-May-1999

C;Accession: A42413

R;Bao, Z.; Muschler, J.; Horwitz, A.F.

J. Biol. Chem. 267, 4974-4980, 1992

A;Title: LBL, a novel, developmentally regulated, laminin-binding lectin.

A;Reference number: A42413; MUID:92165867; PMID:1531660

A;Accession: A42413

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <BAO>

C;Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4  
|||  
Db 12 QTP 14

C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 28-Feb-1997  
 C;Accession: I65478  
 R;Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian, Carcinogenesis 16, 931-939, 1995  
 A;Title: Differences in molecular biological, biological and growth characteristics between  
 A;Reference number: 152734; MUID:95246257; PMID:7728976  
 A;Accession: 165478  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-15 <RES>  
 A;Cross-references: GB:S77069; NID:g914177  
 C;Genetics:  
 A;Gene: c-Ki-ras

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7  
 |||  
 Db 7 VVW 9

RESULT 41  
 S03405  
 hydrogenase (EC 1.18.99.1) small chain - Alcaligenes eutrophus (fragment)  
 C;Species: Alcaligenes eutrophus  
 C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 13-Sep-1998  
 C;Accession: S03405  
 R;Lorenz, B.; Schneider, K.; Kratzin, H.; Schlegel, H.G.  
 Biochim. Biophys. Acta 995, 1-9, 1989  
 A;Title: Immunological comparison of subunits isolated from various hydrogenases of aerob  
 A;Reference number: S03404; MUID:89166625; PMID:2493816  
 A;Accession: S03405  
 A;Molecule type: protein  
 A;Residues: 1-16 <LOR>  
 A;Experimental source: strain H16, DMS 541  
 C;Superfamily: hydrogenase (NiFe) small chain  
 C;Keywords: hydrogen metabolism; iron-sulfur protein; membrane bound; metalloprotein; ni

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5  
 |||  
 Db 7 TPV 9

RESULT 42  
 S11290  
 matrix protein M1 - influenza A virus (strain A/FPV/Rostock/34 [H7N1]) (fragment)  
 C;Species: Influenza A virus  
 C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 18-Jun-1993  
 C;Accession: S11290  
 R;Robertson, J.S.  
 Nucleic Acids Res. 6, 3745-3757, 1979  
 A;Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza  
 A;Reference number: S11286; MUID:80034428; PMID:493121  
 A;Accession: S11290  
 A;Molecule type: genomic RNA  
 A;Residues: 1-16 <ROB>  
 A;Cross-references: EMBL:J02112  
 C;Genetics:  
 A;Map position: segment 7  
 C;Superfamily: influenza virus matrix protein M1

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVW 8  
 |||

Db 14 VVP 16

RESULT 43  
 PS0256  
 22K protein 4208 - rice (strain Nihonbare) (fragment)  
 C;Species: Oryza sativa (rice)  
 C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
 C;Accession: PS0256  
 R;Taigita, A.; Miyatake, N.  
 submitted to JIPID, April 1993  
 A;Reference number: PS0208  
 A;Accession: PS0256  
 A;Molecule type: protein  
 A;Residues: 1-16 <TSU>  
 A;Experimental source: germ, strain Nihonbare  
 C;Comment: molecular weight 22K, pI 6.6.

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7  
 |||  
 Db 4 VVW 6

RESULT 44  
 S09084  
 proteasome chain 3 - rat (fragment)  
 N;Alternate names: multicatalytic proteinase chain 3  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
 C;Accession: S09084  
 R;Lilley, K.S.; Davison, M.D.; Rivett, A.J.  
 FEBS Lett. 262, 327-329, 1990  
 A;Title: N-terminal sequence similarities between components of the multicatalytic prote  
 A;Reference number: S09082; MUID:90242957; PMID:2335214  
 A;Accession: S09084  
 A;Molecule type: protein  
 A;Residues: 1-16 <LIL>

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7  
 |||  
 Db 11 VVW 13

RESULT 45  
 C37520  
 glutathione transferase (EC 2.5.1.18) MII - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 30-Sep-1993  
 C;Accession: C37520; N24735  
 R;Mannervik, B.; Alin, P.; Guthenberg, C.; Jonsson, H.; Tahir, M.K.; Warholm, M.; Jornva  
 Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985  
 A;Title: Identification of three classes of cytosolic glutathione transferase common to  
 A;Reference number: A24735; MUID:86042634; PMID:3864155  
 A;Accession: C37520  
 A;Molecule type: protein  
 A;Residues: 1-17 <MAN>  
 C;Superfamily: glutathione transferase  
 C;Keywords: transferase

Query Match 30.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVW 6  
 |||

Db 9 PVV 11

# RESULT 46

A49237  
45/47K antigen - Mycobacterium bovis (fragment)  
C;Species: Mycobacterium bovis  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Feb-1995  
C;Accession: A49237  
R;Roman, F.; Laqueyrie, A.; Miltzer, P.; Pescher, P.; Chavarot, P.; Legranderie, M.; Infect. Immun. 61, 742-750, 1993.  
A;Title: Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen complex, a  
A;Reference number: A49237; MUID:93138802; PMID:8423100  
A;Contents: BCG  
A;Accession: A49237  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-17 <ROW>  
A;Note: sequence extracted from NCBI backbone (NCBIP:123246)

Query Match 30.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
|||  
Db 8 VPP 10  
|||

# RESULT 47

S66213  
Glucose 1-dehydrogenase (EC 1.1.1.47) - Haloferax mediterranei (fragment)  
C;Species: Haloferax mediterranei  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 30-Oct-1998  
C;Accession: S66213  
R;Bonete, M.J.; Pire, C.; Llorca, F.I.; Camacho, M.L.  
FEBS Lett. 383, 227-229, 1996  
A;Title: Glucose dehydrogenase from the halophilic Archaeon Haloferax mediterranei: enzy  
A;Reference number: S66213; MUID:96198607; PMID:8925901  
A;Accession: S66213  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-17 <BON>  
C;Keywords: oxidoreductase

Query Match 30.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
|||  
Db 13 PV 15  
|||

# RESULT 48

S59481  
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)  
C;Species: Phaseolus vulgaris (kidney bean)  
C;Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998  
C;Accession: S59481  
R;Mohtasez, P.; Trethowan, J.; Bolwell, G.P.  
Plant Mol. Biol. 28, 1075-1087, 1995  
A;Title: Specificity in the immobilisation of cell wall proteins in response to differen  
A;Reference number: S59481; MUID:96011753; PMID:7548825  
A;Accession: S59481  
A;Molecule type: protein  
A;Residues: 1-17 <WOU>  
C;Keywords: glycoprotein, hydroxyproline  
F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
|||  
Db 7 VPP 9  
|||

# RESULT 49

S50742  
Proteinase inhibitor (Kunitz-type) 1-related protein - potato (fragment)  
N;Alternate names: FXPI minor protein  
C;Species: Solanum tuberosum (potato)  
C;Date: 14-Jul-1995 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996  
C;Accession: S50742  
R;Mitsumori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.  
Plant Mol. Biol. 26, 961-969, 1994  
A;Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibit  
A;Reference number: S50741; MUID:95093035; PMID:8000008  
A;Accession: S50742  
A;Molecule type: protein  
A;Residues: 1-17 <MIT>

Query Match 30.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5  
|||  
Db 6 TPV 8  
|||

# RESULT 50

I55612  
thyroid hormone receptor beta - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C;Accession: I55612  
R;Adams, M.; Matthews, C.; Collingwood, T.N.; Tone, Y.; Beck-Peccoz, P.; Chatterjee, K.K.  
J. Clin. Invest. 94, 506-515, 1994  
A;Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to th  
A;Reference number: I55612; MUID:94314950; PMID:8040303  
A;Accession: I55612  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-17 <RES>  
A;Cross-references: GB:S72623; NID:G633779; PIDN:AAB31420.1; PID:G633780  
C;Genetics:  
A;Gene: TRbeta

Query Match 30.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPF 10  
|||  
Db 6 PPF 8  
|||

# RESULT 51

E23734  
insulin-like growth factor-binding protein 3 - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993  
C;Accession: E23734  
R;Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N.  
Mol. Endocrinol. 5, 938-948, 1991  
A;Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-6  
A;Reference number: A23734; MUID:92049376; PMID:1719383  
A;Accession: E23734  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-17 <SHI>

Query Match 30.0%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;  
QY 4 PVV 6  
DB 9 PVV 11

RESULT 52  
I53392  
CD33 antigen homolog - mouse (fragment)  
C:Species: Mus sp. (mouse)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 05-Jun-1998  
C:Accession: I53392  
R:Chies, J.A.; Lembezat, M.P.; Freitas, A.A.  
Eur. J. Immunol. 24, 1657-1664, 1994  
A:Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is n  
A:Reference number: I53392; MUID:94298870; PMID:8026526  
A:Accession: I53392  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-17 <RES>  
A:Cross-references: GB:S71347; NID:9550035  
C:Genetics: I53392  
A:Gene: Ig VHx24b

Query Match 30.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;  
QY 5 VVV 7  
DB 8 VVV 10

RESULT 53  
B25348  
glycogen(starch) synthase (EC 2.4.1.11) P-2 peptide - rabbit (fragment)  
N:Alternate names: UDPglucose-glycogen glucosyltransferase  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 16-Aug-2002  
C:Accession: B25348  
R:Wang, Y.; Bell, A.W.; Hermodson, M.A.; Roach, P.J.  
J. Biol. Chem. 261, 16909-16915, 1986  
A:Title: Liver isozyme of rabbit glycogen synthase. Amino acid sequences surrounding pho  
A:Reference number: A92570; MUID:87057401; PMID:3097016  
A:Accession: B25348  
A:Molecule type: protein  
A:Residues: 1-17 <WAN>  
C:Function:  
A:Description: catalyzes the alpha-1,4-glucosylation of glycogen by UDPglucose producing  
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 30.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;  
QY 7 VPP 9  
DB 8 VPP 10

RESULT 54  
A32220  
T-cell receptor delta chain precursor V region (DN7.3-1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Oct-1989 #sequence\_revision 20-Oct-1989 #text\_change 30-May-1997  
C:Accession: A32220  
R:Korman, A.J.; Maruyama, J.; Raulet, D.H.  
Proc. Natl. Acad. Sci. U.S.A. 86, 267-271, 1989  
A:Title: Rearrangement by inversion of a T-cell receptor delta variable region gene loca  
A:Reference number: A32220; MUID:89098895; PMID:2789518  
A:Accession: A32220

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-18 <KOR>  
A:Cross-references: GB:M23095  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 30.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 8 PPF 10  
DB 7 PPF 9

RESULT 55  
B60277  
pilin - Vibrio parahaemolyticus (strain Ha7) (fragment)  
C:Species: Vibrio parahaemolyticus  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 18-Jun-1993  
C:Accession: B60277  
R:Nakasone, N.; Iwanaga, M.  
Infect. Immun. 59, 726-728, 1991  
A:Title: Purification and characterization of pilin isolated from Vibrio parahaemolyticus  
A:Reference number: A60277; MUID:91100055; PMID:1670933  
A:Accession: B60277  
A:Molecule type: protein  
A:Residues: 1-18 <NAK>

Query Match 30.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 5 VVV 7  
DB 7 VVV 9

RESULT 56  
A60277  
pilin - Vibrio parahaemolyticus (strain Na2) (fragment)  
C:Species: Vibrio parahaemolyticus  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 18-Jun-1993  
C:Accession: A60277  
R:Nakasone, N.; Iwanaga, M.  
Infect. Immun. 59, 726-728, 1991  
A:Title: Purification and characterization of pilin isolated from Vibrio parahaemolyticus  
A:Reference number: A60277; MUID:91100055; PMID:1670933  
A:Accession: A60277  
A:Molecule type: protein  
A:Residues: 1-18 <NAK>

Query Match 30.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0;

QY 5 VVV 7  
DB 7 VVV 9

RESULT 57  
S70612  
alpha-macroglobulin proteinase inhibitor, tetrameric - bloodfluke planorb (fragment)  
C:Species: Biomphalaria glabrata (bloodfluke planorb)  
C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
C:Accession: S70612  
R:Bender, R.C.; Bayne, C.J.  
Biochem. J. 316, 893-900, 1996  
A:Title: Purification and characterization of a tetrameric alpha-macroglobulin proteinas  
A:Reference number: S70612; MUID:96265058; PMID:8670168  
A:Accession: S70612

A:Molecule type: protein  
 A:Residues: 1-18 <BEN>  
 C:Complex: homotetramer  
 C:Function:

A:Description: inhibits proteinases possessing different catalytic mechanisms by steric

Query Match 30.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVP 8  
 |||  
 Db 11 VVP 13

#### RESULT 58

S09026

carboxylesterase (EC 3.1.1.1) MK1, microsomal - crab-eating macaque (fragment)  
 C:Species: Macaca fascicularis (crab-eating macaque)

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 28-Apr-1993

C:Accession: S09026

R:Hosokawa, M.; Maki, T.; Satoh, T.

Arch. Biochem. Biophys. 277, 219-227, 1990

A>Title: Characterization of molecular species of liver microsomal carboxylesterases of

A:Reference number: S09021; MUID:90179180; PMID:2310190

A:Accession: S09026

A:Molecule type: protein

A:Residues: 1-18 <HOS>

C:Keywords: carboxylic ester hydrolase

Query Match 30.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
 |||  
 Db 6 PVV 8

#### RESULT 59

S13046

calreticulin - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996

C:Accession: S13046

R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld

Biochem. J. 271, 473-480, 1990

A>Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage

A:Reference number: S13045; MUID:91054414; PMID:2241926

A:Accession: S13046

A:Molecule type: protein

A:Residues: 1-19 <TRE>

C:Superfamily: calreticulin

Query Match 30.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
 |||  
 Db 2 PVV 4

#### RESULT 60

PC1315

large granule L2 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)

C:Species: Tachyplesus tridentatus

C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999

C:Accession: PC1315

R:Shigenaga, T.; Takayanoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa

J. Biochem. 114, 307-316, 1993

A>Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentatus)

A:Reference number: PC1309; MUID:94110249; PMID:8282718

A:Accession: PC1315

A:Molecule type: protein

A:Residues: 1-19 <SHI>

C:Comment: This protein participates in immobilization of invading microbes.

Query Match 30.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPF 10  
 |||  
 Db 3 PPF 5

#### RESULT 61

PH1352

Ig heavy chain DJ region (clone C100-115) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: PH1352

R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A>Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1352

A:Molecule type: DNA

A:Residues: 1-19 <WAS>

A>Note: the authors translated the stop codon for residue 2 as X

C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
 |||  
 Db 6 VPP 8

#### RESULT 62

A44356

37K adherens junction protein - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: A44356

R:Chiu, M.B.; Jones, J.C.R.; O'Keefe, E.J.

J. Cell Biol. 119, 1689-1700, 1992

A>Title: Restricted tissue distribution of a 37-kD possible adherens junction protein.

A:Reference number: A44356; MUID:93107168; PMID:1469056

A:Accession: A44356

A:Molecule type: protein

A:Residues: 1-19 <CHI>

C:Comment: This protein is restricted to suprabasal cells and localized to punctate regions. This protein is not glycosylated.

Query Match 30.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVV 7  
 |||  
 Db 1 VVV 3

#### RESULT 63

S04961

malate dehydrogenase (EC 1.1.1.37) - Kibdelosporangium aridum (fragment)

C:Species: Kibdelosporangium aridum

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 02-Aug-1994

C:Accession: S04961

R:Rommel, T.O.; Hund, H.K.; Speth, A.R.; Lingsens, P.

Biol. Chem. Hoppe-Seyler 370, 763-768, 1989

A>Title: Purification and N-terminal amino-acid sequences of bacterial malate dehydrogenase



A:Reference number: S04956; MUID:89374824; PMID:2775496  
A:Accession: S04961  
A:Molecule type: protein  
A:Residues: 1-20 <ROM>  
C:Superfamily: L-lactate dehydrogenase  
C:Keywords: oxidoreductase; tricarboxylic acid cycle

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5  
|||  
Db 3 TPV 5

## RESULT 64

S09022  
carboxylesterase (EC 3.1.1.1) RH1, microsomal - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Aug-1998  
C:Accession: S09022

R:Hosokawa, M.; Maki, T.; Satoh, T.  
Arch. Biochem. Biophys. 277, 219-227, 1990  
A:Title: Characterization of molecular species of liver microsomal carboxylesterases of  
A:Reference number: S09021; MUID:90179180; PMID:2310190  
A:Accession: S09022  
A:Molecule type: protein  
A:Residues: 1-20 <HOS>  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
|||  
Db 6 PVV 8

## RESULT 65

S09025  
carboxylesterase (EC 3.1.1.1), microsomal - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Aug-1998  
C:Accession: S09025

R:Hosokawa, M.; Maki, T.; Satoh, T.  
Arch. Biochem. Biophys. 277, 219-227, 1990  
A:Title: Characterization of molecular species of liver microsomal carboxylesterases of  
A:Reference number: S09021; MUID:90179180; PMID:2310190  
A:Accession: S09025  
A:Molecule type: protein  
A:Residues: 1-20 <HOS>  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
|||  
Db 6 PVV 8

## RESULT 66

S09023  
carboxylesterase (EC 3.1.1.1) RL2, microsomal - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Aug-1998  
C:Accession: S09023  
R:Hosokawa, M.; Maki, T.; Satoh, T.

Arch. Biochem. Biophys. 277, 219-227, 1990  
A:Title: Characterization of molecular species of liver microsomal carboxylesterases of  
A:Reference number: S09021; MUID:90179180; PMID:2310190  
A:Accession: S09023  
A:Molecule type: protein  
A:Residues: 1-20 <HOS>  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
|||  
Db 6 PVV 8

## RESULT 67

A05313  
apolipoprotein A-I - red guenon (fragment)  
N:Alternate names: apo-A-I  
C:Species: Erythrocebus patas (red guenon, hussar)  
C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 11-May-2000  
C:Accession: A05313  
R:Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.  
Biochemistry 15, 1928-1933, 1976  
A:Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus  
A:Reference number: A90395; MUID:76184721; PMID:178359  
A:Accession: A05313  
A:Molecule type: protein  
A:Residues: 1-20 <MAH>  
C:Superfamily: apolipoprotein A-I  
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipop

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4  
|||  
Db 5 QTP 7

## RESULT 68

A60372  
Pollen allergen Poa-pI - Kentucky bluegrass (fragment)  
C:Species: Poa pratensis (Kentucky bluegrass)  
C:Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text\_change 09-Jun-2000  
C:Accession: A60372; A33086  
R:Ekrumoddoullah, A.K.M.  
Int. Arch. Allergy Appl. Immunol. 93, 371-377, 1990  
A:Title: Two-dimensional gel electrophoretic analyses of Kentucky bluegrass and rye grass  
ence of Poa p I allergen.

A:Reference number: A60372; MUID:91317571; PMID:2101126  
A:Accession: A60372  
A:Molecule type: protein  
A:Residues: 1-20 <EKR>  
C:Superfamily: expansin  
C:Keywords: hydroxyproline; pollen  
F:5,8/Modified site: hydroxyproline (Pro) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
|||  
Db 4 VPP 6

## RESULT 69

PQ0046

citrate (ei)-synthase (EC 4.1.3.7) - Streptomyces hygroscopicus (fragment)  
 N:Alternate names: citrate condensing enzyme; citrogenase; condensing enzyme; oxaloacetate  
 C:Species: Streptomyces hygroscopicus  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 05-May-2000  
 C:Accession: PQ0046  
 R:Shimotohno, K.W.; Imai, S.; Murakami, T.; Seto, H.  
 Agric. Biol. Chem. 54, 463-470, 1990  
 A:Title: Purification and characterization of citrate synthase from Streptomyces hygroscopicus  
 A:Reference number: PS0106; MUID:90334852; PMID:1368511  
 A:Accession: PQ0046  
 A:Molecule type: protein  
 A:Residues: 1-20 <SHI>  
 A:Experimental source: strain SF-1293  
 C:Comment: This enzyme catalyzes the synthesis of citric acid.  
 C:Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase; tricarboxylic acid cycle

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
 |||  
 Db 17 PVV 19

RESULT 70  
 B44835  
 dTPGlucoase 4,6-dehydratase (EC 4.2.1.46) - Streptomyces peucetius (fragment)  
 C:Species: Streptomyces peucetius  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: B44835  
 R:Thompson, M.W.; Strohl, W.R.; Floss, H.G.  
 J. Gen. Microbiol. 138, 779-786, 1992  
 A:Title: Purification and characterization of TDP-D-glucose 4,6-dehydratase from anthracis  
 A:Reference number: A44835; MUID:92268857; PMID:1598310  
 A:Accession: B44835  
 A:Molecule type: protein  
 A:Residues: 1-20 <THQ>  
 A:Cross-references: PIDN:AB22196.1; PID:G249564  
 A:Experimental source: ATCC 29050  
 A:Note: sequence extracted from NCBI backbone (NCBIP:103673)  
 C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5  
 |||  
 Db 3 TPV 5

RESULT 71  
 S57286  
 translation elongation factor aEF-1 beta - Sulfolobus solfataricus (fragments)  
 C:Species: Sulfolobus solfataricus  
 C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Mar-1999  
 C:Accession: S57286  
 R:Arcari, P.; Raimo, G.; Ianniciello, G.; Gallo, M.; Bocchini, V.  
 Biochim. Biophys. Acta 1263, 86-88, 1995  
 A:Title: The first nucleotide sequence of an archaeal elongation factor 1-beta gene.  
 A:Reference number: S57268; MUID:953559209; PMID:7632739  
 A:Accession: S57286  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <ARC>

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
 |||

Db 11 PVV 13

RESULT 72  
 PA0022  
 protein QAI00011 - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
 C:Accession: PA0022  
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Teugita, A.  
 submitted to JIPID, July 1994  
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
 A:Reference number: PA0001  
 A:Accession: PA0022  
 A:Molecule type: protein  
 A:Residues: 1-20 <KAW>  
 A:Experimental source: callus

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVP 8  
 |||  
 Db 8 VVP 10

RESULT 73  
 PQ0732  
 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 5.7/16K [similarity] - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C:Accession: PQ0732  
 R:Komatsu, S.; Kajiwara, H.; Hirano, H.  
 Theor. Appl. Genet. 86, 935-942, 1993  
 A:Title: A rice protein library; a data-file of rice proteins separated by two-dimensional gel electrophoresis  
 A:Reference number: PQ0696  
 A:Accession: PQ0732  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <KOM>  
 C:Keywords: metalloprotein; oxidoreductase

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVV 7  
 |||  
 Db 18 VVV 20

RESULT 74  
 PS0188  
 superoxide dismutase (EC 1.15.1.1) (Cu-Zn), chloroplast - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 05-Mar-1993 #sequence\_revision 05-Mar-1993 #text\_change 05-Mar-1999  
 C:Accession: PS0188  
 R:Kawakami, T.; Teugita, A.  
 submitted to JIPID, June 1991  
 A:Reference number: PS0187  
 A:Accession: PS0188  
 A:Molecule type: protein  
 A:Residues: 1-20 <KAW>  
 A:Experimental source: leaf  
 C:Function:  
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
 C:Keywords: chloroplast; copper; metalloprotein; oxidoreductase; zinc

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy \* 5 VV 7  
|||  
Db 18 VV 20

## RESULT 75

A38600  
trypsin inhibitor - Atlantic horseshoe crab (fragment)  
C:Species: Limulus polyphemus (Atlantic horseshoe crab)  
C:Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 18-Jun-1993  
C:Accession: A38600  
R:Donovan, M.A.; Laue, T.M.  
J. Biol. Chem. 266, 2121-2125, 1991  
A:Title: A novel trypsin inhibitor from the hemolymph of the horseshoe crab Limulus poly  
A:Reference number: A38600; MUID:91115821; PMID:1989974  
A:Accession: A38600  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <DON>

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPF 10  
|||  
Db 3 PPF 5

Search completed: November 25, 2003, 18:28:26  
Job time : 10.2021 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 4.84043 Seconds  
(without alignments)  
97.154 Million cell updates/sec

Title: US-09-641-801-20  
Perfect score: 10  
Sequence: 1 TQTPVVVPPF 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	30.0	8	1 PK2_PERAM	P82692 periplaneta
2	3	30.0	10	1 BPP_VIPAS	P31351 vipera aspi
3	3	30.0	12	1 FAR7_PENMO	P83322 penaeus mon
4	3	30.0	12	1 H59A_RAT	P82995 rattus norv
5	3	30.0	13	1 IDHP_RAT	P56574 rattus norv
6	3	30.0	14	1 PH1_PRUSE	P29263 prunus sero
7	3	30.0	14	1 UC15_MAIZE	P80621 zea mays (m
8	3	30.0	14	1 UN04_CLOPA	P81349 clostridium
9	3	30.0	15	1 ARCA_STRP5	P58827 streptococc
10	3	30.0	15	1 CHI1_PEA	P21225 pisum sativ
11	3	30.0	15	1 ESTB_SCHGA	P81011 schizaphia
12	3	30.0	15	1 ESTJ_MANSE	P19985 manduca sex
13	3	30.0	15	1 NU08_SOLTU	P80731 solanum tub
14	3	30.0	15	1 PH3_PRUSE	P29265 prunus sero
15	3	30.0	15	1 R13A_SPIOL	P82454 spinacia ol
16	3	30.0	15	1 UC08_MAIZE	P80614 zea mays (m
17	3	30.0	15	1 UP01_METAN	P83440 metarhizium
18	3	30.0	16	1 PH2_PRUSE	P29264 prunus sero
19	3	30.0	17	1 A45K_MYCHO	P80069 mycobacteri
20	3	30.0	19	1 ATPB_CANFA	P99504 canis fami
21	3	30.0	20	1 APAL_ERYPA	P18647 erythrocebu
22	3	30.0	20	1 C15Y_STRHY	P20903 streptomyce
23	3	30.0	20	1 COG4_CHIOP	P34156 chionocete
24	3	30.0	20	1 F1BB_ELENA	P14538 elephas max
25	3	30.0	20	1 MDH_KIBAR	P19978 kibdelospor
26	3	30.0	20	1 OMPW_VIBAL	P83151 vibrio algi
27	3	30.0	20	1 RNKD_PIG	P80551 sus scrofa
28	3	30.0	4	1 RM01_YEAST	P36515 saccharomyc
29	2	20.0	5	1 PSK_DAUCA	P58261 daucus caro
30	2	20.0	5	1 SUGA_ACHDO	P19991 acteta dome
31	2	20.0	6	1 E101_LITRU	P82096 littoria rub
32	2	20.0	7	1 FAP1_HELTI	P41871 helisoma tr
33	2	20.0	7	1 TPFY_PACDA	P83455 pachymedusa

34	2	20.0	7	1 UF04_MOUSE	P38642 mus musculu
35	2	20.0	7	1 UN06_PINPS	P81675 pinus pinas
36	2	20.0	8	1 AKH_LIBAU	P25418 libellula a
37	2	20.0	8	1 AKH_TABAT	P14595 tabanus atr
38	2	20.0	8	1 ALLE_CALVO	P14841 calliphora
39	2	20.0	8	1 ANG2_BOTJA	Q10582 bothrops ja
40	2	20.0	8	1 CLP_THICU	P80488 thriobacillu
41	2	20.0	8	1 FUSS_FUSSO	P81010 fusarium so
42	2	20.0	8	1 HTF2_PERAM	P04549 periplaneta
43	2	20.0	8	1 LMT2_LOCMI	P22396 locusta mig
44	2	20.0	8	1 LPK_LEUNA	P13049 leucophaea
45	2	20.0	8	1 NS3_MYCTU	P81152 mycobacteri
46	2	20.0	8	1 PPK3_PERAM	P82618 periplaneta
47	2	20.0	8	1 UPAL_HUMAN	P30087 homo sapien
48	2	20.0	8	1 VGLG_HSV2B	P81780 herpes simp
49	2	20.0	9	1 CCAP_CARMA	P38556 carcinus ma
50	2	20.0	9	1 COXE_THUOB	P80975 thunnus obe
51	2	20.0	9	1 FAP1_CALVO	P14856 calliphora
52	2	20.0	9	1 FAR2_CALVO	P41865 calliphora
53	2	20.0	9	1 FLA2_TREHY	P80159 treponema h
54	2	20.0	9	1 KNL3_BOMVA	P83058 bombina var
55	2	20.0	9	1 LMT3_LOCMI	P41489 locusta mig
56	2	20.0	9	1 MGMT_BOVIN	P29177 bos taurus
57	2	20.0	9	1 OXYA_SCYCA	P42996 scyllorhinu
58	2	20.0	9	1 OXYF_SCYCA	P42997 scyllorhinu
59	2	20.0	9	1 OXYV_SQUAC	P43000 squalus aca
60	2	20.0	9	1 ULAD_HUMAN	P31929 homo sapien
61	2	20.0	9	1 UPAT_HUMAN	P30093 homo sapien
62	2	20.0	9	1 YBFR_AZOVI	P25825 azotobacter
63	2	20.0	10	1 AH3_PRUSE	P29261 prunus sero
64	2	20.0	10	1 ANGI_BOTJA	Q10581 bothrops ja
65	2	20.0	10	1 ANGT_BOVIN	P01017 bos taurus
66	2	20.0	10	1 ANGT_CHICK	P01018 gallus gall
67	2	20.0	10	1 BPP2_BOTIN	P30422 bothrops in
68	2	20.0	10	1 BPP2_BOTJA	P01022 bothrops ja
69	2	20.0	10	1 BRK_ONCMY	P30426 bothrops in
70	2	20.0	10	1 BRK_ONCMY	Q9PR21 oncorhynch
71	2	20.0	10	1 COXH_ONCMY	P80331 oncorhynch
72	2	20.0	10	1 COXK_ONCMY	P80332 oncorhynch
73	2	20.0	10	1 COXM_RAT	P80431 rattus norv
74	2	20.0	10	1 COXQ_RABIT	P80336 oryctolagus
75	2	20.0	10	1 COXQ_SHEEP	P80337 ovis aries
76	2	20.0	10	1 FAR5_MACRS	P83278 macrobrachi
77	2	20.0	10	1 FAR6_PANRE	P82660 panagrellus
78	2	20.0	10	1 FARP_MANSE	P18523 manduca sex
79	2	20.0	10	1 HTF1_ROMMI	P18110 romalea mic
80	2	20.0	10	1 HTF2_CARMO	P1385 carausius m
81	2	20.0	10	1 HTF_TABAT	P14596 tabanus atr
82	2	20.0	10	1 LPK2_LOCMI	P41488 locusta mig
83	2	20.0	10	1 NS1_MYCTU	P81135 mycobacteri
84	2	20.0	10	1 TMOF_AEDAE	P19425 aedes aegypt
85	2	20.0	10	1 TRP7_LEUNA	P81739 leucophaea
86	2	20.0	10	1 UPAT_HUMAN	P30088 homo sapien
87	2	20.0	10	1 UPAT_HUMAN	P30090 homo sapien
88	2	20.0	10	1 UPAT_HUMAN	P30094 homo sapien
89	2	20.0	10	1 URE3_MORMO	P17339 morganella
90	2	20.0	10	1 UXB1_YEAST	P89012 saccharomyc
91	2	20.0	10	1 ANGT_CRIGE	P09037 crinia geor
92	2	20.0	11	1 BPP3_BOTIN	P30423 bothrops in
93	2	20.0	11	1 BPP4_BOTIN	P30424 bothrops in
94	2	20.0	11	1 BPP4_BOTIN	P01021 agkistrodon
95	2	20.0	11	1 BPP_AKHPA	P04562 agkistrodon
96	2	20.0	11	1 BRK_MEGFL	P12797 magascolia
97	2	20.0	11	1 COR2_PERAM	P14496 periplaneta
98	2	20.0	11	1 CS15_BACSU	P81095 bacillus su
99	2	20.0	11	1 CX5A_CONAL	P58848 conus aulic
100	2	20.0	11		

ALIGNMENTS

RESULT 1

PK2 PERAM  
ID PK2\_PERAM STANDARD; PRT; 8 AA.  
AC P82632;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-2 (Pea-PK-2) (XPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;  
OC Blattellidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=97353923; PubMed=9210163;  
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;  
RT "Isolation and structural elucidation of two pyrokinins from the  
RT retrocerebral complex of the American cockroach.";  
RL Peptides 18:473-478(1997).  
RN [2]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tissue-specific distribution of FXPLamides in the nervous system of  
RT the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
(MYOTROPIC ACTIVITY).  
CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; FALSE NEG.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 8 8  
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;  
Query Match 30.0%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 PPF 10  
DB 2 PPF 4  
RESULT 2  
ID BPP\_VIPAS STANDARD; PRT; 10 AA.  
AC P31351;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide (Angiotensin-converting  
DE enzyme inhibitor).  
OS Vipera aspis (Aspic viper).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;  
OC Viperidae; Viperinae; Vipera.  
OX NCBI\_TaxID=8706;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90382616; PubMed=2169439;  
RA Komori Y., Sugihara H.;  
RT "Characterization of a new inhibitor for angiotensin converting  
RT enzyme from the venom of Vipera aspis aspis.";  
RL Int. J. Biochem. 22:767-771(1990).  
CC -1- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.

DR PIR; A60377; XASNPC.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1  
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;  
Query Match 30.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 VPP 9  
DB 8 VPP 10  
RESULT 3  
ID FAR7\_PENMO STANDARD; PRT; 12 AA.  
AC P83322;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRamide-like neuropeptide FLP7 (GRKKPFNGSIF-amide).  
OS Penaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,  
RA Chaivuthangkura P., Sithigorngul W., Petson A.;  
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk  
RT of the giant tiger prawn Penaeus monodon.";  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 12 12  
SQ SEQUENCE 12 AA; 1383 MW; 31209192EF49D777 CRC64;  
Query Match 30.0%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 PPF 10  
DB 5 PPF 7  
RESULT 4  
ID HS9A\_RAT STANDARD; PRT; 12 AA.  
AC P82955;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Heat shock protein HSP 90-alpha (Fragment).  
GN HSPCA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=21589773; PubMed=11732320;  
RA Langer T., Fasold H.;  
RT "Isolation and quantification of the heat shock protein 90 alpha and  
RT beta isoforms from rat liver.";

```

RL  Protoclasma 218:54-56(2001).
CC  -1- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC  (BY SIMILARITY).
CC  -1- SUBUNIT: Homodimer (By similarity).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR  InterPro; IPR001404; Hsp90.
DR  PROSITE; PS00298; Hsp90; PARTIAL.
KW  Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT  MOD_RES 4 4 PHOSPHORYLATION (BY DS-DNA KINASE) (BY
FT  MOD_RES 6 6 SIMILARITY)
FT  MOD_RES 12 12 PHOSPHORYLATION (BY DS-DNA KINASE) (BY
FT  NON_TER 13 13 SIMILARITY)
SQ  SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOT 3
    |||
Db 4 TOT 6

RESULT 5
IDHP_RAT STANDARD; PRT; 13 AA.
AC P56574;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)
DE (Oxaloacetic decarboxylase) (IDH) (NADP+-specific IDH) (IDP) (ICD-
DE M) (Fragment).
DE IDH2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -1- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY
CC PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE
CC DEHYDROGENASE COMPLEX (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)
CC + NADPH.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT P8) IS: 9.0, ITS MW IS: 42 kDa.
CC -1- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC DEHYDROGENASES FAMILY.
DR InterPro; IPR001804; IsoDH.
DR PROSITE; PS00470; IDH_IDH; PARTIAL.
KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle;
KW Mitochondrion.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1526 MW; 5FB81031723E02C3 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7
    |||
Db 11 VVW 13

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RESULT 6
PH1_PRUSE STANDARD; PRT; 14 AA.
AC P29263;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Prunasin beta-glucosidase I (EC 3.2.1.118) (Prunasin hydrolase
DE isozyme I) (PH 1) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
CC Glucose.
CC -1- SUBUNIT: Monomer.
CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -1- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1575 MW; FB3D7F4FB90CA9CA CRC64;

Query Match 30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6
    |||
Db 4 PVV 6

RESULT 7
UC15_MAIZE STANDARD; PRT; 14 AA.
AC P80621;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC MAIZE-2DPAGE; P80621; COLEOPTILE.
DR Maize2DPAGE; P80621;
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVV 6  
|||  
6 PW 8

## RESULT 8

UN04\_CLOPA STANDARD; PRT; 14 AA.  
AC P81349;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Unknown protein CP 4 from 2D-page (Fragment).  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 4.7, ITS MW IS: 45.7 kDa.  
FT NON TER 14  
SQ SEQUENCE 14 AA; 1608 MW; D424A7069460EBD2 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VVV 7  
|||  
7 VVV 9

## RESULT 9

ARCA\_STRP5 STANDARD; PRT; 15 AA.  
AC PS8827;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD)  
DE (Streptococcal acid glycoprotein) (Fragment).  
GN ARCA OR SAGP.  
OS Streptococcus pyogenes (serotype M5).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=160491;  
RN [1]  
RP SEQUENCE, AND CHARACTERIZATION.  
RC STRAIN=Manfredo / Serotype M5;  
RX MEDLINE=98298018; PubMed=9632565;  
RA Degan B.A., Palmer J.M., Robson T., Jones C.E.D., Fischer M.,  
RA Glanville M., Mellor G.D., Diamond A.G., Kehoe M.A., Goodacre J.A.;  
RT "Inhibition of human peripheral blood mononuclear cell proliferation  
by Streptococcus pyogenes cell extract is associated with arginine  
deiminase activity.";  
RL Infect. Immun. 66:3050-3058(1998).  
CC -!- FUNCTION: Antitumor protein. Has a powerful and dose-dependent  
inhibitory effect on antigen, superantigen, or mitogen-stimulated  
human peripheral blood mononuclear cell (PBMC) proliferation. It  
may inhibit cell proliferation by arresting cell cycle and  
inducing apoptosis.  
CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).  
CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.  
CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -!- SIMILARITY: Belongs to the arginine deiminase family.  
DR HAMAP: MF\_00242; -; 1  
KW Hydrolase; Arginine metabolism; Glycoprotein.  
FT INIT MET 0  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1657 MW; D21150201B00EB46 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QTP 4  
|||  
3 QTP 5

## RESULT 10

CH11\_PEA STANDARD; PRT; 15 AA.  
AC P21225;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Endochitinase A1 (EC 3.2.1.14) (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=cv. Birte; TISSUE=Leaf;  
RA Vad K., Mikkelsen J.D., Collinge D.B.;  
RT "Induction, purification and characterization of chitinase isolated  
from pea leaves inoculated with Ascochyta pisi.";  
RL Planta 184:24-29(1991).  
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN  
CONTAINING FUNGAL PATHOGENS.  
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-  
acetyl-D-glucosamine polymers of chitin.  
CC -!- INDUCTION: By infection with the fungal pathogen Ascochyta pisi.  
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO  
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL  
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL  
HYDROLASES).  
DR InterPro; IPR001002; Chitin binding\_1.  
DR InterPro; IPR000726; Glyco\_hydro\_19.  
DR PROSITE; PS00026; CHITIN BINDING; PARTIAL.  
DR PROSITE; PS00773; CHITINASE\_19\_1; PARTIAL.  
DR PROSITE; PS00774; CHITINASE\_19\_2; PARTIAL.  
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding;  
KW Multigene family.  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1438 MW; 2335ED6BB11E869 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 VPP 9  
|||  
11 VPP 13

## RESULT 11

ESTB\_SCHGA STANDARD; PRT; 15 AA.  
AC P81011;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Esterase 56 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)



(Fragment).  
 DE Schizaphis graminum (Aphid).  
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
 OC Aphidoidea; Aphididae; Aphidini; Schizaphis.  
 OX NCBI\_TaxID=13262;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=97468499; PubMed=9327586;  
 RA Siegfried B.D., Ono M., Swanson J.J.;  
 RT "Purification and characterization of a carboxylesterase associated  
 with organophosphate resistance in the greenbug, Schizaphis graminum  
 (Homoptera: Aphididae).";  
 RL Arch. Insect Biochem. Physiol. 36:229-240(1997).  
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
 carboxylic anion.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC InterPro; IPR002018; CarbesteraseB.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; PARTIAL.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; PARTIAL.  
 KW Hydrolase; Serine esterase.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1609 MW; 1208B2BCCC969482 CRC64;  
 Query Match 30.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 PVW 6  
 Db |||  
 |||  
 2 PVW 4  
 RESULT 12  
 ESTJ\_MANSE STANDARD; PRT; 15 AA.  
 AC P19985;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Juvenile hormone esterase (EC 3.1.1.59) (JH esterase) (Fragment).  
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;  
 OC Sphingidae; Sphinginae; Manduca.  
 OX NCBI\_TaxID=7130;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larval plasma;  
 RX MEDLINE=91072375; PubMed=2254326;  
 RA Venkatesh K., Abdel-Aal Y.A.I., Armstrong F.B., Roe R.M.;  
 RT "Characterization of affinity-purified juvenile hormone esterase from  
 the plasma of the tobacco hornworm, Manduca sexta.";  
 RL J. Biol. Chem. 265:21727-21732(1990).  
 CC -1- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF  
 JH ACTIVITY IN LEPIDOPTERAN INSECTS BY HYDROLYZING THE METHYL  
 ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.  
 CC -1- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-  
 trimethyltrideca-2,6-dienoate + H(2)O = (2E,6E)-(10R,11S)-10,11-  
 epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC PIR; A36527; A36527.  
 DR InterPro; IPR002018; CarbesteraseB.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; PARTIAL.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; PARTIAL.  
 KW Hydrolase; Serine esterase.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1659 MW; D321EA432E58B848 CRC64;  
 Query Match 30.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7  
 Db |||  
 8 VVW 10  
 RESULT 13  
 NU08\_SOLTU STANDARD; PRT; 15 AA.  
 AC P80731;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 12 kDa subunit (EC 1.6.5.3)  
 DE (EC 1.6.59.3) (Complex I-12KD) (CI-12KD) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Bintje; TISSUE=Tuber;  
 RA Herz U., Grohmann L.;  
 RL Submitted (DEC-1996) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
 CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
 TO BE UBIQUINONE.  
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -1- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
 CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER  
 MEMBRANE.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1668 MW; EDC87B30AD155854 CRC64;  
 Query Match 30.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 VPP 9  
 Db |||  
 9 VPP 11  
 RESULT 14  
 PH3\_PRUSE STANDARD; PRT; 15 AA.  
 AC P29265;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase  
 isozyme IIB) (PH IIB) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-  
 glucose.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 EMBRYONAL TISSUES.

CC -1- PTM: GLYCOSYLATED.  
 KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1635 MW; 4F3D7F4FB90CFE4C CRC64;

Query Match 30.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
 Db 5 PVV 7

RESULT 15  
 R13A SPIOL  
 ID R13A SPIOL STANDARD; PRT; 15 AA.  
 AC P82454;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 60S ribosomal protein L13a (Fragment).  
 GN RPL13A.  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Alwato; TISSUE=Leaf;  
 RA Yanaguchi K., Subramanian A.R.;  
 RT "N-terminal sequence of spinach cytosolic 60S ribosomal protein L13a.";  
 RL Submitted (APR-2000) to the SWISS-PROT data bank.  
 CC -1- SIMILARITY: BELONGS TO THE L13P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro: IPR005822; Rib prot L13.  
 DR PROSITE: PS00783; RIBOSOMAL\_L13; PARTIAL.  
 KW Ribosomal protein.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1489 MW; C7B9C80F5A099EB3 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVV 7  
 Db 11 VVV 13

RESULT 16  
 UC08 MAIZE  
 ID UC08 MAIZE STANDARD; PRT; 15 AA.  
 AC P80614;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159) (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated genome analysis program.";  
 RT Theor. Appl. Genet. 93:997-1005 (1996).

CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.4. ITS MW IS: 38.8 kDa.  
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase  
 CC family.  
 DR Maize-2DPAGE; P80614; COLEOPTILE.  
 DR MaizeDB; 123934; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6ABADD8D CRC64;

Query Match 30.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
 Db 9 PVV 11

RESULT 17  
 UP01 METAN  
 ID UP01 METAN STANDARD; PRT; 15 AA.  
 AC P83440;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Unknown protein (Fragment).  
 OS Metarhizium anisopliae.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Clavicipitaceae;  
 OC mitosporic Clavicipitaceae; Metarhizium.  
 OX NCBI\_TaxID=5530;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=54A-1b;  
 RX MEDLINE=22343006; PubMed=12455610;  
 RA Kamp A.M., Bidochka M.J.;  
 RT "Protein analysis in a pleomorphically deteriorated strain of the insect-pathogenic fungus Metarhizium anisopliae.";  
 RL Can. J. Microbiol. 48:787-792 (2002).  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1651 MW; FBD76D669E1F0F4F CRC64;

Query Match 30.0%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
 Db 4 PVV 6

RESULT 18  
 PH2 PRUSE  
 ID PH2 PRUSE STANDARD; PRT; 16 AA.  
 AC P29264;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Prunasin beta-glucosidase IIA (EC 3.2.1.118) (Prunasin hydrolase isozyme IIA) (PH IIA) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurossids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290 (1992).  
 CC -1- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-

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CC CC glucose.
CC -1- SUBUNIT: Homodimer.
CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT. THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -1- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON TER 16
SQ SEQUENCE 16 AA; 1703 MW; FC4D7F4FB90CFE01 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVW 6
DB 6 PVW 8

RESULT 19
A45K_MYCBO
ID A45K_MYCBO STANDARD; PRT; 17 AA.
AC P80069;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 45/47 kDa antigen (Fragment).
OS Mycobacterium bovis.
CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / Paris 1173 P2;
RA MEDLINE=93138802; PubMed=8423100;
RA Romain F., Laquerriere A., Miltzer P., Pescher P., Chavarot P.,
RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;
RT Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen
RT complex, an immunodominant target for antibody response after
RT immunization with living bacteria."
RL Infect. Immun. 61:742-750(1993).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: TO M.LEPRAE NL43, AND M.TUBERCULOSIS MPT32.
DR PIR; A49237; A49237.
KW Antigen.
FT NON TER 17
SQ SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VPP 9
DB 8 VPP 10

RESULT 20
ATPB_CANFA
ID ATPB_CANFA STANDARD; PRT; 19 AA.
AC P99504;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP synthase beta chain, mitochondrial (EC 3.6.3.14) (Fragment).
GN ATP5B.
OS Canis familiaris (Dog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.

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RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
CC SUBUNIT.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
DR HSC-2DPAGE; P99504; DOG.
DR InterPro; IPR000194; ATPase_a/bcentra.
DR PROSITE; PS00152; ATPASE ALPHA BETA; PARTIAL.
KW ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; ATP-binding;
KW Mitochondrion.
FT UNSURE 8
FT UNSURE 17
FT NON TER 19
SQ SEQUENCE 19 AA; 1871 MW; BB9C163FDC60BB42 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TQT 3
DB 2 TQT 4

RESULT 21
APAL_ERYPA
ID APAL_ERYPA STANDARD; PRT; 20 AA.
AC P18647;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein A-I (Apo-AI) (Fragment).
GN APOA1
OS Erythrocebus patas (Red guenon) (Husar).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
CC Cercopitheinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=76184721; PubMed=178359;
RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
RT "Characterization of the plasma lipoproteins and apoproteins of the
RT Erythrocebus patas monkey."
RL Biochemistry 15:1928-1933(1976).
CC -1- FUNCTION: APOA-I PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
DR PIR; A05313; A05313.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism.
FT NON TER 20
SQ SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 QTP 4
Db      5 QTP 7

RESULT 22
CISY_STRHY STANDARD; PRT; 20 AA.
ID _CISY_STRHY STANDARD; PRT; 20 AA.
AC P20903;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Citrate synthase (EC 2.3.3.1) (Fragment).
GN GLTA.
OS Streptomyces hygroscopicus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1912;
RN [1]
RP SEQUENCE
RC STRAIN=SF1293;
RX MEDLINE=90334852; PubMed=1368511;
RA Shimotohno K.W., Imai S., Murakami T., Seto H.;
RT "Purification and characterization of citrate synthase from
RT Streptomyces hygroscopicus SP-1293 and comparison of its properties
RT with those of 2-phosphinomethylmalic acid synthase.";
RL Agric. Biol. Chem. 54:463-470(1990).
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate +
CC CoA.
CC -1- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY NADH.
CC -1- PATHWAY: Tricarboxylic acid cycle.
CC -1- SUBUNIT: Homohexamer.
CC -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
CC CAPABLE OF OXIDATIVE METABOLISM.
CC -1- SIMILARITY: Belongs to the citrate synthase family.
DR PIR; PQ0046;
DR InterPro: IPR002020; Citrate synt.
DR PROSITE; PS00480; CITRATE SYNTHASE; PARTIAL.
KW Transferase; Tricarboxylic acid cycle; Allosteric enzyme.
FT NON TER 20
SQ SEQUENCE 20 AA; 2234 MW; C527EC7A87119597 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PVV 6
Db      17 PVV 19

RESULT 23
COG4_CHIOP STANDARD; PRT; 20 AA.
AC P34156;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagenolytic protease 23 kDa (EC 3.4.24.7) (Fragment).
OS Chionocetes opilio (Crab-beetle).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Majoidae; Majidae; Chionoecetes.
OX NCBI_TaxID=41210;
RN [1]
RP SEQUENCE
RC TISSUE=Hepatopancreas;
RX MEDLINE=92120073; PubMed=1663026;
RA Klimova O.A., Vedishcheva Y.V., Strongin A.Y.;
RT "Isolation and characteristics of collagenolytic enzymes from the
RT hepatopancreas of the crab Chionoecetes opilio.";
RL Dokl. Akad. Nauk SSSR 317:482-484(1991).

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CC -1- FUNCTION: THIS ENZYME IS A METAL PROTEASE CAPABLE OF DEGRADING
CC THE NATIVE TRIPLE HELIX OF COLLAGEN.
CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-[Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where pi' is a
CC hydrophobic residue.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
DR MEROPS; M12.001; -.
DR InterPro; IPR006025; Zn_MTPeptidse.
DR PROSITE; PS00142; ZINC_PROTEASE; PARTIAL.
KW Hydrolase; Metalloprotease; Zinc; Collagen degradation.
FT NON TER 20
SQ SEQUENCE 20 AA; 2108 MW; 2BC7A93D022A97D8 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VVP 8
Db      14 VVP 16

RESULT 24
FIBB_ELEMA STANDARD; PRT; 20 AA.
ID _FIBB_ELEMA STANDARD; PRT; 20 AA.
AC P14538;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Elephas maximus (Indian elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantiidae; Elephas.
OX NCBI_TaxID=9783;
RN [1]
RP SEQUENCE.
RA O'Neil P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 20 FIBRINOPEPTIDE B.
FT MOD_RES 20 4 SULFATION.
FT NON TER 20
SQ SEQUENCE 20 AA; 2107 MW; B4F52B9599933273 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 VPP 9
Db      13 VPP 15

RESULT 25
MDH_KIBAR STANDARD; PRT; 20 AA.
ID _MDH_KIBAR

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AC P19578;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
GN MDH
OS Kibdelosporangium aridum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardaceae; Kibdelosporangium.
OX NCBI_TaxID=2030;
RN [1]
RP SEQUENCE.
RX MEDLINE=89374824; PubMed=2775496;
RA Rommel T.O., Hund H.-K., Speth A.R., Lingens F.;
RT "Purification and N-terminal amino-acid sequences of bacterial malate
RT dehydrogenases from six actinomycetales strains and from
RT phenylobacterium immobile, strain E.";
RL Biol. Chem. Hoppe-Seyler 370:763-768 (1989).
CC -|- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
CC -|- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
DR PIR; S04961; S04961.
DR InterPro; IPR001252; Mdh.
DR PROSITE; PS00068; MDH: PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 20
SQ SEQUENCE 20 AA; 1989 MW; 795876F58C00AC9 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5
Db 3 TPV 5

RESULT 26
OMPW_VIBAL
ID OMPW_VIBAL STANDARD; PRT; 20 AA.
AC P83151;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein W (Outer membrane protein 25Va) (Omp25Va)
DE (Fragment).
GN OMPW.
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 1903T;
RA Onji M., Hirabayashi J., Suzuki S.;
RT "Characterization of major outer membrane proteins of Vibrio
RT alginolyticus and the stability against proteases.";
RL Microbes Environ. 0:0-0(2002).
CC -|- SUBCELLULAR LOCATION: Outer membrane.
CC -|- SIMILARITY: BELONGS TO THE OMPW/ALKL FAMILY.
KW Outer membrane.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2096 MW; D29EE7FCA16C0D37 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVP 8
Db 15 VVP 17

RESULT 27

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RNKD_PIG
ID RNKD_PIG STANDARD; PRT; 20 AA.
AC P80551;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nonsecretory ribonuclease (EC 3.1.27.5) (Eosinophil-derived
DE neurotoxin) (Fragment).
GN RNASE2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=96242065; PubMed=8645990;
RA Fornhem C., Peterson C.G.B., Alving K.;
RT "Isolation and characterization of porcine cationic eosinophil
RT granule proteins.";
RL Int. Arch. Allergy Immunol. 110:132-142 (1996).
CC -|- FUNCTION: THIS IS A NON-SECRETORY RIBONUCLEASE. IT IS A PYRIMIDINE
CC SPECIFIC NUCLEASE WITH A SLIGHT PREFERENCE FOR U.
CC -|- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-cyclic phosphonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -|- SUBCELLULAR LOCATION: LYSOSOMAL (PROBABLE); MATRIX OF EOSINOPHIL'S
CC LARGE SPECIFIC GRANULE.
CC -|- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR InterPro; IPR001427; RNaseA.
DR PROSITE; PS00127; RNASE_PANCREATIC; PARTIAL.
KW Hydrolase; Nuclease; Endonuclease; Eosinophil.
FT ACT_SITE 16
FT NON_TER 20
SQ SEQUENCE 20 AA; 2142 MW; 2CDOA6E1ABAE8A6A CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9
Db 1 VPP 3

RESULT 28
RM01_YEAST
ID RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56 (1991).
DR PIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4

Db 3 TP 4

#### RESULT 29

PSK\_DAUCA  
ID PSK\_DAUCA STANDARD; PRT; 5 AA.  
AC P58261;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].  
OS Daucus carota (Carrot).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; campanulids; Apiales; Apiaceae; Daucus.  
OX NCBI\_TaxID=4039;  
RN [1]  
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.  
RC STRAIN=cv. US-Harumakigosun;  
RX MEDLINE=2012743; PubMed=10750705;  
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,  
RA Kamada H., Sakagami Y.;  
RT "A secreted peptide growth factor, phytosulfokine, acting as a  
stimulatory factor of carrot somatic embryo formation.";  
RL Plant Cell Physiol. 41:27-32(2000).  
CC -1- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE  
CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC  
EMBRYOS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A  
PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.  
KW Growth factor; Sulfation.  
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.  
FT MOD\_RES 1 1 SULFATION.  
FT MOD\_RES 3 3 SULFATION.  
SQ SEQUENCE 5 AA; 687 MW; 76C1BB504B300000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;

Qy 1 TQ 2

Db 4 TQ 5

#### RESULT 30

SUGA\_ACHDO  
ID SUGA\_ACHDO STANDARD; PRT; 5 AA.  
AC P19931;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Subesophageal ganglion pentapeptide.  
OS Acheta domestica (House cricket).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
OC Acheta.  
OX NCBI\_TaxID=6997;  
RN [1]  
RP SEQUENCE.  
RA Wicker C.;  
RT "Isolation and structure of a peptide isolated from the  
subesophageal ganglion of Acheta domestica (Orthoptera).";  
RL Comp. Biochem. Physiol. 88C:185-187(1987).  
CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL  
GANGLIA.

DR PIR; JS0319; JS0319.

SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;

Qy 9 PF 10

Db 4 PF 5

#### RESULT 31

EI01\_LITRU  
ID EI01\_LITRU STANDARD; PRT; 6 AA.  
AC P82036;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litoria electrica. Comparison with the skin peptides from Litoria  
rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 6 6 AMIDATION.  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;

Qy 7 VP 8

Db 2 VP 3

#### RESULT 32

FAR1\_HELTI  
ID FAR1\_HELTI STANDARD; PRT; 7 AA.  
AC P41871;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRamide-like neuropeptide GDPFLRF-amide.  
OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;  
OC Lymnaeidae; Planorbidae; Helisoma.  
OX NCBI\_TaxID=27815;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRamide-related peptides from the kidney of the snail, Helisoma  
trivolvis.";  
RL Peptides 15:31-36(1994).  
CC -1- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING  
THE KIDNEY, MANTLE AND SKIN.  
CC -1- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
FAMILY.

```
KW Neuropeptide; Amidation.
FT MOD RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PF 10
   ||
Db 3 PF 4

RESULT 33
TPFY PACDA STANDARD; PRT; 7 AA.
AC P8345;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (Pdt-1).
OS Pachymedusa dactinolor (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyllidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactinolor tryptophyllin-1 (Pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD RES 3 3 HYDROXYLATION.
FT MOD RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VP 8
   ||
Db 6 VP 7

RESULT 34
UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=9500907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PP 9
   ||
Db 3 PP 4

RESULT 35
UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PF 10
   ||
Db 6 PF 7

RESULT 36
AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
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RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
DB 5 TP 6

RESULT 37
AKH TABAT
ID AKH TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP TISSUE=Head;
RC MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A33995; A33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
DB 5 TP 6

RESULT 38
ALL5_CALVO
ID ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP TISSUE=Head;
RC MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -1- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; E47393; E47393.
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD RES 3 3 HYDROXYLATION (20%).
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PP 9
DB 2 PP 3

RESULT 39
ANG2 BOTJA
ID ANG2 BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP TISSUE=Plasma;
RC MEDLINE=96208932; PubMed=8929801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8

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SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PF 10  
 ||  
 7 PF 8

Db

RESULT 40

CLP\_THICU

ID CLP\_THICU STANDARD; PRT; 8 AA.

AC P80488;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Chemolithotroph-specific protein (fragment).

OS Thiobacillus cuprinus.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

CC Comamonadaceae; Thiomonas.

OX NCBI\_TaxID=36860;

RN [1]

RP SEQUENCE.

RC STRAIN=DSM 5494;

RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;

RL Submitted (SEP-1995) to the SWISS-PROT data bank.

CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED

CC -!- CHEMOLITHOTROPHICALLY.

FT NON TER 8

SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PV 5  
 ||  
 2 PV 3

Db

RESULT 41

FUSS\_FUSSO

ID FUSS\_FUSSO STANDARD; PRT; 8 AA.

AC P81010;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Allergen Fus s 13596\* (fragment).

OS Fusarium solani (subsp. pisi) (Nectria haematococca).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

CC Hypocnemycetidae; Hypocreales; Nectriaceae; Nectria.

OX NCBI\_TaxID=70791;

RN [1]

RP SEQUENCE.

RC STRAIN=IARI 3596; TISSUE=Mycelium;

RA Verna J., Gangal S.V.;

RL Submitted (JUL-1997) to the SWISS-PROT data bank.

KW Allergen.

FT NON TER 8

SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VP 8  
 ||  
 7 VP 8

Db

RESULT 42

HTF2\_PERAM

ID HTF2\_PERAM STANDARD; PRT; 8 AA.

AC P04549;

DT 13-AUG-1987 (Rel. 05, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypertrihaloaemic factor II (Neuropeptide M-II) (Periplanetin CC-2) (Pea-CAH-II) (LeP-CC-II) (Hypertrihaloaemic neuropeptide II).

OS Periplaneta americana (American cockroach).

OS Leptinotarsa decemlineata (Colorado potato beetle), and

OS Blatta orientalis (Oriental cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;

OC Blattidae; Periplaneta.

OX NCBI\_TaxID=6978, 7539, 6976;

RN [1]

RP SEQUENCE.

RC SPECIES=P.americana;

RX MEDLINE=85046530; PubMed=6548628;

RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Henling M.E.,

RA Rinehart K.L. Jr.;

RT "Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry.";

RT Biochem. Biophys. Res. Commun. 124:350-358 (1984).

RN [2]

RP SEQUENCE.

RC SPECIES=P.americana;

RX MEDLINE=84298179; PubMed=6591205;

RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,

RA Miller C.A., Schooley D.A.;

RT "Isolation and primary structure of two peptides with cardioacceleratory and hyperglycemic activity from the corpora cardiaca of Periplaneta americana.";

RT proc. Nacl. Acad. Sci. U.S.A. 81:5575-5579 (1984).

RN [3]

RP SEQUENCE.

RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;

RX MEDLINE=90160053; PubMed=2576128;

RA Gaede G., Kellner R.;

RT "The metabolic neuropeptides of the corpus cardiaca from the potato beetle and the American cockroach are identical.";

RL Peptides 10:1287-1289 (1989).

RN [4]

RP SEQUENCE.

RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;

RX MEDLINE=90253659; PubMed=2340112;

RA Gaede G., Rinehart K.L. Jr.;

RT "Primary structures of hypertrihaloaemic neuropeptides isolated from the corpora cardiaca of the cockroaches Leucophaea maderae, Gromphadorhina portentosa, Blattella germanica and Blatta orientalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry.";

RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).

CC -!- FUNCTION: HYPERTRHALOAEIC FACTORS ARE NEUROPEPTIDES THAT ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).

CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.

DR PIR; B44960; B44960.

DR PIR; B49823; B49823.

DR PIR; S08996; S08996.

DR InterPro; IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.

KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 8 8 AMIDATION.

SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4  
 ||  
 ||

Db 5 TP 6

## RESULT 43

LMT2\_L0CMI STANDARD; PRT; 8 AA.  
 AC P22396;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE Locustamyotropin 2 (LOM-MT-2).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OK NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Corpora cardiaca;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
 RT "Isolation, identification and synthesis of locustamyotropin II, an  
 RT additional neuropeptide of Locusta migratoria. Member of the  
 RT cephalomyotropic peptide family.";  
 RL Insect Biochem. 20:479-484(1990).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 (MYOTROPIC ACTIVITY).  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro; IPR001484; Pyrokinin.  
 KW PROSITE; PS00539; PYROKININ; 1.  
 DR Neuropeptide; Amidation; Pyrokinin.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 934 MW; 26341771A9CA87B CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4

Db 5 TP 6

## RESULT 44

LPK\_LEUMA STANDARD; PRT; 8 AA.  
 AC P13049;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leukopyrokinin (LPK) (LEM-PK).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OK NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.

RC MEDLINE=86269041; PubMed=3015140;  
 RA Nachman R.J., Holman G.M., Cook B.J.;  
 RT "Active fragments and analogs of the insect neuropeptide  
 RT leucopyrokinin: structure-function studies.";  
 RL Biochem. Biophys. Res. Commun. 137:936-942(1986).  
 CC [2]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RX MEDLINE=87052651; PubMed=2877794;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Primary structure and synthesis of a blocked myotropic  
 RT neuropeptide isolated from the cockroach, Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 85C:219-224(1986).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 (MYOTROPIC ACTIVITY).

-1- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS

CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE  
 CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST  
 CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE  
 CC PENTAPEPTIDE FRAGMENT FTPL.  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR PIR; A23967; A23967.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin; Pyroglutamate carboxylic acid.  
 FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QT 3

Db 1 QT 2

## RESULT 45

NS3\_MYCTU STANDARD; PRT; 8 AA.  
 AC P81152;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 30 kDa non-secretory protein 3 (Fragment).  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OK NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=H37Rv;  
 RA Prasad H.K., Annappurna P.S.;  
 RL Submitted (DEC-1997) to the SWISS-PROT data bank.  
 CC -1- CAUTION: We are unable to find this protein in the translation of  
 CC the genome of strain H37Rv.  
 CC NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDC2D2 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VV 6

Db 1 VV 2

## RESULT 46

PK3\_PERAM STANDARD; PRT; 8 AA.  
 AC P82618;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-3 (Psa-PK-3) (EXPRU-amide).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OK NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Retrocerebral complex;  
 RX MEDLINE=99212469; PubMed=10196736;  
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
 RT "Differential distribution of pyrokinin-isoforms in cerebral and

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RT abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144 (1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tigma-specific distribution of FXPRLamides in the nervous system of
the American cockroach.";
RL J. Comp. Neurol. 419:352-363 (2000).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VP 8
Db 2 VP 3

RESULT 47
UPAL_HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714 (1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.9, ITS MW IS: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON_TER 1
FT UNSURE 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VP 8
Db 6 VP 7

RESULT 48
VGLG_HSV2B STANDARD; PRT; 8 AA.
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).

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OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RX Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
2: GH, GB, GC, GD, GI, AND GF.
CC -1- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
HSV-1.
KW Glycoprotein.
FT NON_TER 8
SQ SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VP 8
Db 4 VP 5

RESULT 49
CCAP_CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RX SPECIES=C.maenas; TISSUE=Pericardial organs;
RX Stangler J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579 (1987).
RN [2]
RP SEQUENCE.
RX SPECIES=M.sexta;
RX MEDLINE=93050243; PubMed=1426284;
RX Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168 (1992).
RN [3]
RP SEQUENCE.
RX SPECIES=S.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RX Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RX Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074 (1993).
CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
INTO THE HEMOLYMPH.
DR PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3
FT MOD_RES 9
SQ SEQUENCE 9 AMIDATION.

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SQ SEQUENCE 9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PF 10  
DB 1 PF 2

RESULT 50  
COXE THUOB  
ID COXE THUOB STANDARD; PRT; 9 AA.  
AC P80975; 9 AA.  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).  
OS Thunus obesus (Bigeye tuna). Craniata; Vertebrata; Euteleostomi;  
OC Eukaryota; Metazoa; Chordata.  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
OC Scombridae; Thunnus.  
OX NCBI\_TaxID=8241;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Heart;  
RX MEDLINE=97454291; PubMed=9310366;  
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,  
RA Kadenbach B.;  
RT "The subunit structure of cytochrome-c oxidase from tuna heart and liver.";  
RL Eur. J. Biochem. 248:99-103(1997).  
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.  
CC -1- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome c + 2 H2(O).  
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.  
DR PIR; S77984; S77984.  
DR InterPro; IPR001349; COX6A.  
DR PROSITE; PS01329; COX6A; PARTIAL.  
KW Oxidoreductase; inner membrane; Mitochondrion.  
FT NON TER 1 1  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VP 8  
DB 7 VP 8

RESULT 51  
FAR1 CALVO  
ID FAR1 CALVO STANDARD; PRT; 9 AA.  
AC P41856; 9 AA.  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CallifMRamide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated callifMRFamides) from the blowfly Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
DR PIR; A41978; A41978.  
KW Neuropeptide; Amidation.  
FT MOD RES 9  
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4  
DB 1 TP 2

RESULT 52  
FAR2 CALVO  
ID FAR2 CALVO STANDARD; PRT; 9 AA.  
AC P41857;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CallifMRamide 2.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated callifMRFamides) from the blowfly Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
DR PIR; B41978; B41978.  
KW Neuropeptide; Amidation.  
FT MOD RES 9  
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4  
DB 1 TP 2

RESULT 53  
FARA CALVO  
ID FARA CALVO STANDARD; PRT; 9 AA.  
AC P41865;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliphridae 10.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Renfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliphrin) from the blowfly  
 RT Calliphora vomitoria.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
 CC -1- FAMILY.  
 DR PIR; A44787; A44787.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 FT UNSURE 1 1 OR S OR A.  
 SQ SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;  
  
 Query Match 20.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 3 TP 4  
 DB 1 TP 2  
  
 RESULT 54  
 ID FLA2\_TREHY STANDARD; PRT; 9 AA.  
 AC P80159;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Flagellar filament outer layer protein flia2 (35 kDa sheath protein)  
 DE (Fragment).  
 GN FLA2.  
 OS Treponema hyodysenteriae (Serpulina hyodysenteriae).  
 OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.  
 OX NCBI\_TaxID=159;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=C5;  
 RX MEDLINE=93139764; PubMed=1487733;  
 RA Koopman M.B.H., Baate E., van Vorstenbosch C.J.A.H.V.,  
 RA van der Zeijst B.A.M., Kusters J.G.;  
 RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are  
 RT composed of two sheath proteins and three core proteins.";  
 RL J. Gen. Microbiol. 138:2697-2706(1992).  
 CC -1- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.  
 CC -1- SURUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO  
 CC SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE  
 CC THAT CONTAINS THREE PROTEINS FLA3 (37 kDa), FLA2 (34 kDa) AND  
 CC FLA3 (32 kDa).  
 CC -1- SUBCELLULAR LOCATION: Periplasmic flagellum.  
 KW Flagella; Periplasmic.  
 FT UNSURE 2 2  
 FT NON\_TER 8 9  
 SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;  
  
 Query Match 20.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 7 VP 8

DB 3 VP 4  
 RESULT 55  
 ID KNL3\_BOMVA STANDARD; PRT; 9 AA.  
 AC P83058;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE [Thr6]bradykinin.  
 OS Bombina variegata (Yellow-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=8348;  
 RN [1]  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;  
 RT "Cloning and post-translational processing of frog skin kininogens.";  
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat  
 CC arterial smooth muscle and constriction of intestinal smooth  
 CC muscle.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
 KW Amphibian defense peptide; Vasodilator; Bradykinin.  
 SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;  
  
 Query Match 20.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 3 TP 4  
 DB 6 TP 7  
  
 RESULT 56  
 ID LMT3\_LOCMI STANDARD; PRT; 9 AA.  
 AC P41489;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Locustamyotropin 3 (LOW-MT-3).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,  
 RA de Loof A.;  
 RT "Isolation, identification and synthesis of locustamyotropin III and  
 RT IV, two additional neuropeptides of Locusta migratoria: members of the  
 RT locustamyotropin peptide family.";  
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).  
 CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR PIR; A61620; A61620.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 9  
 SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;  
  
 Query Match 20.0%; Score 2; DB 1; Length 9;

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PF 10
DB 4 PF 5

RESULT 57
MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
  methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
  methyltransferase."
RL Nucleic Acids Res. 18:17-21(1990).
CC -I- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
  TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
  RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
  IRREVERSIBLY INACTIVATED.
CC -I- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein
  [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
  S-methyl-L-cysteine.
CC -I- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
  WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT, PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TP 4
DB 7 TP 8

RESULT 58
OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42956;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyliorhinus canicula (spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PF 10
DB 4 PF 5

RESULT 59
OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Phasvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
  fishes: asvatocin and phasvatocin, two oxytocin-like peptides
  isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -I- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -I- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PV 5
DB 7 PV 8

RESULT 60
OXYV_SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

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RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
  fishes: asvatocin and phasvatocin, two oxytocin-like peptides
  isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -I- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -I- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PV 5
DB 7 PV 8

RESULT 59
OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Phasvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
  fishes: asvatocin and phasvatocin, two oxytocin-like peptides
  isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -I- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -I- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PV 5
DB 7 PV 8

RESULT 60
OXYV_SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

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DE valitocin.  
OS Squalus acanthias (Spiny dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.  
OX NCBI\_TaxID=7797;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=73031727; PubMed=5083097;  
RA Acher R., Chauvet J., Chauvet M.-T.;  
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides  
RT isolated from a cartilaginous fish, Squalus acanthias.";  
RL Eur. J. Biochem. 29:12-19(1972).  
RN [2]  
RP SEQUENCE.  
RX MEDLINE=72128038; PubMed=4622083;  
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;  
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-  
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the  
RT spiny dog-fish (Squalus acanthias).";  
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).  
CC -I- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR InterPro; IPR000981; Neurohyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD RES 9 9 AMIDATION.  
FT SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PV 5  
DB 7 PV 8

RESULT 61  
ULAD HUMAN  
ID ULAD HUMAN STANDARD; PRT; 9 AA.  
AC P31929;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Liver;  
RX MEDLINE=94147969; PubMed=8313870;  
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
RA Tissot J.-D., Balroger A., Appel R.D., Hochstrasser D.F.;  
RT "Human liver protein map: update 1993.";  
RL Electrophoresis 14:1216-1222(1993).  
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6, ITS MW IS: 15 kDa.  
DR SWISS-2DPAGE; P31929; HUMAN.  
FT NON TER 9  
FT SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OT 3  
DB 5 OT 6

RESULT 62  
UPA7 HUMAN  
ID UPA7 HUMAN STANDARD; PRT; 9 AA.  
AC P30093;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RL Electrophoresis 13:707-714(1992).  
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.  
DR SWISS-2DPAGE; P30093; HUMAN.  
FT NON TER 1 1  
FT UNSURE 5 5  
FT NON TER 9 9  
FT SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 VP 8  
DB 3 VP 4

RESULT 63  
YBFR AZOVI  
ID YBFR AZOVI STANDARD; PRT; 9 AA.  
AC P25825;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein in bfr 3' region (Fragment).  
OS Azotobacter vinelandii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Azotobacter.  
OX NCBI\_TaxID=354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92196129; PubMed=1549605;  
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,  
RA Stiefel E.I.;  
RT "Unification of the ferritin family of proteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M83692; AAA22122.1; -;  
DR PIR; B41983; B41983  
KW Hypothetical protein.  
FT NON TER 9  
FT SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PP 9  
||  
Db 3 PP 4

## RESULT 64

ANGT\_PRUSE  
ID \_AH3\_PRUSE STANDARD; PRT; 10 AA.  
AC P29261;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase isozyme II) (AH II) (Fragment).  
OS Prunus serotina (Black cherry).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
OX NCBI\_TaxID=23207;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Seed;  
RA Li C.P., Swain E., Poulton J.E.;  
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";   
RL Plant Physiol. 100:282-290(1992).  
CC -1- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-glucose.  
CC -1- SUBUNIT: Monomer.  
CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR EMBRYONAL TISSUES.  
CC -1- PTM: GLYCOSYLATED.  
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 9.5e+03; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PP 9  
||  
Db 3 PP 4

## RESULT 65

ANGT\_BOTJA  
ID \_ANGI\_BOTJA STANDARD; PRT; 10 AA.  
AC Q10581;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Angiotensin-like peptide I (fragment).  
OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=96208932; PubMed=8829801;  
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
RT "Isolation and identification of angiotensin-like peptides from the plasma of the snake Bothrops jararaca.";   
RL Comp. Biochem. Physiol. 113B:467-473(1996).  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR InterPro; IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.

KW Vasoconstrictor; Plasma; Serpin.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.5e+03; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PP 10  
||  
Db 7 PP 8

## RESULT 66

ANGT\_BOVIN  
ID \_ANGT\_BOVIN STANDARD; PRT; 10 AA.  
AC P01017;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)] (Fragment).  
DE NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RA Elliott D.F., Peart W.S.;  
RT "The amino acid sequence in a hypertensin.";   
RL Biochem. J. 65:246-254(1957).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II. THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the plasma.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR PIR; A90345; A90345.  
DR PDB; 3ERS; 15-JUL-92.  
DR InterPro; IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin; 3D-structure.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT PEPTIDE 2 8 ANGIOTENSIN III.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.5e+03; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PP 10  
||  
Db 7 PP 8

## RESULT 67

ANGT\_CHICK  
ID \_ANGT\_CHICK STANDARD; PRT; 10 AA.  
AC P01018;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]



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DE (Fragment).
GN AGT OR SERPINAS.
OS Gallus gallus (Chicken), and
OS Cocurnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031, 93934;
RN [1]
RP SEQUENCE.
RC SPECIES=Chicken; PubMed=4361802;
RX MEDLINE=74127845;
RA Nakayama T., Nakajima T., Sokabe H.;
RT "Comparative studies on angiotensins. 3. Structure of fowl
  angiotensin and its identification by DNS-method.";
RL Chem. Pharm. Bull. 21:2085-2087(1973).
RN [2]
RP SEQUENCE.
RC SPECIES=C.c.japonica;
RX MEDLINE=90284684; PubMed=2191893;
RA Takei Y., Hasegawa Y.;
RT "Vasopressor and depressor effects of native angiotensins and
  inhibition of these effects in the Japanese quail.";
RL Gen. Comp. Endocrinol. 79:12-22(1990).
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
  CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
  CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
  PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II. THE MOST POTENT
  PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
  BALANCE OF BODY FLUIDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR; A60624; A60624.
DR PIR; A90917; A90917.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasopressor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PP 10
Db 7 PP 8

RESULT 68
BPP2 BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
  enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating

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RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
  angiotensin-converting enzyme and enhances the action of
  bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C741F773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PP 9
Db 9 PP 10

RESULT 69
BPP2 BOTJA STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
  inhibitor V-6-II).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
  Kocoy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
  jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -1- FUNCTION: This peptide both inhibits the activity of the
  angiotensin-converting enzyme and enhances the action of
  bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01255; XAVI6B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PP 9
Db 9 PP 10

RESULT 70
BPP8 BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
  enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

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OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RP peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 CC PIR: H37196; H37196.  
 DR Hypotensive agent; Pyrrolidone carboxylic acid.  
 KW MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;  
 SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 PP 9  
 Db 9 PP 10  
 RESULT 71  
 BRK ONCMY STANDARD; PRT; 10 AA.  
 ID AC Q9PRZ1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lysyl-bradykinin-like.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94039817; PubMed=8224232;  
 RA Conlon J.M., Olson K.R.;  
 RT "Purification of a vasoactive peptide related to lysyl-bradykinin from  
 RT trout plasma.";  
 RL FEBS Lett. 334:75-78(1993).  
 CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR  
 CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Plasma.  
 CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
 DR PIR: S39030; S39030.  
 KW Bradykinin; Vasodilator.  
 SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 PP 9  
 Db 3 PP 4  
 RESULT 72  
 COXH ONCMY STANDARD; PRT; 10 AA.  
 ID AC P80331;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)

DE Cytochrome c oxidase polypeptide VIc (EC 1.9.3.1) (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94237150; PubMed=8181469;  
 RA Freund R., Kadenbach B.;  
 RT "Identification of tissue-specific isoforms for subunits Vb and VIIa  
 RT of cytochrome c oxidase isolated from rainbow trout.";  
 RL Eur. J. Biochem. 221:1111-1116(1994).  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 DR PIR: S43630; S43630.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 977 MW; E11B40769DC772DA CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 VP 8  
 Db 4 VP 5  
 RESULT 73  
 COXH ONCMY STANDARD; PRT; 10 AA.  
 ID AC P80332;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIIa-heart (EC 1.9.3.1) (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=94237150; PubMed=8181469;  
 RA Freund R., Kadenbach B.;  
 RT "Identification of tissue-specific isoforms for subunits Vb and VIIa  
 RT of cytochrome c oxidase isolated from rainbow trout.";  
 RL Eur. J. Biochem. 221:1111-1116(1994).  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.  
 DR PIR: S43631; S43631.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1174 MW; 4C8D81CAFA772C3 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 VP 8  
 Db 4 VP 5

Db ' 4 VP 5

## RESULT 74

COXM\_RAT

ID\_CoxM\_RAT STANDARD; PRT; 10 AA.  
 AC P80431;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)  
 DE (Fragment).  
 GN COX7B.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Liver;  
 RX MEDLINE=95324529; PubMed=7601105;  
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;  
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and  
 RT amino-terminal sequences suggest identity of the fetal heart and the  
 RT adult liver isoform."  
 RL Eur. J. Biochem. 230:235-241(1995).  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 DR PIR; S65387; S65387.  
 KW Oxidoreductase; Mitochondrion.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 9.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4

Db 6 TP 7

## RESULT 75

COXQ\_RABIT

ID\_CoxQ\_RABIT STANDARD; PRT; 10 AA.  
 AC P80336;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)  
 DE (Fragment).  
 GN COX8H.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 RA Freund R., Kadenbach B.;  
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 KW Oxidoreductase; Mitochondrion.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 9.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TP 4

Db 8 TP 9

Search completed: November 25, 2003, 18:17:37  
 Job time : 5.84043 secs

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90 Q9WSV4 hepatitis g  
 91 Q8BB62 human papil  
 92 Q9PS63 gallus gall  
 93 Q8XY54 raiatonia s  
 94 Q8RGY4 fusobacteri  
 95 Q50556 actinobacil  
 96 Q47029 enterobacte  
 97 Q8NHH7 homo sapien  
 98 P92214 amblyopyrum  
 99 P92393 hordeum vul  
 100 P92403 lophopyrum

## ALIGNMENTS

## RESULT 1

Q8TCJ7 PRELIMINARY; PRT; 13 AA.  
 ID Q8TCJ7  
 AC Q8TCJ7; (Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN DFEZP667B0210.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph node;  
 RA Dusterthof A., Lauber J., Mewes H.W., Weil B., Wiemann S.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL713797; CAD28550.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 13 AA; 1289 MW; 96E82229FC482865 CRC64;

Query Match 40.0%; Score 4; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WVPP 9  
 Db 9 WVPP 12

## RESULT 2

Q9R5A0 PRELIMINARY; PRT; 15 AA.  
 ID Q9R5A0  
 AC Q9R5A0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE DNA topoisomerase I (Fragment).  
 OS Micrococcus luteus (Micrococcus lysodeikticus).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococcales; Micrococcaceae; Micrococcus.  
 OX NCBI\_TaxID=1270;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93249439; PubMed=8387285;  
 RA Anderluzzi D., Pedrini A.M.;  
 RT "Structural similarities between M. luteus and E. coli DNA  
 topoisomerase I";  
 RL Biochem. Biophys. Res. Commun. 192:657-664(1993).  
 SQ SEQUENCE 15 AA; 1602 MW; 285457836F151383 CRC64;

Query Match 40.0%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
 Db 6 QTPV 9

## RESULT 3

Q93UW3 PRELIMINARY; PRT; 17 AA.  
 ID Q93UW3  
 AC Q93UW3; (Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE RepA protein (Fragment).  
 GN REPA.  
 OS Agrobacterium tumefaciens.  
 OG Plasmid pRI44b.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=358;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A4;  
 RA Liang Y., Aoyama T., Oka A.;  
 RT "Organization of the conjugal transfer genes of the hairy-root-  
 inducing plasmid A4";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB050904; BAB47270.1; -.  
 KW Plasmid.  
 FT NON\_TER  
 SQ SEQUENCE 17 AA; 1655 MW; 4455CAD15C1A5520 CRC64;

Query Match 40.0%; Score 4; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVVV 7  
 Db 10 PVVV 13

## RESULT 4

Q9TRU8 PRELIMINARY; PRT; 17 AA.  
 ID Q9TRU8  
 AC Q9TRU8; (Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Leukemia inhibitory factor, LIF=INHIBITOR of aortic endothelial cell  
 growth (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92115728; PubMed=1370585;  
 RA Ferrata N., Winer J., Henzel W.J.;  
 RT "Pituitary follicular cells secrete an inhibitor of aortic endothelial  
 cell growth: identification as leukemia inhibitory factor";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:698-702(1992).  
 FT NON\_TER  
 SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 40.0%; Score 4; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPVV 6  
 Db 6 TPVV 9

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RESULT 5
Q9UWL5 PRELIMINARY; PRT; 20 AA.
ID Q9UWL5
AC Q9UWL5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Membrane-associated ATPase alpha subunit (Fragment).
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=2188;
RN [1]
RP SEQUENCE.
RX MEDLINE=93374865; PubMed=8366053;
RA Chen W., Konisky J.;
RT "Characterization of a membrane-associated ATPase from Methanococcus
RL voltae, a methanogenic member of the Archaea.";
RL J. Bacteriol. 175:5677-5682(1993).
SQ SEQUENCE 20 AA; 1965 MW; 8251D2DCB4483FA5 CRC64;

Query Match 40.0%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 7
Db 11 PVV 14

RESULT 6
Q9TR55 PRELIMINARY; PRT; 20 AA.
ID Q9TR55
AC Q9TR55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE INS(1,3,4,5)P4 receptor (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=95398635; PubMed=7669040;
RA Reiser G., Kunzelmann U., Hulseer E., Stricker R., Hoppe J.,
RA Lottspeich F., Kalbacher H.;
RT "Peptide-specific antibodies indicate species heterogeneity of a 42
RT kDa high-affinity inositol 1,3,4,5-tetrakisphosphate receptor protein
RT from brain.";
RL Biochem. Biophys. Res. Commun. 214:20-27(1995).
SQ SEQUENCE 20 AA; 2274 MW; 6E18218F2A579796 CRC64;

Query Match 40.0%; Score 4; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10
Db 15 VPPF 18

RESULT 7
Q912B0 PRELIMINARY; PRT; 20 AA.
ID Q912B0
AC Q912B0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 7.5-kDa nonstructural protein (Fragment).
GN 7.5-KDA.

OS Human parvovirus B19.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.
OX NCBI_TaxID=10798;
RN [1]
RP SEQUENCE FROM N.A.

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OS Human erythrovirus VX.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.
OX NCBI_TaxID=104382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RS9;
RA Nguyen Q.T.;
RT "Molecular cloning and sequencing of a novel human erythrovirus
RT genome: new species beside B19 in the genus Erythrovirus.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249877; CAC80693.1; -.
KW Nonstructural protein.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 1967 MW; 4D9971E8578CE493 CRC64;

Query Match 40.0%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5
Db 9 QTPV 12

RESULT 8
Q912B4 PRELIMINARY; PRT; 20 AA.
ID Q912B4
AC Q912B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 7.5-kDa nonstructural protein (Fragment).
GN 7.5-KDA.
OS Human erythrovirus V9.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.
OX NCBI_TaxID=72197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R234;
RA Nguyen Q.T.;
RT "Molecular cloning and sequencing of a novel human erythrovirus
RT genome: new species beside B19 in the genus Erythrovirus.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249875; CAC80689.1; -.
KW Nonstructural protein.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 1977 MW; F00971E8578CE490 CRC64;

Query Match 40.0%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5
Db 9 QTPV 12

RESULT 9
Q912B2 PRELIMINARY; PRT; 20 AA.
ID Q912B2
AC Q912B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 7.5-kDa nonstructural protein (Fragment).
GN 7.5-KDA.
OS Human parvovirus B19.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.
OX NCBI_TaxID=10798;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=R82;
RA Nguyen Q.T.;
RT "Molecular cloning and sequencing of a novel human erythrovirus
RL genome: new species beside B19 in the genus Erythrovirus.";
DR EMBL; AJ249876; CAC80691.1; -.
KW Nonstructural protein.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2008 MW; F00971B8578CE5D5 CRC64;

Query Match 40.0%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5
Db 9 QTPV 12

RESULT 10
Q9QK11 PRELIMINARY; PRT; 20 AA.
AC Q9QK11; 2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22204V3.4;
RX MEDLINE=9909499; PubMed=9878014;
RA Van Dyke R.B., Korber B.T., Popek E., Macken C., Widmayer S.M.,
RA Bardequez A., Hansen I.C., Wiznia A., Luzuriaga K., Viscarello R.R.,
RA Wolinsky S., the Ariel Core Investigators;
RT "The Ariel Project: A prospective cohort study of maternal-child
RT transmission of human immunodeficiency virus type 1 in the era of
RT maternal antiretroviral therapy.";
RL J. Infect. Dis. 179:319-328(1999).
DR EMBL; AF112557; AAF13335.1; -.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2200 MW; 7C3CD47A96615726 CRC64;

Query Match 40.0%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVVU 7
Db 1 PVVU 4

RESULT 11
Q99P40 PRELIMINARY; PRT; 8 AA.
AC Q99P40;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Repressor of GATA (Fragment).
GN ROG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B6;
RA Miao S., Ho I.;

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RT "ROG is a NF-AT target gene that partly rescues the phenotype of NF-
RT ATC2/NF-ATc3 deficient Th cells.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335542; AAG59843.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 943 MW; FE3411B771B6C766 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4
Db 3 QTP 5

RESULT 12
Q9P8E5 PRELIMINARY; PRT; 9 AA.
AC Q9P8E5; 2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE His4 protein (Fragment).
GN HIS4.
OS Kluyveromyces fragilis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL-Y1140;
RX MEDLINE=99448382; PubMed=10518937;
RA Lamas-Macielas M., Esperanza Cerdan E., Freire-Picos M.A.;
RT "Kluyveromyces fragilis His4 transcriptional regulation: similarities
RT and differences to Saccharomyces cerevisiae His4 gene.";
RL FEBS Lett. 458:72-76(1999).
DR EMBL; AJ238494; CAB87125.1; -.
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772B2D767 CRC64;

Query Match 30.0%; Score 3; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6
Db 3 PVV 5

RESULT 13
Q88612 PRELIMINARY; PRT; 9 AA.
AC Q88612;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Structural polyprotein (Fragment).
OS Middelburg virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11023;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83039346; PubMed=6291034;
RA Ou J.H., Rice C.M., Dalgarno L., Strauss E.G., Strauss J.H.;
RT "Sequence studies of several alphavirus genomic RNAs in the region
RT containing the start of the subgenomic RNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:5235-5239(1982).
DR EMBL; J02246; AAA96655.1; -.
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1114 MW; 00E8B6C1B7604B54 CRC64;

```



Query Match 30.0%; Score 3; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TOT 3  
 |||  
 Db 6 TOT 8

## RESULT 14

Q9UCR0 PRELIMINARY; PRT; 10 AA.  
 ID Q9UCR0  
 AC Q9UCR0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE AUTOTAXIN (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=92129337; PubMed=1733949;  
 RA Stracke M.L., Krutzech H.C., Unsworth E.J., Arestad A., Cioce V.,  
 RA Schiffmann E., Liotta L.A.;  
 RT "Identification, purification, and partial sequence analysis of  
 RT autotaxin, a novel motility-stimulating protein.";  
 RL J. Biol. Chem. 267:2524-2529(1992).  
 FT NON\_TER 1  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1193 MW; 3E01FB40544B19D7 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 PPF 10  
 |||  
 Db 2 PPF 4

## RESULT 15

Q9SHF5 PRELIMINARY; PRT; 10 AA.  
 ID Q9SHF5  
 AC Q9SHF5;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class I antigen (Fragment).  
 GN PAAN-AG.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Papio.  
 OX NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;  
 RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;  
 RA "The baboon placenta contains unique tissue-specific messages derived  
 RT from the class Ib major histocompatibility complex gene, Paan-AG.";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY055037; AAL23595.1; -.  
 KW MHC.

FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 30.0%; Score 3; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TOT 3  
 |||  
 Db 6 TOT 8

## RESULT 16

Q9SHF9 PRELIMINARY; PRT; 10 AA.  
 ID Q9SHF9  
 AC Q9SHF9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class I antigen (Fragment).  
 GN PAAN-AG.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Papio.  
 OX NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;  
 RT "The baboon placenta contains unique tissue-specific messages derived  
 RT from the class Ib major histocompatibility complex gene, Paan-AG.";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY055033; AAL23591.1; -.  
 KW MHC.

FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 30.0%; Score 3; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TOT 3  
 |||  
 Db 6 TOT 8

## RESULT 17

Q9SHF6 PRELIMINARY; PRT; 10 AA.  
 ID Q9SHF6  
 AC Q9SHF6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class I antigen (Fragment).  
 GN PAAN-AG.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Papio.  
 OX NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;  
 RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;  
 RA "The baboon placenta contains unique tissue-specific messages derived  
 RT from the class Ib major histocompatibility complex gene, Paan-AG.";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY055036; AAL23594.1; -.  
 KW MHC.

FT NON\_TER 1  
 SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 30.0%; Score 3; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TOT 3  
 |||  
 Db 6 TOT 8

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RESULT 18
Q95HF7      PRELIMINARY;      PRT;      10 AA.
ID Q95HF7
AC Q95HF7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC class I antigen (Fragment).
GN PAAN-AG.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;
RT "The baboon placenta contains unique tissue-specific messages derived
RL from the class Ib major histocompatibility complex gene, Paan-AG.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055035; AAL23593.1; -.
KW MHC.
FT NON TER
SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 30.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQT 3
Db 6 TQT 8

RESULT 19
Q95HF4      PRELIMINARY;      PRT;      10 AA.
ID Q95HF4
AC Q95HF4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC class I antigen (Fragment).
GN PAAN-AG.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;
RT "The baboon placenta contains unique tissue-specific messages derived
RL from the class Ib major histocompatibility complex gene, Paan-AG.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055038; AAL23596.1; -.
KW MHC.
FT NON TER
SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 30.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQT 3
Db 6 TQT 8

RESULT 20
Q95H99      PRELIMINARY;      PRT;      10 AA.
ID Q95H99
AC Q95H99;

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Q95HF8      PRELIMINARY;      PRT;      10 AA.
ID Q95HF8
AC Q95HF8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC class I antigen (Fragment).
GN PAAN-AG.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;
RT "The baboon placenta contains unique tissue-specific messages derived
RL from the class Ib major histocompatibility complex gene, Paan-AG.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055034; AAL23592.1; -.
KW MHC.
FT NON TER
SQ SEQUENCE 10 AA; 1213 MW; 5C7EB7B6C1ADC1A3 CRC64;

Query Match 30.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQT 3
Db 6 TQT 8

RESULT 21
Q95HG0      PRELIMINARY;      PRT;      10 AA.
ID Q95HG0
AC Q95HG0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC class I antigen (Fragment).
GN PAAN-AG.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Langat D.K., Morales P.J., Fazleabas A.T., Mwenda J.M., Hunt J.S.;
RT "The baboon placenta contains unique tissue-specific messages derived
RL from the class Ib major histocompatibility complex gene, Paan-AG.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055032; AAL23590.1; -.
KW MHC.
FT NON TER
SQ SEQUENCE 10 AA; 1226 MW; 5C7EB7B6C1ADD443 CRC64;

Query Match 30.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQT 3
Db 6 TQT 8

RESULT 22
Q95H99      PRELIMINARY;      PRT;      10 AA.
ID Q95H99
AC Q95H99;

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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class I antigen (Fragment).
GN PAAN-AG.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUB=Endomericum;
RA Langat D.K., Morales P.J., Farleabas A.T., Mwenda J.M., Hunt J.S.;
RT "The baboon placenta contains unique tissue-specific messages derived
RT from the class Ib major histocompatibility complex gene, Paan-AG.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055031; AAL3589.1; -.
KW MHC.
FT NON TER 1
SQ SEQUENCE 10 AA; 1213 MW; 5C7EB7B6C1ADC1A3 CRC64;

Query Match 30.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOT 3
   |||
Db 6 TOT 8

RESULT 23
Q9J1G8 PRELIMINARY; PRT; 10 AA.
AC Q9J1G8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ORF2.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TTV-SC232;
RX MEDLINE=20251008; PubMed=10790123;
RA Niel C., Saback F.L., Lampe E.;
RT "Coinfection with Multiple TT Virus Strains Belonging to Different
RT Genotypes Is a Common Event in Brazilian Healthy Adults.";
RL J. Clin. Microbiol. 38:1926-1930(2000).
DR EMBL; AF216453; AAF66889.1; -.
SQ SEQUENCE 10 AA; 1124 MW; 64FE2BD771B5B9CE CRC64;

Query Match 30.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5
   |||
Db 6 TPV 8

RESULT 24
O94785 PRELIMINARY; PRT; 11 AA.
AC O94785
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Thrombopoietin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki Y., Takahashi T., Nakamura K., Okuno Y., Nakao K.;
RT "Production of Thrombopoietin by Human Carcinomas and Its Novel mRNA
RT Isoforms.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB014683; BAA34932.1; -.
FT NON TER 1
SQ SEQUENCE 11 AA; 1203 MW; 5FE19F44B6C1A877 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOT 3
   |||
Db 6 TOT 8

RESULT 25
Q8NI03 PRELIMINARY; PRT; 11 AA.
AC Q8NI03
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 25 hydroxyvitamin d3 1-alpha hydroxylase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert R., Schneider D., Jovanovic M., Adamski J., Jakob F.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF500480; AAM21669.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1298 MW; 82C14E84CB533731 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOT 3
   |||
Db 2 TOT 4

RESULT 26
Q9TQSO PRELIMINARY; PRT; 11 AA.
AC Q9TQSO
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE C-KIT (Fragment).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
RT "A polymorphism in the bovine c-kit gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243424; CAB60775.1; -.
DR EMBL; AJ243060; CAB60774.1; -.
FT NON TER 1
FT NON TER 11
SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

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Query Match      30.0%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PVV 6
   |||
Db 5 PVV 7

RESULT 27
Q9UEX7 PRELIMINARY; PRT; 11 AA.
AC Q9UEX7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Human leucocyte antigen B (Fragment).
GN HLA-A*03.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fae I., Krika D., Cernava B., Fischer G.F.;
RT "An novel HLA-A*03 allele."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ252283; CAB65736.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1118 MW; 5191BC69C1A72DD7 CRC64;

Query Match      30.0%; Score 3; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TOT 3
   |||
Db 7 TOT 9

RESULT 28
Q9S8Z9 PRELIMINARY; PRT; 11 AA.
AC Q9S8Z9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE W1 peptide (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytochemistry 31:731-735(1992).
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1120 MW; 8391BABCDD77772D1 CRC64;

Query Match      30.0%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VPP 9
   |||
Db 5 VPP 7

us-09-641-801-20.oligo.rspt

RESULT 29
Q61797 PRELIMINARY; PRT; 11 AA.
AC Q61797;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 1.1 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1;
RX MEDLINE=86215264; PubMed=3754749;
RA Tanaka S., Fujimoto H.;
RT "A postmeiotically expressed clone encodes lactate dehydrogenase
isozyme X."
RL Biochem. Biophys. Res. Commun. 136:760-766(1986).
DR EMBL; M12781; AAA88313.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1122 MW; 32810C52476EA2D7 CRC64;

Query Match      30.0%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPV 5
   |||
Db 3 TPV 5

RESULT 30
Q64296 PRELIMINARY; PRT; 12 AA.
AC Q64296;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CD44 antigen (Fragment).
GN CD44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER;
RA Yu Q., Toole B.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER;
RA Yu Q., Toole B.P.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U57612; AAC52806.1; -.
DR EMBL; U57611; AAB08756.1; -.
DR MGD; MGI:88338; Cd44.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 12 AA; 1235 MW; CBFDEB7444ADC2D2 CRC64;

Query Match      30.0%; Score 3; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVV 7
   |||
Db 4 VVV 6

```

## RESULT 31

Q9QVK6 PRELIMINARY; PRT; 13 AA.  
 AC Q9QVK6;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DE 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DT Phosphoglycerate mutase P29 (EC 2.7.5.3) (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91373341; PubMed=1832670;  
 RA Hoppner W., Beckert L., Buck F., Seitz H.J.;  
 RT "Is the p29 protein involved in the rapid regulation of  
 RT phosphoenolpyruvate carboxykinase (GTP)?";  
 RL J. Biol. Chem. 266:17257-17260(1991).  
 SQ SEQUENCE 13 AA; 1456 MW; 39099D8CBBAA6D2D7 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVW 6  
 Db 6 PVV 8

## RESULT 32

Q16484 PRELIMINARY; PRT; 14 AA.  
 AC Q16484;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE DMD protein (Fragment).  
 GN DMD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92366490; PubMed=1380160;  
 RA Hugnot J.P., Gilgenkrantz H., Vincent N., Chafey P., Morris G.E.,  
 RA Monaco A.P., Berwald-Netter Y., Koulakoff A., Kaplan J.C., Kahn A.,  
 RA et al;  
 RT "Distal transcript of the dystrophin gene initiated from an  
 RT alternative first exon and encoding a 75-kDa protein widely  
 RT distributed in nonmuscle tissues";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:7506-7510(1992).  
 DR EMBL; S42206; AAD13820.1; -.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1662 MW; 2D5889B6976E28E8 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOT 3  
 Db 10 TOT 12

## RESULT 33

P82216 PRELIMINARY; PRT; 14 AA.  
 AC P82216;  
 DT 01-OCT-2001 (TReMBLrel. 18, Created)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)

DE Unknown protein from 2D-page (Fragment).  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE.  
 RX STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;  
 RC MEDLINE=21177481; PubMed=11280994;  
 RA Zhong B.X.;  
 RT "Protein database for several tissues derived from five instar of  
 RT silkworm.";  
 RL I Chuan Heuh Pao 28:217-224(2001).  
 CC -!- SIMILARITY: TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1619 MW; 86C63995B983BC45 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
 Db 4 PVV 6

## RESULT 34

P82340 PRELIMINARY; PRT; 14 AA.  
 AC P82340;  
 DT 01-JUN-2000 (TReMBLrel. 14, Created)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last sequence update)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
 DE Unknown protein from 2D-page of thylakoid lumen (SPOT204) (Fragment).  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 OX NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
 RX STRAIN=cv. DE GRACE; TISSUE=LEAF;  
 RX MEDLINE=20181728; PubMed=10715320;  
 RA Adamska I., van Wijk K.J.;  
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
 RA "Proteomics of the chloroplast: systematic identification and  
 RT targeting analysis of luminal and peripheral thylakoid proteins.";  
 RL Plant Cell 12:319-341(2000).  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.  
 CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
 KW Chloroplast; Thylakoid membrane.  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1505 MW; 2EABFAF980F3D7D7 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
 Db 7 PVV 9

## RESULT 35

P83424 PRELIMINARY; PRT; 14 AA.  
 AC P83424;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Agglutinin I, beta chain (MNA I beta) (Fragment).  
 OS Morus nigra.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eurosids I; Rosales; Moraceae; Morus.  
 OX NCBI\_TaxID=85232;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Bark, and Root;  
 RA Angel C.E., Pickford W.J., Grant G., Kelly D.;  
 RT "Purification and characterisation of Morus nigra agglutinins I and II";  
 RL Submitted (JUL-2002) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: N-ACETYL-GALACTOSAMINE AND D-GALACTOSE SPECIFIC LECTIN.  
 CC BINDS THE TN-ANTIGEN STRUCTURE GALNAC-ALPHA-1-O-SER, T-ANTIGEN  
 CC STRUCTURE GAL-BETA1-3-GALNAC AND IGA.  
 CC -1- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.  
 KW Lectin; Glycoprotein; IGA-binding protein.  
 FT NON TER 14 14  
 SQ SEQUENCE 14 AA; 1443 MW; 880D0F49D2285D05 CRC64;  
 Query Match 30.0%; Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 VVW 7  
 Db 11 VVW 13  
 RESULT 36  
 Q9QVF3 ID Q9QVF3 PRELIMINARY; PRT; 14 AA.  
 AC Q9QVF3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE TRANSFERRIN-PEPTIDE 35 (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=92165927; PubMed=1791188;  
 RA Cavanaugh P.G., Nicolson G.L.;  
 RT "Lung-derived growth factor that stimulates the growth of lung-  
 RT metastasizing tumor cells: identification as transferrin.";  
 RL J. Cell. Biochem. 47:261-271(1991).  
 DR InterPro: IPR001156; Transferrin.  
 DR Pfam: PF00405; transferrin; 1.  
 FT NON TER 1 1  
 FT NON TER 14 14  
 SQ SEQUENCE 14 AA; 1499 MW; 01AE8289E54E3224 CRC64;  
 Query Match 30.0%; Score 3; DB 11; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 PVV 6  
 Db 10 PVV 12  
 RESULT 37  
 Q07378 ID Q07378 PRELIMINARY; PRT; 14 AA.  
 AC Q07378;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Pairedbox and homeobox (Fragment).  
 GN PAX-QNR.

OS Coturnix coturnix (Common quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archoeauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Coturnix.  
 OX NCBI\_TaxID=9091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ssp. japonicus; TISSUE=Spinal cord;  
 RX MEDLINE=93264300; PubMed=8098617;  
 RA Dozier C., Carriere C., Grevin D.;  
 RT "Structure and DNA binding properties of PAX-QNR, a paired Box- and  
 RT Homeobox-containing Gene.";  
 RL Cell Growth Differ. 4:281-289(1993).  
 DR EMBL: X68169; CAA48271.1; .  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON TER 1 1  
 SQ SEQUENCE 14 AA; 1412 MW; 8EBB4EE821E0B9D5 CRC64;  
 Query Match 30.0%; Score 3; DB 13; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 TPV 5  
 Db 3 TPV 5  
 RESULT 38  
 Q9R4P5 ID Q9R4P5 PRELIMINARY; PRT; 15 AA.  
 AC Q9R4P5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Ribosomal protein L24 (Fragment).  
 OS Brevundimonas diminuta (Pseudomonas diminuta).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;  
 OC Caulobacteraceae; Brevundimonas.  
 OX NCBI\_TaxID=293;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95244309; PubMed=7727274;  
 RA Ochi K.;  
 RT "Comparative ribosomal protein sequence analyses of a phylogenetically  
 RT defined genus, Pseudomonas, and its relatives.";  
 RL Int. J. Syst. Bacteriol. 45:268-273(1995).  
 SQ SEQUENCE 15 AA; 1513 MW; 8BA258CFA725914F CRC64;  
 Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 VVW 7  
 Db 10 VVW 12  
 RESULT 39  
 Q9R4J8 ID Q9R4J8 PRELIMINARY; PRT; 15 AA.  
 AC Q9R4J8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Steroid monooxygenase (Fragment).  
 OS Rhodococcus rhodochrous.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Nocardiaceae; Rhodococcus.  
 OX NCBI\_TaxID=1829;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95399430; PubMed=7669800;  
 RA Miyamoto M., Matsumoto J., Iwaya T., Itagaki E.;

RT "Bacterial steroid monooxygenase catalyzing the Baeyer-Villiger  
 RT oxidation of C21-ketosteroids from Rhodococcus rhodochrous: the  
 RT isolation and characterization."  
 RL Biochim. Biophys. Acta 1251:115-124(1995).  
 SQ SEQUENCE 15 AA; 1562 MW; C405FC41DF057BEB CRC64;

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7  
 Db 8 VVW 10

## RESULT 40

Q53290 ID Q53290 PRELIMINARY; PRT; 15 AA.

AC Q53290; 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Orf protein (Fragment).  
 GN ORF.

OS Mycobacterium paratuberculosis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1770;

RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=93089535; PubMed=1455629;  
 RA Thomas T.J., Andrews R.E.Jr., Thoen C.O.;  
 RT "Molecular cloning and characterization of Mycobacterium  
 RT paratuberculosis promoters in Escherichia coli."  
 RL Vet. Microbiol. 32:351-362(1992).  
 DR EMBL; S50756; AAB24385.1; -;  
 FT NON\_TER . 15  
 SQ SEQUENCE 15 AA; 1629 MW; C29B5EC0D88556BB CRC64;

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5  
 Db 6 TPV 8

## RESULT 41

Q9R5T1 ID Q9R5T1 PRELIMINARY; PRT; 15 AA.

AC Q9R5T1; 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE 3-HYDROXYPHENYLACETATE 6-hydroxylase, FAD-dependent monooxygenase  
 DE (Fragment).  
 OS Flavobacterium.

OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;  
 OC Flavobacteriaceae.

OX NCBI\_TaxID=237;  
 RN [1]

RP SEQUENCE.

RX MEDLINE=92037613; PubMed=1935954;  
 RA van Berkel W.J., van Den Tweel W.J.;

RT "Purification and characterisation of 3-hydroxyphenylacetate 6-  
 RT hydroxylase: a novel FAD-dependent monooxygenase from a Flavobacterium  
 RT species."  
 RL Eur. J. Biochem. 201:585-592(1991).

FT NON\_TER 1  
 FT NON\_TER 15

SQ SEQUENCE 15 AA; 1416 MW; D673378E0221F9D9 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
 Db 13 VPP 15

## RESULT 42

Q9TRP0 ID Q9TRP0 PRELIMINARY; PRT; 15 AA.

AC Q9TRP0; 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE LOW MR zona pellucida binding protein (fragment).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE.

RX MEDLINE=92379826; PubMed=1510840;

RA Parry R.V., Barker P.J., Jones R.;

RT "Characterization of low Mr zona pellucida binding proteins from boar

RT spermatozoa and seminal plasma."

RL Mol. Reprod. Dev. 33:108-115(1992).

SQ SEQUENCE 15 AA; 1525 MW; CC800E1028CF2058 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7  
 Db 12 VVW 14

## RESULT 43

Q9TNQ1 ID Q9TNQ1 PRELIMINARY; PRT; 15 AA.

AC Q9TNQ1; 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Beta 2M- class I-binding PEPTIDE-MAJOR histocompatibility complex

DE H-2KB-specific molecule POORLY associated with beta 2-microglobulin

DE (Fragment).

OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10095;

RN [1]

RP SEQUENCE.

RX MEDLINE=94240094; PubMed=8183884;

RA Joyce S., Kuzushima K., Kepecs G., Angeletti R.H., Nathanson S.G.;

RT "Characterization of an incompletely assembled major

RT histocompatibility class I molecule (H-2KB) associated with unusually

RT long peptides: implications for antigen processing and presentation."

RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).

KW MHC.

FT NON\_TER 1

FT NON\_TER 15

SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;

Query Match 30.0%; Score 3; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6  
 Db 8 PVV 10

## RESULT 44

Q9UWK4 PRELIMINARY; PRT; 16 AA.  
 ID Q9UWK4  
 AC Q9UWK4  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE 53 kDa tungsten containing formylmethanofuran dehydrogenase (Fragment).  
 OS Methanobacterium thermoautotrophicum.  
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanothermobacter.  
 OX NCBI\_TaxID=187420;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94213570; PubMed=8161283;  
 RA Bartram P.A., Schmitz R.A., Linder D., Thauer R.K.;  
 RT "Tungstate can substitute for molybdate in sustaining growth of Methanobacterium thermoautotrophicum. Identification and characterization of a tungsten isoenzyme of formylmethanofuran dehydrogenase.";  
 RL Arch. Microbiol. 161:220-228(1994).  
 SQ SEQUENCE 16 AA; 1838 MW; 03AC809D4685199 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVP 8  
 Db 7 VVP 9

## RESULT 45

Q9L925 PRELIMINARY; PRT; 16 AA.  
 ID Q9L925  
 AC Q9L925  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Antiterminator (Fragment).  
 GN BGLG.  
 OS Shigella flexneri.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Shigella.  
 OX NCBI\_TaxID=623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPXR;  
 RA Kharat A.S., Mahadevan S.;  
 RT "Molecular characterization of the bglR and bglG genes of Shigella dysenteriae (SPXR).";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF185095; AAF61643.1; -.  
 DR InterPro; IPR004341; CAT\_RBD.  
 DR Pfam; PF03123; CAT\_RBD; 1.  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1830 MW; 6597358CAD4E21EE CRC64;

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7  
 Db 13 VVW 15

## RESULT 46

Q9KJ10 PRELIMINARY; PRT; 16 AA.  
 ID Q9KJ10

Q9KJ10;  
 AC 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Heparin-binding protein (Fragment).  
 OS Staphylococcus haemolyticus.  
 OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.  
 OX NCBI\_TaxID=1283;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SM131;  
 RX MEDLINE=21284478; PubMed=11393292;  
 RA Fallgren C., Utt M., Ljungh A.;  
 RT "Isolation and characterization of a 17-kDa staphylococcal heparin-binding protein with broad specificity.";  
 RL J. Med. Microbiol. 50:547-557(2001).  
 DR EMBL; AF169242; AAF89664.1; -.  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1909 MW; 30C19B931B50FF11 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOT 3  
 Db 3 TOT 5

## RESULT 47

Q9L923 PRELIMINARY; PRT; 16 AA.  
 ID Q9L923  
 AC Q9L923  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Antiterminator (Fragment).  
 GN BGLG.  
 OS Shigella boydii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Shigella.  
 OX NCBI\_TaxID=621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SBYR;  
 RA Kharat A.S., Mahadevan S.;  
 RT "Molecular characterization of the bglR and bglG genes of Shigella boydii (SBYR).";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF185096; AAF61645.1; -.  
 DR InterPro; IPR004341; CAT\_RBD.  
 DR Pfam; PF03123; CAT\_RBD; 1.  
 FT NON TER 16  
 SQ SEQUENCE 16 AA; 1830 MW; 6597358CAD4E21EE CRC64;

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVW 7  
 Db 13 VVW 15

## RESULT 48

Q9L927 PRELIMINARY; PRT; 16 AA.  
 ID Q9L927  
 AC Q9L927; Q9L929;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Antiterminator (Fragment).  
 GN BGLG.



OS Shigella sonnei.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Shigella.  
 OX NCBI\_TaxID=624;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=CR+;  
 RC Kharat A.S., Mahadevan S.;  
 RA "Molecular characterization of the bglR and bglG genes of Shigella sonnei CR+";  
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RL SEQUENCE FROM N.A.  
 RP STRAIN=CR-;  
 RC Kharat A.S., Mahadevan S.;  
 RA "Molecular characterization of the bglR and bglG genes of Shigella sonnei CR-";  
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF185094; AAF61641.1; -;  
 DR EMBL; AF185093; AAF61639.1; -;  
 DR InterPro: IPR004341; CAT\_RBD.  
 DR Pfam: PF03123; CAT\_RBD; I.  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1830 MW; 6597358CAD4E21EE CRC64;  
 Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 VVW 7  
 Db 13 VVW 15  
 RESULT 49  
 ID Q8VNS8 PRELIMINARY; PRT; 16 AA.  
 AC Q8VNS8;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE CadC protein (Fragment).  
 GN CADC.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=413/89-1;  
 RC Benkel P., Chakraborty T.;  
 RA "Genetic organisation and sequence of the LEE II locus in Shiga toxin-producing Escherichia coli";  
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AJ277443; CAC81838.1; -;  
 DR EMBL; AJ277443; CAC81838.1; -;  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1826 MW; 0D5EA97E0C676A12 CRC64;  
 Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 PVV 6  
 Db 4 PVV 6  
 RESULT 50  
 ID Q9UC52 PRELIMINARY; PRT; 16 AA.  
 AC Q9UC52;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Carboxylesterase isozyme (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE.  
 RP MEDLINE=96170127; PubMed=8597091;  
 RA Satoh T., Hosokawa M.;  
 RT "Molecular aspects of carboxylesterase isoforms in comparison with other esterases";  
 RL Toxicol. Lett. 82:439-445(1995).  
 SQ SEQUENCE 16 AA; 1599 MW; 5DA6286D3C6BFFED CRC64;  
 Query Match 30.0%; Score 3; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 PVV 6  
 Db 6 PVV 8  
 RESULT 51  
 ID Q9T2V8 PRELIMINARY; PRT; 16 AA.  
 AC Q9T2V8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 2-enoyl-CoA hydratase (Fragment).  
 OS Homo sapiens (Human).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=95046784; PubMed=7958339;  
 RA Middleton B.;  
 RT "The mitochondrial long-chain trifunctional enzyme: 2-enoyl-CoA hydratase, 3-hydroxyacyl-CoA dehydrogenase and 3-oxoacyl-CoA thiolase";  
 RL Biochem. Soc. Trans. 22:427-431(1994).  
 SQ SEQUENCE 16 AA; 1763 MW; 31AD66A3080B019A CRC64;  
 Query Match 30.0%; Score 3; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 VVW 7  
 Db 7 VVW 9  
 RESULT 52  
 ID Q9T2R0 PRELIMINARY; PRT; 16 AA.  
 AC Q9T2R0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Cytochrome-C reductase 14 kDa subunit (EC 1.10.2.2) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OG Mitochondrion.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 [1]  
 RN SEQUENCE.  
 RP MEDLINE=94198758; PubMed=7764624;

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RA Braun H.P., Kruft V., Schmitz U.K.;
RL Planta 193:99-106(1994). 1946 MW; B6C625F8E4A4C8E7 CRC64;
SQ SEQUENCE 16 AA; 1946 MW; 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 30.0%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4
Db 13 QTP 15

RESULT 53
Q9SPV1 PRELIMINARY; PRT; 16 AA.
AC Q9SPV1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Hypothetical 1.7 kDa protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20023723; PubMed=10561067;
RA Foster E., Hattori J., Labbe H., Ouellet T., Fobert P.R., James L.E.,
RA Iyer V.N., Miki B.L.;
RT "A tobacco cryptic constitutive promoter, tCUP, revealed by T-DNA
tagging.";
RL Plant Mol. Biol. 41:45-55(1999).
DR EMBL; AF133844; AAC56607.1; -.
KW Hypothetical protein.
FT NON TER 16
SQ SEQUENCE 16 AA; 1725 MW; 6A4C8A093666240D CRC64;

Query Match 30.0%; Score 3; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPF 10
Db 12 PPF 14

RESULT 54
O89560 PRELIMINARY; PRT; 16 AA.
AC O89560;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Minor capsid protein (Fragment).
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=41951;
RC MEDLINE=99034644; PubMed=9815212;
RA LaDuca J.R., Love J.L., Abbott L.Z., Dube S., Freidman-Kien A.E.,
RA Polesz B.J.;
RT "Detection of human herpesvirus 8 DNA sequences in tissues and bodily
fluids.";
RL Infect. Dis. 178:1610-1615(1998).
DR EMBL; AF042149; AAC25060.1; -.
FT NON TER 1
SQ SEQUENCE 16 AA; 1787 MW; 2B505B0137B39DFF CRC64;

Query Match 30.0%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVP 8
Db 14 VVP 16

RESULT 55
Q9FOP3 PRELIMINARY; PRT; 17 AA.
AC Q9FOP3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Electron transfer flavoprotein subunit A (Fragment).
GN ETFA.
OS Paracoccus denitrificans.
OG Plasmid pLE20.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OX NCBI_TaxID=266;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93388590; PubMed=8376381;
RA Bedzyk L.A., Escudero K.W., Gill R.E., Griffin K.J., Frerman F.E.;
RT "Cloning, sequencing, and expression of the genes encoding subunits of
Paracoccus denitrificans electron transfer flavoprotein.";
RL J. Biol. Chem. 268:20211-20217(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21101849; PubMed=1160087;
RA Fales L., Kryszak L., Zellstra-Ryalls J.;
RT "Control of hemA expression in Rhodobacter sphaeroides 2.4.1: Effect
of a Transposon Insertion in the hbdA Gene.";
RL J. Bacteriol. 183:1568-1576(2001).
DR EMBL; AF212164; AAG43534.1; -.
KW Plasmid.
FT NON TER 1
SQ SEQUENCE 17 AA; 1744 MW; F277E1E18F28DEA2 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVP 8
Db 9 VVP 11

RESULT 56
Q9NQY8 PRELIMINARY; PRT; 17 AA.
AC Q9NQY8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Transcription factor 12 (Fragment).
GN TCF12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gan T.-I., O'Sickey T., Zhang Y., Kim U.-J., Bina M.;
RT "Organization of the HTF4 Gene.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF271610; AAF82574.1; -.
FT NON TER 1
FT NON TER 17
SQ SEQUENCE 17 AA; 1802 MW; E26E7FB1D7903679 CRC64;

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Query Match 30.0%; Score 3; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9  
 ||||  
 Db 10 VPP 12

RESULT 57  
 Q9TWf6 PRELIMINARY; PRT; 17 AA.  
 ID Q9TWf6  
 AC Q9TWf6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Valyl-tRNA synthetase (Fragment).  
 OS Artemia (brine shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;  
 OC Artemiidae.  
 OX NCBI\_TaxID=6660;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96061959; PubMed=7588756;  
 RA Brandema M., Kerjan P., Dijk J., Janssen G.M., Moller W.;  
 RT "Valyl-tRNA synthetase from Artemia. Purification and association with  
 elongation factor 1.";  
 RL Eur. J. Biochem. 233:277-282(1995).  
 SQ SEQUENCE 17 AA; 1806 MW; 92F60AC52AB27FD7 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPF 10  
 ||||  
 Db 4 PPF 6

RESULT 58  
 Q9TRY8 PRELIMINARY; PRT; 17 AA.  
 ID Q9TRY8  
 AC Q9TRY8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Insulin-like growth factor-binding protein-3, IGFBP-3 (Fragment).  
 OS Sus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9826;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92049376; PubMed=1719383;  
 RA Shimaaki S., Gao L., Shimonaka M., Ling N.;  
 RT "Isolation and molecular cloning of insulin-like growth factor-binding  
 protein-6.";  
 RL Mol. Endocrinol. 5:938-948(1991).  
 FT NON\_TER 1  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1618 MW; 14B17C38D32A400F CRC64;

Query Match 30.0%; Score 3; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PW 6  
 ||||  
 Db 9 PV 11

RESULT 59

Q9S8K1 PRELIMINARY; PRT; 17 AA.  
 ID Q9S8K1  
 AC Q9S8K1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 20 kDa kunitz-type proteinase inhibitor (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95093035; PubMed=8000008;  
 RA Mitsumori C., Yamagishi K., Fujino K., Kikuta Y.;  
 RT "Detection of immunologically related Kunitz and Bowman-Birk  
 proteinase inhibitors expressed during potato tuber development.";  
 RL Plant Mol. Biol. 26:961-969(1994).  
 SQ SEQUENCE 17 AA; 1872 MW; 44F34F575B0F832 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5  
 ||||  
 Db 6 TPV 8

RESULT 60  
 Q84098 PRELIMINARY; PRT; 17 AA.  
 ID Q84098  
 AC Q84098;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Influenza A/epv/rostock/34 (H7n1), matrix protein (Seg 7), 3' end of  
 DE vrna (Initiator region for protein coding) (Fragment).  
 OS Influenzavirus A.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses.  
 OX NCBI\_TaxID=197911;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90034428; PubMed=493121;  
 RA Robertson J.S.;  
 RT "5' and 3' terminal nucleotide sequences of the rna genome segments of  
 RT influenza virus.";  
 RL Nucleic Acids Res. 6:3745-3757(1979).  
 DR EMBL: J02112; AAA43305.1; -.  
 DR InterPro: IPR001561; Flu\_M1.  
 DR Pfam: PF00598; Flu\_M1; 1.  
 KW Matrix protein.  
 FT NON\_TER 17  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1795 MW; C0D59B0984ED10E1 CRC64;

Query Match 30.0%; Score 3; DB 12; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVP 8  
 ||||  
 Db 14 VVP 16

RESULT 61  
 Q9R4C3 PRELIMINARY; PRT; 18 AA.  
 ID Q9R4C3  
 AC Q9R4C3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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DE Protocatechuate 3,4-dioxygenase type I beta subunit (EC 1.13.11.3)
DE (Fragment).
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE
RX MEDLINE=96337865; PubMed=8772173;
RA Hammer A., Stolz A., Knackmuss H.;
RT "Purification and characterization of a novel type of protocatechuate
RT 3,4-dioxygenase with the ability to oxidize 4-sulfocatechol.";
RL Arch. Microbiol. 166:92-100(1996).
SQ SEQUENCE 18 AA; 2008 MW; C7BD971BBE59BE9 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOT 3
Db 2 TOT 4

RESULT 62
Q9UCL4 PRELIMINARY; PRT; 18 AA.
ID Q9UCL4
AC Q9UCL4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Insulin-like growth factor binding protein 30 kDa form (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=93091816; PubMed=1726837;
RA Roghani M., Segovia B., Whitechurch O., Binoux M.;
RT "Purification from human cerebrospinal fluid of insulin-like growth
RT factor binding proteins (IGFBPs). Isolation of IGFBP-2, an altered form
RT of IGFBP-3 and a new IGFBP species.";
RL Growth Regul. 1:125-130(1991).
SQ SEQUENCE 18 AA; 1689 MW; 10F5516240C6298B CRC64;

Query Match 30.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6
Db 9 PVV 11

RESULT 63
Q9TWE0 PRELIMINARY; PRT; 18 AA.
ID Q9TWE0
AC Q9TWE0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Alpha-macroglobulin (Fragment).
OS Biomphalaria glabrata (Bloodfluke planorb).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Biomphalaria.
OX NCBI_TaxID=6526;
RN [1]
RP SEQUENCE
RX MEDLINE=96265058; PubMed=8670168;
RA Bender R.C., Bayne C.J.;
RT "Purification and characterization of a tetrameric alpha-macroglobulin
RT proteinase inhibitor from the gastropod mollusc Biomphalaria

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RT glabrata.";
RL Biochem. J. 316:893-900(1996).
SQ SEQUENCE 18 AA; 1955 MW; E9B34ED1EBE20942 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVP 8
Db 11 VVP 13

RESULT 64
Q9IBW7 PRELIMINARY; PRT; 18 AA.
ID Q9IBW7
AC Q9IBW7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE P10 peptide (Fragment).
OS Autographa californica nuclear polyhedrosis virus (ACMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90085829; PubMed=2688302;
RA Kuzio J., Jaques R., Faulkner P.;
RT "Identification of p74, a gene essential for virulence of baculovirus
RT occlusion bodies.";
RL Virology 173:759-763(1989).
DR EMBL; M31301; AAA46728.2; -
FT NON_TER
SQ SEQUENCE 18 AA; 1923 MW; FAA5B122C2BFD17A CRC64;

Query Match 30.0%; Score 3; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVV 7
Db 10 VVV 12

RESULT 65
Q9R4T8 PRELIMINARY; PRT; 19 AA.
ID Q9R4T8
AC Q9R4T8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Type 3 fimbriae (Fragment).
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE
RX MEDLINE=95102231; PubMed=7803933;
RA Stolpe H., Grund S., Schroder W.;
RT "Purification and partial characterization of type 3 fimbriae from
RT Salmonella typhimurium var. copenhagen.";
RL Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis. 281:8-15(1994).
SQ SEQUENCE 19 AA; 1910 MW; 9AD8B59D411E5B51 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVP 8
Db 2 VVP 4

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RESULT 66
O87732 PRELIMINARY; PRT; 19 AA.
AC O87732;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE NusG-like protein (Transcription antitermination protein nusG)
DE (Fragment).
DE NUSG.
GN Streptomyces lavendulae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1914;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA406 A-1;
RX MEDLINE=98401489; PubMed=97131302;
RA Kawamoto S., Ochi K.;
RT "Comparative ribosomal protein (L11 and L30) sequence analyses of
RT several Streptomyces sp. commonly used in genetic studies.";
RL Int. J. Syst. Bacteriol. 48:597-600(1998).
CC -1- FUNCTION: INFLUENCES TRANSCRIPTION TERMINATION AND
CC ANTITERMINATION. ACTS AS A COMPONENT OF THE TRANSCRIPTION COMPLEX,
CC AND INTERACTS WITH THE TERMINATION FACTOR RHO AND RNA POLYMERASE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUSG FAMILY.
DR EMBL; D87847; BAA31975.1; -.
DR InterPro; IPR001062; NusG.
DR PROSITE; PS01014; NUSG; 1.
KW Transcription; Transcription termination.
FT NON TER 1
FT SEQUENCE 19 AA; 2250 MW; 2B44F981A68BFF18 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5
Db 7 TPV 9

RESULT 67
P82600 PRELIMINARY; PRT; 19 AA.
AC P82600;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Chorion peroxidase (EC 1.11.1.7).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Liverpool / Blackeye; TISSUE=Ovary;
RX MEDLINE=20326865; PubMed=10871050;
RA Han Q., Li G., Li J.;
RT "Purification and characterization of chorion peroxidase from Aedes
RT aegypti eggs.";
RL Arch. Biochem. Biophys. 378:107-115(2000).
RN [2]
RP FUNCTION.
RC STRAIN=Liverpool / Blackeye; TISSUE=Ovary;
RX MEDLINE=97056259; PubMed=8900599;
RA Li J., Hodgeman B.A., Christensen B.M.;
RT "Involvement of peroxidase in chorion hardening in Aedes aegypti.";
RL Insect Biochem. Mol. Biol. 26:309-317(1996).
CC -1- FUNCTION: INVOLVED IN THE FORMATION OF A RIGID AND INSOLUBLE EGG

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CC CHORION BY CATALYZING CHORION PROTEIN CROSSLINKING THROUGH
CC DITYROSINE FORMATION.
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
CC -1- COFACTOR: BINDS HEME.
CC -1- ENZYME REGULATION: EXTREMELY RESISTANT TO DENATURATING AGENTS,
CC SUCH AS SDS AND ORGANIC SOLVENTS.
CC -1- SUBCELLULAR LOCATION: IN THE CHORION LAYER OF THE MATURE EGGS.
CC -1- MISCELLANEOUS: HAS HIGHEST ACTIVITY AT PH 8.0 WITH GUAIACOL AS A
CC REDUCING AGENT.
KW Oxidoreductase; Glycoprotein; Peroxidase; Heme; Chorion.
FT CARBOHYD 9
FT SEQUENCE 19 AA; 2172 MW; 022F95BA72E14998 CRC64;
RN [1]
RP N-LINKED (GLCNAC... ) (POTENTIAL).
RC SEQUENCE 19 AA; 2172 MW; 022F95BA72E14998 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPP 9
Db 5 VPP 7

RESULT 68
Q9S8G9 PRELIMINARY; PRT; 19 AA.
AC Q9S8G9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Proline-rich protein (fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=95277008; PubMed=7757337;
RA Esaka M., Hayakawa H.;
RT "Specific secretion of proline-rich proteins by salt-adapted winged
RT bean cells.";
RL Plant Cell Physiol. 36:441-446(1995).
SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0F8779A CRC64;

Query Match 30.0%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVV 6
Db 11 PVV 13

RESULT 69
Q9QUY7 PRELIMINARY; PRT; 19 AA.
AC Q9QUY7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Oligodendrocyte-specific UDP-galactose:ceramide galactosyltransferase
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RC MEDLINE=96085162; PubMed=8521863;
RA Schulte S., Stoffel W.;
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate
RT transporter. Copurification, separation and characterization of the two

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RT glycoproteins."; 233:947-953(1995).
RL Eur. J. Biochem. 233:947-953(1995).
SQ SEQUENCE 19 AA; 2217 MW; 85BE441C727321D1 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VPP 9
DB 6 VPP 8

RESULT 70
ID O90628 PRELIMINARY; PRT; 19 AA.
AC O90628;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
DE Glycoprotein G (Fragment).
GN US4.
OS Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1504-11;
RA Eberle R., Smith A., Black D.;
RT "Molecular evidence for distinct genotypes of monkey B virus
(Herpesvirus simiae) which are related to the Macaque host species.";
RL J. Virol. 0:0-0(1998).
DR EMBL; AF082807; AAC34456.1; -.
FT NON TER 1
SQ SEQUENCE 19 AA; 2135 MW; E08736736CE8E98B CRC64;

Query Match 30.0%; Score 3; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTP 4
DB 2 QTP 4

RESULT 71
ID O11338 PRELIMINARY; PRT; 19 AA.
AC O11338;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE H1-7-1 protein (Fragment).
GN H1-7-1.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RA Moratilla M., Agronayor M., Nunez A., Punes J.M., Varas A.J.,
RA Lopez-Estebaranz J.L., Estebaranz M., Martin-Gallardo A.;
RT "A Random DNA Sequencing, Computer-Based Approach for the Generation
of a Gene Map of Molluscum Contagiosum Virus.";
RL Virus Genes 0:0-0(1997).
DR EMBL; U86916; AAB57971.1; -.
DR InterPro; IPR004900; Pox_P35.
DR Pfam; PF03213; Pox_P35; 1.
FT NON TER 19
SQ SEQUENCE 19 AA; 2018 MW; 1ECAF8E98F95ED65 CRC64;

Query Match 30.0%; Score 3; DB 12; Length 19;

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Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PTV 6
DB 14 PTV 16

RESULT 72
ID O90622 PRELIMINARY; PRT; 19 AA.
AC O90622;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
DE Glycoprotein G (Fragment).
GN US4.
OS Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kumquat;
RA Eberle R., Smith A., Black D.;
RT "Molecular evidence for distinct genotypes of monkey B virus
(Herpesvirus simiae) which are related to the Macaque host species.";
RL J. Virol. 0:0-0(1998).
DR EMBL; AF082805; AAC34450.1; -.
FT NON TER 1
SQ SEQUENCE 19 AA; 2135 MW; E08736736CE8E98B CRC64;

Query Match 30.0%; Score 3; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTP 4
DB 2 QTP 4

RESULT 73
ID Q9UWJ2 PRELIMINARY; PRT; 20 AA.
AC Q9UWJ2;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)
DE 35 kDa flagellin (Fragment).
OS Methanospirillum hungatei.
OC Archaea; Euryarchaeota; Methanococci; Methanomicrobiales;
OC Methanospirillaceae; Methanospirillum.
OX NCBI_TaxID=2203;
RN [1]
RP SEQUENCE.
RX MEDLINE=95095917; PubMed=8002572;
RA Feguy D.M., Koval S.F., Jarrell K.F.;
RT "Physical characterization of the flagella and flagellins from
Methanospirillum hungatei.";
RL J. Bacteriol. 176:7491-7498(1994).
SQ SEQUENCE 20 AA; 2036 MW; B2244BC7818F799 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVV 7
DB 14 VVV 16

RESULT 74
ID Q9R519

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ID Q9R5L9 PRELIMINARY; PRT; 20 AA.  
 AC Q9R5L9;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE ISONICOTINATE dehydrogenase (Fragment).  
 OS Mycobacterium.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae.  
 OX NCBI\_TaxID=1763;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94103749; PubMed=8277257;  
 RA Kretzer A., Frunzke K., Andresen J.R.;  
 RT "Catabolism of isonicotinate by Mycobacterium sp. INAI: extended  
 RT description of the pathway and purification of the molybdoenzyme  
 RT isonicotinate dehydrogenase.";  
 RL J. Gen. Microbiol. 139:2763-2772(1993).  
 SQ SEQUENCE 20 AA; 2280 MW; 874DAA8637BB07C1 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTP 4  
 Db 11 QTP 13

## RESULT 75

ID Q9R5L1 PRELIMINARY; PRT; 20 AA.  
 AC Q9R5L1;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Thymidine 5'-diphosphate D-glucose 4,6-dehydratase (EC 4.2.1.46)  
 DE (Fragment).  
 OS Streptomyces peucetius.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1950;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92268857; PubMed=1588310;  
 RA Thompson M.W., Strohl W.R., Floss H.G.;  
 RT "Purification and characterization of TDP-D-glucose 4,6-dehydratase  
 RT from anthracycline-producing streptomyces.";  
 RL J. Gen. Microbiol. 138:779-786(1992).  
 SQ SEQUENCE 20 AA; 1943 MW; 7958730238C00AC9 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPV 5  
 Db 3 TPV 5

Search completed: November 25, 2003, 18:25:47  
 Job time : 26.1457 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 32.3936 Seconds  
(without alignments)  
48.999 Million cell updates/sec

Title: US-09-641-801-20

Perfect score: 10

Sequence: 1 TQTPVVVPPF 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq 19Jun03.\*

1: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1992.DAT.\*  
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21: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA2001.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA2002.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	22	Colostrin derive
2	10	100.0	10	22	Colostrin peptid
3	10	100.0	10	22	Colostrin peptid
4	10	100.0	10	22	Ewe colostrin pep
5	10	100.0	10	23	Colostrin consti
6	10	100.0	10	23	Colostrin consti
7	10	100.0	10	23	Neural cell regula
8	9	90.0	10	15	ACE inhibitor pept
9	7	70.0	9	22	Colostrin peptid

10	7	70.0	10	22	AAE07203	Modified colostrin
11	6	60.0	6	15	AAE48291	ACE inhibitor pept
12	6	60.0	6	22	AAG62323	Casein-related pep
13	6	60.0	7	19	AAW66745	Dolastatin-15 deri
14	6	60.0	7	22	AAG62320	Casein-related pep
15	6	60.0	8	22	AAG62317	Casein-related pep
16	6	60.0	8	23	ABG32210	Sheep colostrin
17	5	50.0	5	15	AAE48290	ACE inhibitor pept
18	5	50.0	5	16	AAW93990	Antineoplastic pep
19	5	50.0	5	16	AAE88265	Intermediate XI fo
20	5	50.0	5	16	AAE88259	Benzylamide hydroc
21	5	50.0	5	18	AAW50300	Antineoplastic pep
22	5	50.0	5	18	AAW29053	Dolastatin-15 deri
23	5	50.0	5	19	AAW11169	Pentapeptide usef
24	5	50.0	5	19	AAW66736	Dolastatin-15 deri
25	5	50.0	5	20	AAW08841	Dolastatin-15 deri
26	5	50.0	5	20	AAW08834	Dolastatin-15 deri
27	5	50.0	5	22	AAU07305	Antineoplastic pep
28	5	50.0	5	22	AAG62324	Casein-related pep
29	5	50.0	5	22	AAG62326	Casein-related pep
30	5	50.0	5	23	ABW84004	Transglutaminase i
31	5	50.0	6	18	AAW50303	Antineoplastic pep
32	5	50.0	6	18	AAW29043	Dolastatin analogu
33	5	50.0	6	18	AAW29044	Dolastatin analogu
34	5	50.0	6	19	AAW29045	Dolastatin-15 deri
35	5	50.0	6	19	AAW66746	Dolastatin-15 deri
36	5	50.0	6	22	AAU07308	Antineoplastic pep
37	5	50.0	6	22	AAG62321	Casein-related pep
38	5	50.0	7	16	AAW93991	Antineoplastic pep
39	5	50.0	7	18	AAW11170	Heptapeptide compo
40	5	50.0	7	19	AAW66747	Dolastatin-15 deri
41	5	50.0	7	19	AAW66748	Dolastatin-15 deri
42	5	50.0	7	19	AAW66734	Dolastatin-15 deri
43	5	50.0	7	20	AAW08847	Dolastatin-15 deri
44	5	50.0	7	20	AAW08848	Dolastatin-15 deri
45	5	50.0	7	20	AAW08840	Dolastatin-15 deri
46	5	50.0	7	20	AAW08833	Dolastatin-15 deri
47	5	50.0	7	20	AAW08838	Dolastatin-15 deri
48	5	50.0	7	22	AAW62318	Casein-related pep
49	5	50.0	9	24	ABU19910	MHC binding peptid
50	5	50.0	10	23	ABW84044	Transglutaminase i
51	5	50.0	14	22	AAW97801	Human peptid #107
52	5	50.0	15	21	AAW00054	Angiotensin peptid
53	5	50.0	16	21	AAW84247	Consensus site for
54	5	50.0	16	24	ABU64607	Motif-specific and
55	4	40.0	4	13	AAE48289	ACE inhibitor pept
56	4	40.0	4	16	AAW93980	Antineoplastic pep
57	4	40.0	4	16	AAE88264	Intermediate X for
58	4	40.0	4	16	AAE88266	Intermediate V for
59	4	40.0	4	16	AAE88260	Intermediate II fo
60	4	40.0	4	16	AAE88261	Intermediate III f
61	4	40.0	4	16	AAE88262	Intermediate IX fo
62	4	40.0	4	19	AAW66735	Dolastatin-15 deri
63	4	40.0	4	19	AAW66566	Peptide useful as
64	4	40.0	4	22	AAU07306	Antineoplastic pep
65	4	40.0	4	22	AAG62329	Cell growth inhibi
66	4	40.0	4	22	AAG62325	Casein-related pep
67	4	40.0	4	22	AAG62327	Casein-related pep
68	4	40.0	4	22	AAG62327	Antineoplastic pep
69	4	40.0	5	18	AAW50302	Dolastatin analogu
70	4	40.0	5	19	AAW29046	Dolastatin-15 deri
71	4	40.0	5	19	AAW66739	ACE inhibitor pept
72	4	40.0	5	21	AAE69982	Casein-related pep
73	4	40.0	5	22	AAG62322	Genome derived ant
74	4	40.0	5	24	AAE33698	Antineoplastic pep
75	4	40.0	6	16	AAW93997	Dolastatin analogu
76	4	40.0	6	18	AAW29050	Dolastatin analogu
77	4	40.0	6	18	AAW29051	Dolastatin analogu
78	4	40.0	6	18	AAW29052	Casein-related pep
79	4	40.0	6	22	AAG62319	Sheep colostrin
80	4	40.0	6	23	ABG32213	Antineoplastic pep
81	4	40.0	7	16	AAW93995	
82	4	40.0				

83 4 40.0 7 16 AAW93996 Antineoplastic pep  
 84 4 40.0 7 16 AAR73908 Human monocyte che  
 85 4 40.0 7 16 AAR73907 Human monocyte che  
 86 4 40.0 7 19 AAW66744 Dolastatin-15 deri  
 87 4 40.0 7 20 AAW08846 Dolastatin-15 deri  
 88 4 40.0 7 22 AAB66376 Hepatitis C virus  
 89 4 40.0 7 24 AAE33699 Genome derived ant  
 90 4 40.0 8 18 AAW46416 Peptide T259 deriv  
 91 4 40.0 8 19 AAW81765 Synthetic metallo  
 92 4 40.0 8 22 AAG62330 Casein-related pep  
 93 4 40.0 8 22 AAJ00291 Hepatitis C virus  
 94 4 40.0 8 22 AAJ01329 Hepatitis C virus  
 95 4 40.0 8 24 AAE33700 Genome derived ant  
 96 4 40.0 8 24 AAE33704 Genome derived ant  
 97 4 40.0 8 24 ABG72765 Human FNfn10 FG lo  
 98 4 40.0 8 24 ABG72767 Human FNfn10 FG lo  
 99 4 40.0 9 14 AAR54620 Listeria p60 pepti  
 100 4 40.0 9 18 AAW41628 Peptide used in de

## ALIGNMENTS

## RESULT 1

AAB72265  
 ID AAB72265 standard; peptide; 10 AA.

XX  
 AC AAB72265;

DT 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 20.

XX Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX  
 SQ

Sequence 10 AA;

Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPVVVPPF 10  
 |||||

Db 1 TQTPVVVPPF 10  
 |||||

## RESULT 2

AAB72518  
 ID AAB72518 standard; Peptide; 10 AA.

XX  
 AC AAB72518;

XX 09-MAY-2001 (first entry)

XX Colostrinin peptide #19.

XX Dermatological; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22665.

XX 17-AUG-1999; 99US-0149310.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -

XX Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.

XX  
 SQ

Sequence 10 AA;

Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPVVVPPF 10  
 |||||

Db 1 TQTPVVVPPF 10  
 |||||

## RESULT 3

AAB72550  
 ID AAB72550 standard; Peptide; 10 AA.

XX  
 AC AAB72550;

XX 09-MAY-2001 (first entry)

XX

```

DE Colostrinin peptide #19.
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX Unidentified.
XX WO200112651-A2.
XX 22-FEB-2001.
XX 17-AUG-2000; 2000WO-US22774.
XX 17-AUG-1999; 99US-0149633.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Boldogh I;
XX WPI; 2001-226545/23.
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient -
XX Claim 6; Page 21; 35pp; English.
XX The present invention relates to a method for promoting neural cell
XX differentiation and treating damaged neural cells, using colostrinin and
XX colostrinin constituent peptides (e.g. the present peptide) as a neural
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX Sequence 10 AA;
XX Query Match 100.0%; Score 10; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.00053;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TQTPVVVPPF 10
Db 1 TQTPVVVPPF 10
RESULT 4
AAB59328
ID AAB59328 standard; Peptide; 10 AA.
XX AAB59328;
XX 21-MAR-2001 (first entry)
XX Ewe colostrinin peptide fragment C-3.
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX Ovis sp.
XX WO2000075173-A2.
XX 14-DEC-2000.
XX 02-JUN-2000; 2000WO-GB02128.
XX 02-JUN-1999; 99GB-0012852.
XX (REGC-) REGEN THERAPEUTICS PLC.
XX Georgiades JA;
XX WPI; 2001-071058/08.
XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX Claim 7; Page 27; 63pp; English.
XX The present invention provides the sequences of a number of peptides
XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX fragment of colostrum. These peptides can be used in the treatment of
XX central nervous system disorders such as senile dementia, Parkinson's
XX disease, Alzheimer's disease, psychosis and neurosis, immune system
XX disorders such as bacterial and viral infections, to improve the
XX development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques.
XX Sequence 10 AA;
XX Query Match 100.0%; Score 10; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.00053;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TQTPVVVPPF 10
Db 1 TQTPVVVPPF 10
RESULT 5
AAE20247
ID AAE20247 standard; peptide; 10 AA.
XX AAE20247;
XX 18-JUN-2002 (first entry)
XX Colostrinin constituent peptide #19.
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
XX therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX transplantation; implantation; dermatological; vulnery.
XX Unidentified.
XX Key Location/Qualifiers
XX Modified-site 10 /note= "Optionally C-terminal amide"
XX WO200213850-A1.
XX 21-FEB-2002.
XX 17-AUG-2000; 2000WO-US22776.
XX 17-AUG-2000; 2000WO-US22776.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2002-269151/31.
XX Composition useful for the modulation of blood cell proliferation in a
XX patient comprises a blood cell regulator selected from colostrinin, its
XX constituent peptide and/or analog -
XX Claim 6; Page 25; 51pp; English.
XX The invention relates to a composition which comprises a blood cell
XX regulator selected from colostrinin, its constituent peptide and/or
XX analogue. The invention is used for modulating the oxidative stress
XX level in a cell e.g. mammalian or human cell present in a cell culture,
XX tissue, organ, or organism; or for treating oxidative damage to the skin
XX of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 10 AA;  
 Query Match 100.0%; Score 10; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPVVVPPF 10  
 Db 1 TQTPVVVPPF 10

## RESULT 6

AA014596  
 ID AAM51054 standard; Peptide; 10 AA.

AC AAM51054;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide (casein amino acids 93-102).

KW Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Modified-site 10 /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. It is  
 CC classified as having a beta-casein homologue precursor, and  
 CC corresponds to casein amino acids 93-102. Methods are claimed for:  
 CC inducing a cytokine in a cell by contact with an immunological  
 CC regulator, where the cell is present in a cell culture, a tissue,  
 CC an organ or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide. Cytokines  
 CC induced by this peptide in human leucocyte cultures include  
 CC interferon-gamma, tumour necrosis factor-alpha and interleukin-10.

SQ Sequence 10 AA;  
 Query Match 100.0%; Score 10; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPVVVPPF 10  
 Db 1 TQTPVVVPPF 10

## RESULT 7

AA014596

ID AAO14596 standard; peptide; 10 AA.

AC AAO14596;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostrinin peptide 19.

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

OS Unidentified.

PH Key Location/Qualifiers

FT Modified-site 10 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.

SQ Sequence 10 AA;

Query Match 100.0%; Score 10; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00053;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPVVVPPF 10

Db 1 TQTPVVVPPF 10

RESULT 8

AAR48292  
 ID AAR48292 standard; peptide; 10 AA.

AC AAR48292;

XX 25-MAR-2003 (updated)

DT 08-JUL-1994 (first entry)

XX ACE inhibitor peptide.

XX ACE inhibitor; angiotensin converting enzyme inhibitor; hypotensive;  
 KW hypertension; high blood pressure; lactic acid bacterium; yeast.

OS Synthetic.

XX EPS83074-A2.

XX 16-FEB-1994.

PF 14-JUL-1993; 93EP-0305507.

XX 23-JUL-1992; 92JP-0197239.

XX (CALV ) CALPIS FOOD IND CO LTD.

XX (CALV ) CALPIS SHOKUHIN KOGYO KK.

XX Nakamura Y, Takano T;

XX WPI; 1994-050387/07.

XX New angiotensin converting enzyme inhibitor peptide(s) - contg.

PT 3-10 amino acids and the amino acid residue sequence

PT Valine-Proline-Proline

PS Example 3; Page 7; 8pp; English.

XX ACE inhibitors having the sequences given in AAR48287-95 are prepared  
 CC by solid phase synthesis or by fermentation of e.g. milk, casein,  
 CC corn, wheat or soybean products using lactic acid bacteria or yeast.  
 CC They exhibit high safety and effective hypotensive activity when  
 CC administered orally at low doses.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 10 AA;

Query Match

Best Local Similarity 90.0%; Score 9; DB 15; Length 10;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPVVVPP 9

Db 2 TQTPVVVPP 10

RESULT 9

AAE07193

ID AAE07193 standard; peptide; 9 AA.

XX AAE07193;

XX 06-NOV-2001 (first entry)

XX Colostrinin peptide 9.

XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral.

XX Unidentified.

XX WO200155199-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-GB00329.

XX 26-JAN-2000; 2000GB-0001825.

XX (REGE-) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -

XX Claim 1; Page 15; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is colostrinin peptide 9 related to the invention.  
 CC Colostrinin peptide 9 corresponds to position 97-105 of beta-caesin.

XX Sequence 9 AA;

Query Match

Best Local Similarity 70.0%; Score 7; DB 22; Length 9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVVVPFF 10

Db 1 PVVVPFF 7

RESULT 10

AAE07203

ID AAE07203 standard; peptide; 10 AA.

XX

AAE07203;  
 06-NOV-2001 (first entry)  
 Modified colostrinin cyclic peptide #9.  
 Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 central nervous system disorder; neurodegenerative disorder; weight loss;  
 beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 acquired immunological deficiency; neurological disorder; dementia;  
 antiviral; cyclic.  
 Synthetic.  
 Key Location/Qualifiers  
 Modified-site 1  
 /note= "N-terminal acetyl; this residue forms a cyclic  
 linkage with Gln found at the C-terminal end"  
 WO200155199-A1.  
 02-AUG-2001.  
 26-JAN-2001; 2001WO-GB00329.  
 26-JAN-2000; 2000GB-0001825.  
 (REGE-) REGEN THERAPEUTICS PLC.  
 Georgiades JA;  
 WPI; 2001-488775/53.  
 Peptide useful as an inter alia in the treatment of e.g. disorders of  
 the immune system and the central nervous system comprises ten  
 amino-terminal amino acid sequence derived from peptides present in  
 colostrinin -  
 Example 2; Page 9; 40pp; English.  
 The invention relates to colostrinin peptide fragments which are useful,  
 inter alia, in the treatment of chronic disorders of the immune system  
 and the central nervous system. Colostrinin peptides are used as a  
 medicament in the treatment of neurological disorders e.g., dementia,  
 neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 disease e.g., Parkinson's disease, mental disorders e.g., psychosis and  
 neurosis, in acquired immunological deficiencies, chronic bacterial and  
 viral infections and diseases characterised by the presence of beta-  
 amyloid plaques and as a dietary supplement for babies, small children,  
 adults and senile persons, who have been subjected to chemotherapy or  
 have suffered from cachexia or weight loss due to the chronic disease.  
 Colostrinin peptides are also used as food additives and as an auxiliary  
 withdrawal treatment for drug addicts, after a period of detoxification  
 and in persons dependent on stimulants. Colostrinin peptides are used to  
 prepare antibodies and to treat emotional disturbances, e.g. emotional  
 disturbances of psychiatric patients in a state of depression. These  
 colostrinin peptides improves the development of immune system in a new  
 born child and to correct the immunological deficiencies in a child.  
 The present sequence is modified colostrinin cyclic peptide #9 related to  
 the invention.  
 Sequence 10 AA;  
 Query Match 70.0%; Score 7; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.59;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 PVVVPPF 10  
 Db 2 PVVVPPF 8

RESULT 11  
 AAR48291  
 ID AAR48291 standard; peptide; 6 AA.  
 XX  
 AC AAR48291;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 08-JUL-1994 (first entry)  
 XX  
 DE ACE inhibitor peptide.  
 XX  
 KW ACE inhibitor; angiotensin converting enzyme inhibitor; hypotensive;  
 KW hypertension; high blood pressure; lactic acid bacterium; yeast.  
 XX  
 OS Synthetic.  
 XX  
 XX EP583074-A2.  
 PN  
 XX  
 PD 16-FEB-1994.  
 XX  
 XX 14-JUL-1993; 93EP-0305507.  
 PF  
 XX  
 PR 23-JUL-1992; 92JP-0197239.  
 XX  
 PA (CALV ) CALPIS FOOD IND CO LTD.  
 PA (CALV ) CALPIS SHOKUHN KOGYO KK.  
 XX  
 PI Nakamura Y, Takano T;  
 XX  
 DR WPI; 1994-050387/07.  
 XX  
 XX New angiotensin converting enzyme inhibitor peptide(s) - contg.  
 PT 3-10 amino acids and the amino acid residue sequence  
 PT Valine-Proline-Proline  
 XX  
 XX Example 3; Page 7; 8pp; English.  
 PS  
 XX  
 CC ACE inhibitors having the sequences given in AAR48287-95 are prepared  
 CC by solid phase synthesis or by fermentation of e.g. milk, casein,  
 CC corn, wheat or soybean products using lactic acid bacteria or yeast.  
 CC They exhibit high safety and effective hypotensive activity when  
 CC administered orally at low doses.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 6 AA;  
 Query Match 60.0%; Score 6; DB 15; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 PVVVPP 9  
 Db 1 PVVVPP 6  
 RESULT 12  
 AAG62323  
 ID AAG62323 standard; peptide; 6 AA.  
 XX  
 AC AAG62323;  
 XX  
 DT 24-AUG-2001 (first entry)  
 XX  
 DE Casein-related peptide SEQ ID 22.  
 XX  
 KW Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200134828-A1.  
 XX  
 PD 17-MAY-2001.  
 XX



PT Production of tripeptides for treating hypertension and stress by  
XX processing casein with proteinase and peptidase -  
PS Claim 3; Page 25; 32pp; Japanese.  
XX  
CC This invention relates to a method for the production of tripeptides. The  
CC method comprises treating material containing milk casein with a  
CC proteinase to produce intermediate peptide containing Valpropro or  
CC IleProPro with no proline residue any where else in the peptide. Use of  
CC the peptides may result in hypotensive and tranquiliser activity. The  
CC peptide can be used in treatments to lower blood pressure and in the  
CC treatment of stress. The present sequence represents an intermediate  
CC peptide of the invention.  
XX  
SQ Sequence 7 AA;  
Query Match 60.0%; Score 6; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 5 VVVPFF 10  
Db 1 VVVPFF 6  
RESULT 15  
AAG62317  
ID AAG62317 standard; peptide; 8 AA.  
XX AC AAG62317;  
XX AC AAG62317;  
DT 24-AUG-2001 (first entry)  
DE Casein-related peptide SEQ ID 16.  
XX  
KW Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.  
OS Synthetic.  
XX WO200134828-A1.  
XX  
PD 17-MAY-2001.  
XX  
PF 10-NOV-2000; 2000WO-JP07930.  
XX  
PR 11-NOV-1999; 99JP-0321084.  
XX (CALV ) CALPIS CO LTD.  
XX Yamamoto N, Ueno K, Ejiri M;  
XX WPI; 2001-343606/36.  
XX  
PT Production of tripeptides for treating hypertension and stress by  
PT processing casein with proteinase and peptidase -  
XX  
PS Claim 3; Page 25; 32pp; Japanese.  
XX  
CC This invention relates to a method for the production of tripeptides. The  
CC method comprises treating material containing milk casein with a  
CC proteinase to produce intermediate peptide containing Valpropro or  
CC IleProPro with no proline residue any where else in the peptide. Use of  
CC the peptides may result in hypotensive and tranquiliser activity. The  
CC peptide can be used in treatments to lower blood pressure and in the  
CC treatment of stress. The present sequence represents an intermediate  
CC peptide of the invention.  
XX  
SQ Sequence 8 AA;  
Query Match 60.0%; Score 6; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 VVVPFF 10  
Db 1 VVVPFF 6  
RESULT 16  
ABG32210  
ID ABG32210 standard; peptide; 8 AA.  
XX AC ABG32210;  
XX AC ABG32210;  
DT 05-NOV-2002 (first entry)  
XX  
DE Sheep colostrinin derived peptide #4.  
XX  
KW Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia;  
KW central nervous system disorder; neurological disorder; neurosis;  
KW mental disorder; psychosis; neurodegenerative disorder;  
KW Alzheimer's disease; motor neuron disease; immune system disorder;  
KW acquired immunological deficiency; bacterial infection; viral infection;  
KW amyloid plaque; dietary supplement; cachexia; weight loss;  
KW senile dementia; Parkinson's disease; emotional disturbance; depression;  
KW drug addiction; drug withdrawal.  
XX  
OS Ovis aries.  
XX WO200246211-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 05-DEC-2001; 2001WO-GB053376.  
XX  
PR 06-DEC-2000; 2000GB-0029777.  
XX (REGE-) REGEN THERAPEUTICS PLC.  
XX  
PI Georgiades JA;  
XX  
DR WPI; 2002-619016/66.  
XX  
PT Novel peptides isolated from colostrinin polypeptide, useful for  
PT treating viral and bacterial infections, disorders of immune system and  
PT central nervous system e.g., Alzheimer's disease, dementia, and as food  
PT additive -  
XX  
PS Claim 1; Page 8; 16pp; English.  
XX  
CC The invention relates to a peptide derived from colostrinin (a colostrum  
CC protein known to be a cytokine inducer) substantially entirely consists  
CC of the peptide sequences appearing as ABG32207-ABG32223. Also included  
CC are a composition comprising two or more of the peptides in combination  
CC with a carrier, a dietary supplement comprising an orally ingestible  
CC combination of the peptide in combination with a carrier and an antibody  
CC which binds to the peptide, and which is obtainable by using peptide as  
CC an antigen. The peptide is useful as a medicament for treating chronic  
CC disorders of central nervous system e.g., neurological disorders and/or  
CC mental disorders such as psychosis and/or neurosis, dementia,  
CC neurodegenerative disorders such as Alzheimer's disease, motor  
CC neuron disease, chronic disorders of immune system, diseases  
CC with bacterial and viral etiology, acquired immunological deficiencies,  
CC chronic bacterial, viral infections. The peptide is also useful for  
CC treating diseases characterised by presence of amyloid plaque. The  
CC peptide is also useful as a dietary supplement for babies, small  
CC children, adults who have been subjected to chemotherapy and/or  
CC adults who have suffered from cachexia or weight loss due to chronic  
CC disease. The peptide is also useful for treating senile dementia,  
CC Parkinson's disease, emotional disturbances and depression. The peptides  
CC may also be used as an auxiliary withdrawal treatment for drug addicts,  
CC after a period of detoxification, and in persons dependent on stimulants.  
CC The present sequence is a colostrinin derived peptide of the invention.  
XX  
SQ Sequence 8 AA;



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Query Match      60.0%; Score 6; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 6
Db 3 TOTPV 8

RESULT 17
AAR48290
ID AAR48290 standard; peptide; 5 AA.
XX
AC AAR48290;
XX
DT 25-MAR-2003 (updated)
DT 08-JUL-1994 (first entry)
XX
DE ACE inhibitor peptide.
XX
KW ACE inhibitor; angiotensin converting enzyme inhibitor; hypotensive;
KW hypertension; high blood pressure; lactic acid bacterium; yeast.
XX
OS Synthetic.
XX
PN EP583074-A2.
XX
PD 16-FEB-1994.
XX
PF 14-JUL-1993; 93EP-0305507.
XX
PR 23-JUL-1992; 92JP-0197239.
XX
PA (CALV ) CALPIS FOOD IND CO LTD.
PA (CALV ) CALPIS SHOKUHIN KOGYO KK.
XX
PI Nakamura Y, Takano T;
XX
DR WPI; 1994-050387/07.
XX
XX
XX New angiotensin converting enzyme inhibitor peptide(s) - contg.
XX 3-10 amino acids and the amino acid residue sequence
XX Valine-Proline-Proline
XX
XX Example 3; Page 7; 8pp; English.
XX
XX ACE inhibitors having the sequences given in AAR48287-95 are prepared
XX by solid phase synthesis or by fermentation of e.g. milk, casein,
XX corn, wheat or soybean products using lactic acid bacteria or yeast.
XX They exhibit high safety and effective hypotensive activity when
XX administered orally at low doses.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 5 AA;

Query Match      50.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVWPP 9
Db 1 VVWPP 5

RESULT 18
AAW93990
ID AAW93990 standard; peptide; 5 AA.
XX
AC AAW93990;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antineoplastic peptide 11.

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XX Tetrapeptide; tumour; dolastatin; antineoplastic activity; lung; breast;
KW intestine; bladder; rectum; uterus; prostate; leukaemia; lymphoma;
KW neoplastic disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Me2-Val"
FT Modified-site 3
FT /note= "Me-Val"
FT Modified-site 5
FT /note= "Pro-NHBzl"
XX
XX DE4415998-A1.
XX
XX 09-NOV-1995.
XX
XX 06-MAY-1994; 94DE-4415998.
XX
XX 06-MAY-1994; 94DE-4415998.
XX
XX (BADI ) BASF AG.
XX
XX Amberg W, Bernhard H, Buschmann E, De Potzulli B;
XX Haupt A, Janitschke L, Janssen B, Karl U, Kling A;
XX Mueller S, Ritter K, Thyes M, Zierke T;
XX
XX WPI; 1995-393582/51.
XX
XX Prepn. of proline contg. tetra:peptide derivs. - comprises
XX condensing tri:peptide with protected amino acid, deprotection, and
XX N-di:methylation, useful as e.g. intermediates for dolastatin
XX
XX Example 4; Page 6; 8pp; German.
XX
XX This invention describes a method for the production of tetrapeptides
XX which comprises reacting a tripeptide with an amino acid, removing Z and
XX methylating the free amino group twice. R1-R4 = 1-6C alkyl; and Z =
XX optional ring substituted benzyloxycarbonyl. The products of the
XX invention are intermediates for dolastatin 15 which have high
XX antineoplastic activity. The peptides of the invention are active against
XX solid tumours (of lung, breast, intestine, bladder, rectum, uterus and
XX prostate), leukaemia, lymphoma and other neoplastic diseases. The
XX peptides can now be produced from material available in large quantities,
XX without racemisation and without requiring very expensive or hazardous
XX reagents.
XX
SQ Sequence 5 AA;

Query Match      50.0%; Score 5; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVWPP 9
Db 1 VVWPP 5

RESULT 19
AAR88265
ID AAR88265 standard; peptide; 5 AA.
XX
AC AAR88265;
XX
XX
DT 25-MAR-2003 (updated)
DT 13-JUN-1996 (first entry)
XX
XX Intermediate XI for prepn. of Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl.
XX
KW Anti-neoplastic agent; solid tumour; leukaemia; lymphoma; treatment;
KW crystalline; non-racemic; intermediate; benzylamide hydrochloride salt.

```

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "protected Z-Val, where Z is benzyloxy-carbonyl, opt. ring substd."

FT Modified-site 3

FT /label= OTHER

FT Modified-site 5

FT /note= "MeVal"

FT /note= "Pro-NHbenzyl"

XX DE4415997-A1.

XX 09-NOV-1995.

XX 06-MAY-1994; 94DE-4415997.

XX 06-MAY-1994; 94DE-4415997.

XX (BADI ) BASF AG.

XX Amberg W, Bernard H, Buschmann E, Haupt A, Janitschke L;

PI Janssen B, Karl U, Kling A, Mueller S, Potzolli B, Ritter K;

PI Zierke T, Thyges M;

XX WPI; 1995-393581/51.

XX Benzyl:amide hydrochloride salt of anti-neoplastic penta:peptide -

PT can be produced without racemisation and in easily crystallisable form

XX Claim 5; Page 8; 8pp; German.

XX The salt Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl is prepared by one of the following methods:

CC (1). claimed intermediate II (AAR88260) is deprotected by removal of Z to give claimed intermediate III (AAR88261) which is methylated twice

CC and the product is hydrolysed to give intermediate (V) (AAR88266).

CC This cpd. is pref. converted to the claimed mixed anhydride VII

CC (AAR88262) before reaction with proline benzylamide and conversion to the hydrochloride salt; or

CC (2). intermediate II is hydrolysed to claimed intermediate IX

CC (AAR88263), which is pref. converted to the claimed mixed anhydride X (AAR88264) before reaction with proline benzylamide; then Z is removed, N-methyl introduced as above and product converted to hydrochloride. The free base form of the pentapeptide is known as an anti-neoplastic agent suitable for treatment of solid tumours, leukaemia, lymphoma and other neoplastic diseases. The benzylamide hydrochloride salt is easily crystallisable and can be produced in high yield without racemisation or the use of expensive or dangerous reagents.

CC The present sequence is that of intermediate XI.

CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 5; DB 16; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPPP 9

Db 1 VVPPP 5

RESULT 20

AAR88259

ID AAR88259 standard; peptide; 5 AA.

XX AC AAR88259;

XX DT 25-MAR-2003 (updated)

DT 13-JUN-1996 (first entry)

XX Benzylamide hydrochloride salt of anti-neoplastic pentapeptide.

XX Anti-neoplastic agent; solid tumour; leukaemia; lymphoma; treatment; crystalline; non-racemic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT Modified-site 3

FT /label= OTHER

FT Modified-site 5

FT /note= "MeVal"

FT /note= "Pro-NHbenzyl"

XX DE4415997-A1.

XX 09-NOV-1995.

XX 06-MAY-1994; 94DE-4415997.

XX 06-MAY-1994; 94DE-4415997.

XX (BADI ) BASF AG.

XX Amberg W, Bernard H, Buschmann E, Haupt A, Janitschke L;

PI Janssen B, Karl U, Kling A, Mueller S, Potzolli B, Ritter K;

PI Zierke T, Thyges M;

XX WPI; 1995-393581/51.

XX Benzyl:amide hydrochloride salt of anti-neoplastic penta:peptide -

PT can be produced without racemisation and in easily crystallisable form

XX Claim 1; Page 8; 8pp; German.

XX The benzylamide hydrochloride salt of the present pentapeptide sequence is claimed. In its free base form, the peptide is known as an anti-neoplastic agent suitable for treatment of solid tumours, leukaemia, lymphoma and other neoplastic disease. The salt is easily crystallisable and can be produced in high yield without racemisation or the use of expensive or dangerous reagents.

XX (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 5; DB 16; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPPP 9

Db 1 VVPPP 5

RESULT 21

AAW50300

ID AAW50300 standard; peptide; 5 AA.

XX AC AAW50300;

XX DT 08-JUL-1998 (first entry)

XX Antineoplastic peptide.

XX Antineoplastic; antitumour agent; Dolastatin; tumour; cancer; Dolastatin 10.

## SYNTHETIC.

OS XX Key Location/Qualifiers  
 XX FH Modified-site 1  
 FT FT Modified-site 3 /note= "N,N-dimethylvaline"  
 FT FT Modified-site 5 /note= "N-methylvaline"  
 FT FT Modified-site 5 /note= "Amide substituted by a wide variety of substituents"  
 XX XX WO9722621-A2.  
 XX XX 26-JUN-1997.  
 XX XX 11-DEC-1996; 96WO-EP05518.  
 XX XX 15-DEC-1995; 95US-0573422.  
 XX XX (BADI ) BASF AG.  
 XX PI Amberg W, Barlozzari T, Bernard H, Buschmann E;  
 PI Haupt A, Hege H, Janssen B, Kling A, Lietz H, Ritter K;  
 PI Ullrich M, Weymann J, Zierke T;  
 XX DR WPI; 1997-341627/31.

PT New peptide(s) with anti-neoplastic activity - useful for treating  
 PT solid tumours and haematological malignancies

XX FS Claim 6; Page 50; 54pp; English.

XX XX This sequence represents a specifically claimed peptide of the formula  
 CC R1R2N-CHX-CO-A-B-D-E-(G)s-K (1), in which R1 = H, Me or Et; R2 = Me or  
 CC Et; or R1R2N = a pyrrolidine ring; A = valyl, isoleucyl, allo-isoleucyl,  
 CC 2-tert-butylglycyl, 2-ethylglycyl, norleucyl or norvalyl residue; B =  
 CC N-methyl-valyl, N-methyl-norvalyl, N-methylleucyl, N-methylisoleucyl, N-  
 CC methyl-2- tert-butylglycyl, N-methyl-2-ethylglycyl or N-methyl-norleucyl  
 CC residue; D = prolyl, homoprolyl, hydroxyprolyl or thiazolidine-4-  
 CC carbonyl residue; E = prolyl, homoprolyl, hydroxyprolyl, thiazolidine-  
 CC 4-carbonyl, trans- or cis-4-fluoro-L-prolyl, or trans- or cis-4-chloro-L-  
 CC prolyl residue; X = Et, propyl, butyl, isopropyl, sec.butyl, tert.butyl,  
 CC cyclopropyl or cyclopentyl; G = L- or D-2-tert-butylglycyl, D-valyl,  
 CC D-isoleucyl, D-leucyl, D-norvalyl, 1-aminopentyl-1-carbonyl or 2,2-  
 CC dimethylglycyl residue; s = 0 or 1; K = -NH-(1-8C alkyl), -NH-(3-8C  
 CC alkenyl), -NH-(3-8C alkenyl), -NH-(6-8C cycloalkyl), -NH-(1-4C alkenyl)-  
 CC (3-8C cycloalkyl) or 1-4C alkyl-N(1-8C alkyl)-, in which one CH2 is  
 CC optionally replaced by O or S, one H is optionally replaced by Ph or CN,  
 CC or 1-3 H are optionally replaced by F, except the N-methoxy-N-  
 CC methylamino; N-benzylamino or N-methyl-N-benzylamino residue; or K is  
 CC thiazolidino, morpholino, azetidino, bicyclo(3.3.0)octan-1-yl-amino,  
 CC 4-methyl-tetrahydrofuran-4-yl-amino, 2,6-dimethyl-anilino, 1,2,3,4-  
 CC tetrahydronaphthalen-1-yl-amino, indan-1-yl-amino, indan-2-yl-amino,  
 CC 1-methyl-cyclopropylamino, 1-methyl-cyclobutylamino, 1-methyl-  
 CC cyclopentylamino, 1-methyl-cyclohexylamino, 1-aminocarbonyl-1-methyl-  
 CC ethylamino, fluoren-9-yl-amino, tetrahydrofuran-2-ylmethyl-amino,  
 CC isindolino or adamantan-1-yl-amino. The peptides are useful for  
 CC treating neoplastic diseases, particularly solid tumours (e.g. lung,  
 CC breast, colon, prostate, bladder, rectum or endometrial tumours) or  
 CC haematological malignancies (e.g. leukaemias, lymphomas). They are  
 CC resistant to enzymatic degradation and can be administered orally.

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 5; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPPP 9  
 |||||  
 Db 1 VVPPP 5

## RESULT 22

AAW29053  
 XX ID AAW29053 standard; peptide; 5 AA.  
 XX AC AAW29053;  
 XX DT 05-MAR-1998 (first entry)  
 XX DE Dolastatin-15 derivative Me2Val-Val-MeVal-Pro-Pro-ester.  
 XX KW dolastatin; antitumour; antineoplastic; ester; hydroxylamine; oxime.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 XX FT Modified-site 1 /note= "Me2Val"  
 XX FT Modified-site 3 /note= "this residue is Meval in the preparative  
 FT FT examples, but is subsequently referred to as  
 FT FT Val in Tables"  
 XX FT Modified-site 5 /note= "this proline is derivatised into a wide  
 FT FT variety of substituted or unsubstituted alkyl,  
 FT FT hydroxylamine or oxime esters; e.g.  
 FT FT Pro-cyclohexyl ester, Pro-dodecyl ester, or  
 FT FT Pro-benzophenone oxime ester"

XX PN WO9717364-A1.

XX PD 15-MAY-1997.

XX PP 30-OCT-1996; 96WO-EP04709.

XX PR 09-NOV-1995; 95US-0554897.

XX PA (BADI ) BASF AG.

XX PI Amberg W, Barlozzari T, Bernard H, Buschmann E;  
 PI De Arruda M, Haupt A, Janssen B, Kling A, Muller S;  
 PI Ritter K, Robinson S, Zierke T, Mueller S;

XX DR WPI; 1997-280979/25.

XX PT New peptide derivatives of dolastatin 15 - useful for treating  
 PT neoplastic diseases, including both solid tumours and haematological  
 PT malignancies

XX PS Examples; Pages 32-59; 76pp; English.

XX CC New peptides are provided which are of general formula A-B-D-E-F-L,  
 CC where A, B, D, E and F are a broadly defined set of amino acid residues  
 CC and L (representing a modification of the C-terminal amino acid F) is  
 CC an alkyl, hydroxylamino or oxime residue. The peptides are dolastatin-15  
 CC derivatives which are used to treat neoplastic diseases. They can be  
 CC used to treat or inhibit solid tumours (e.g. tumours of the lung,  
 CC breast, colon, prostate, bladder, rectum or endometrium) or  
 CC haematological malignancies (e.g. leukaemias or lymphomas). The present  
 CC sequence is one of three specific sequences given in the patent for  
 CC which a large number of ester groups L are exemplified.

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 5; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPPP 9  
 |||||  
 Db 1 VVPPP 5

## RESULT 23

```

AAW11169
ID AAW11169 standard; peptide; 5 AA.
XX
AC AAW11169;
XX
XX 27-NOV-1997 (first entry)
XX
DE Pentapeptide useful as antineoplastic compound.
XX
XX dolastatin; antineoplastic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N,N-dimethyl-Val"
FT Modified-site 3
FT Modified-site /label= MeVal
FT Modified-site /note= "N-methyl-valine"
FT Modified-site 5
FT /note= "Pro-NHCH(CH3)2"
XX
XX WO9840092-A1.
PN
XX 17-SEP-1998.
PD
XX
XX 09-MAR-1998; 98WO-US04594.
PF
XX
XX 13-MAR-1997; 97US-0819101.
PR
XX
XX (BADI ) BASF AG.
PA
XX (BADI ) BASF BIORESEARCH CORP.
XX
XX Barlozzari T, Haupt A;
PI
XX WPI; 1998-520790/44.
DR
XX
XX Composition used for treating cancer - comprises paclitaxel,
PT taxotere or modified taxane or taxoid analogs and tetra- to hepta-
PT peptide(s)
XX
XX Example 1B; Page 38; 114pp; English.
XX
XX The invention relates to a composition for the treatment of cancer. The
CC composition comprises: (a) paclitaxel, taxotere or modified taxane or
CC taxoid analogs; (b) tetra- to hepta- peptides of formula
CC R1R2N-CH-CO-A-B-D-(E)s-(F)t-(G)u-K (I) or their salts and optionally (c)
CC a carrier. R1 = alkyl, cycloalkyl, alkylsulphonyl, fluoroalkyl or
CC aminosulphonyl; R2 = H, alkyl, fluoroalkyl, or cycloalkyl or NR1R2 =
CC pyrrolidino or piperidino; A = valyl, isoleucyl, leucyl, alioisoleucyl,
CC 2,2-dimethylglycyl, 2-cyclopropylglycyl, 2-cyclohexylglycyl,
CC 3-tert-butylalanyl, 2-tert-butylglycyl, 3-cyclohexylalanyl,
CC 2-ethylglycyl, 2-cyclohexylglycyl, norleucyl or norvalyl; B = an N-alkyl
CC derivative of A except alioisoleucyl or cyclohexylalanyl; D, E = prolyl,
CC homoprolyl, hydroxyprolyl, 3,4-dihydroxyprolyl, 4-fluoroprolyl, 3-, 4- or
CC 5- methylprolyl, azetidine-2-carbonyl, 3,3-dimethylprolyl,
CC 4,4-difluoroprolyl, oxazolidine-4-carbonyl, or thiazolidine-4-carbonyl;
CC F, G = prolyl, homoprolyl, hydroxyprolyl, thiazolidine-4-carbonyl,
CC 1-aminopentyl-1-carbonyl, valyl, 2-tert-butylglycyl, isoleucyl, leucyl,
CC 3-cyclohexylalanyl, phenylalanyl, N-methyl-phenylalanyl, 3-pyridylalanyl,
CC tetrahydroisoquinolyl-2-histidyl, 1-aminoinidyl-1-carbonyl,
CC 2-cyclohexylglycyl, norleucyl, norvalyl, neopentylglycyl, tryptophanyl,
CC glycyl, 2,2-dimethylglycyl, alanyl, beta-alanyl or 3-naphthylalanyl; X =
CC H, alkyl, cycloalkyl, methylcyclohexyl or arylalkyl; s, t, u = 0 or 1 and
CC K = hydroxy, alkoxy, phenoxy, benzyloxy or amino (optionally
CC substituted). The composition is used for treating lung, breast, colon,
CC prostate, bladder, rectal, endometrial and haematological cancers e.g.
CC leukaemias and lymphomas. The present sequence represents a specific
CC example of a peptide disclosed in the specification.
XX
SQ Sequence 5 AA;
XX
Query Match 50.0%; Score 5; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 VVVPP 9
DB 1 VVVPP 5
XX
RESULT 24
AAW66736
ID AAW66736 standard; peptide; 5 AA.
XX
AC AAW66736;
XX
XX 02-DEC-1998 (first entry)
XX
DE Dolastatin-15 derivative in composition for treatment of cancer.
XX
XX dolastatin-15; cancer; paclitaxel; taxane; taxoid; taxotere.
XX
KW

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AAW08841
ID AAW08841 standard; peptide; 5 AA.
XX
AC AAW08841;
XX
DT 06-JUL-1999 (first entry)
XX
DE Dolastatin-15 derivative for treatment of rheumatoid arthritis.
XX
KW Dolastatin; antiarthritic; rheumatoid arthritis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 3 /note= "N,N-dimethyl-Val"
FT Modified-site 3 /note= "N-methyl-Val"
FT Modified-site 5
FT /note= "Pro-NH-iPr or Pro-NH-tBu"
XX
PN WO9917792-A1.
XX
PD 15-APR-1999.
XX
PF 24-SEP-1998; 98WO-US19841.
XX
PR 06-OCT-1997; 97US-0944479.
XX
PA (BADI ) BASF AG.
XX
PI Banerjee S, Barlozzari T, Haupt A;
XX
DR WPI; 1999-277207/23.
XX
PT Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,
PT alone or in combination with other antiarthritic drugs
XX
PS Disclosure; Pages 39, 42; 106pp; English.
XX
CC The invention relates to a method for treating rheumatoid arthritis
CC using dolastatin-15 derivatives. The present peptide is a specific
CC example of a dolastatin compound which was prepared for use in the
CC method.
XX
SQ Sequence 5 AA;
XX
Query Match 50.0%; Score 5; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 VVVPP 9
Db 1 VVVPP 5
XX
RESULT 26
AAW08834
ID AAW08834 standard; peptide; 5 AA.
XX
AC AAW08834;
XX
DT 06-JUL-1999 (first entry)
XX
DE Dolastatin-15 derivative for treating rheumatoid arthritis.
XX
KW Dolastatin; antiarthritic; rheumatoid arthritis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 3 /note= "N,N-dimethyl-Val"
FT Modified-site 3 /note= "N-methyl valine"
FT Modified-site 5
FT /note= "Pro-NHCH(CH3)2"
XX
PN US2001009901-A1.
XX
PD 26-JUL-2001.
XX
PF 09-JAN-2001; 2001US-0757142.
XX
PR 12-JUN-1998; 98US-0097184.
PR 11-DEC-1996; 96WO-EP05518.
XX
Query Match 50.0%; Score 5; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 VVVPP 9
Db 1 VVVPP 5
XX
RESULT 27
AAU07305
ID AAU07305 standard; Peptide; 5 AA.
XX
AC AAU07305;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antineoplastic peptide #1.
XX
KW Antineoplastic; tumour; cytostatic; therapeutic; lung; breast;
KW colon; prostate; bladder; rectum; endometrial tumour; leukaemia;
KW haematological malignancy; lymphoma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Me2-valine"
FT Modified-site 3 /label= MeVal
FT /note= "N-methyl valine"
FT Modified-site 5 /note= "Pro-NHCH(CH3)2"
XX
PN US2001009901-A1.
XX
PD 26-JUL-2001.
XX
PF 09-JAN-2001; 2001US-0757142.
XX
PR 12-JUN-1998; 98US-0097184.
PR 11-DEC-1996; 96WO-EP05518.
XX
Query Match 50.0%; Score 5; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 VVVPP 9
Db 1 VVVPP 5
XX
RESULT 27
AAU07305
ID AAU07305 standard; Peptide; 5 AA.
XX
AC AAU07305;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antineoplastic peptide #1.
XX
KW Antineoplastic; tumour; cytostatic; therapeutic; lung; breast;
KW colon; prostate; bladder; rectum; endometrial tumour; leukaemia;
KW haematological malignancy; lymphoma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Me2-valine"
FT Modified-site 3 /label= MeVal
FT /note= "N-methyl valine"
FT Modified-site 5 /note= "Pro-NHCH(CH3)2"
XX
PN US2001009901-A1.
XX
PD 26-JUL-2001.
XX
PF 09-JAN-2001; 2001US-0757142.
XX
PR 12-JUN-1998; 98US-0097184.
PR 11-DEC-1996; 96WO-EP05518.
XX

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XX (BADI ) BASF AG.  
 XX  
 PI Amberg W, Barlozzari T, Bernard H, Buschmann E, Haupt A, Hege H;  
 PI Janssen B, Kling A, Lietz H, Ritter K, Ullrich M, Weymann J;  
 PI Zierke T;  
 XX  
 DR WPI; 2001-529023/58.  
 XX  
 XX New penta- and hexapeptides, which are resistant to enzymatic  
 PT degradation, are used to inhibit or treat solid tumours e.g. of the  
 PT lung, colon, prostate, bladder and rectum, and leukaemias and lymphomas  
 PT -  
 XX  
 XX Example 1; Page 5; 22pp; English.  
 PS  
 XX The invention relates to novel antineoplastic peptides of formula (I):  
 CC N(R1)(R2)-CHX-C(O)-A-B-D-E-(G)s-K. Where R1 = H, CH3 or C2H5;  
 CC R2 = CH3 or C2H5; or NR1R2 = pyrrolidine; A = valyl, isoleucyl, allo-  
 CC isoleucyl, 2-tert-butylglycyl, 2-ethylglycyl, norleucyl or norvalyl  
 CC residue; B = N-methyl-valyl, N-methyl-norvalyl, N-methyl-leucyl,  
 CC N-methyl-isoleucyl, N-methyl-2-tertbutylglycyl, N-methyl-2-ethylglycyl  
 CC or N-methyl-norleucyl; D = prolyl, homoprolyl, thiazolidine-4-  
 CC thiazolidine-4-carboxyl residue; E = prolyl, homoprolyl, trans-4-chloro-  
 CC carbonyl, trans-4-fluoro-L-prolyl, cis-4-fluoro-L-prolyl, trans-4-chloro-  
 CC L-prolyl or cis-4-chloro-L-prolyl; X = C2H5, C3H7, C4H9, isopropyl, sec-  
 CC butyl, tert-butyl, cyclopropyl or cyclopentyl; G = L-2-tert-butylglycyl,  
 CC D-2-tert-butylglycyl, D-valyl, D-isoleucyl, D-leucyl, D-norvalyl,  
 CC 1-aminopentyl-1-carboxyl or 2,2-dimethylglycyl; s = 0 or 1; K' = NH-1-8C  
 CC alkyl, NH-3-8C alkynyl, -NH-3-8C alkynyl, -NH-6-8C cycloalkyl, -NH1-4C  
 CC alkene-3-8C cycloalkyl, 1-4C alkyl-N-1-6C alkyl (one CH2 group may be  
 CC replaced by O or S, one H by phenyl or CN, or mono, di or tri-H by F,  
 CC except for N-methoxy-N-methylamino, N-benzylamino or N-methyl-N-  
 CC benzylamino residue), morpholine, azetidine, thiazolidine, hexahydro-  
 CC pentalen-3a-ylamine, methyl-(4-methyl-tetrahydro-pyran-4-yl) amine,  
 CC 2,6-dimethyl-phenylamine, 1,2,3,4-tetrahydro-naphthalen-1-ylamine,  
 CC indan-1-ylamine, indan-2-ylamine, 1-methyl-cyclopropylamine,  
 CC 1-methyl-cyclobutylamine, 1-methyl-cyclopentylamine,  
 CC 1-methyl-cyclohexylamine, tetrahydro-furan-2-yl methylamine,  
 CC 2,3-dihydro-1H-isindole, adamantan-1-yl amine, NH-C(CH3)2(CONH2) or  
 CC 9-fluorenylamine. The peptides are used to inhibit or otherwise treat  
 CC solid tumours (e.g. tumours of the lungs, breast, colon, prostate,  
 CC bladder, rectum or endometrial tumours) or haematological malignancies  
 CC (e.g. leukaemias, lymphomas). The peptide is resistant to enzymatic  
 CC degradation and can also be administered orally. The present sequence  
 CC represents antineoplastic peptide #1 used in an example of the invention.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 50.0%; Score 5; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 VVPPP 9  
 DB 1 VVPPP 5  
 RESULT 28  
 AAG62324  
 ID AAG62324 standard; peptide; 5 AA.  
 XX  
 AC AAG62324;  
 XX  
 XX 24-AUG-2001 (first entry)  
 DT Casein-related peptide SEQ ID 23.  
 DE Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200134828-A1.

XX 17-MAY-2001.  
 PD  
 XX  
 XX 10-NOV-2000; 2000WO-JP07930.  
 PF  
 XX  
 XX 11-NOV-1999; 99JP-0321084.  
 PR  
 XX  
 XX (CALV ) CALPIS CO LTD.  
 PA  
 XX Yamamoto N, Ueno K, Ejiri M;  
 PI WPI; 2001-343606/36.  
 XX  
 XX Production of tripeptides for treating hypertension and stress by  
 PT processing casein with proteinase and peptidase -  
 PT  
 XX Claim 3; Page 26; 32pp; Japanese.  
 PS  
 XX This invention relates to a method for the production of tripeptides. The  
 CC method comprises treating material containing milk casein with a  
 CC proteinase to produce intermediate peptide containing ValProPro or  
 CC IleProPro with no proline residue any where else in the peptide. Use of  
 CC the peptide may result in hypotensive and tranquilliser activity. The  
 CC peptide can be used in treatments to lower blood pressure and in the  
 CC treatment of stress. The present sequence represents an intermediate  
 CC peptide of the invention.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 50.0%; Score 5; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VVPPP 10  
 DB 1 VVPPP 5  
 RESULT 29  
 AAG62326  
 ID AAG62326 standard; peptide; 5 AA.  
 XX  
 AC AAG62326;  
 XX  
 XX 24-AUG-2001 (first entry)  
 DT Casein-related peptide SEQ ID 25.  
 DE Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200134828-A1.  
 XX  
 XX 17-MAY-2001.  
 PD  
 XX  
 XX 10-NOV-2000; 2000WO-JP07930.  
 PF  
 XX  
 XX 11-NOV-1999; 99JP-0321084.  
 PR  
 XX  
 XX (CALV ) CALPIS CO LTD.  
 PA  
 XX Yamamoto N, Ueno K, Ejiri M;  
 PI WPI; 2001-343606/36.  
 XX  
 XX Production of tripeptides for treating hypertension and stress by  
 PT processing casein with proteinase and peptidase -  
 PT  
 XX Claim 3; Page 27; 32pp; Japanese.  
 PS  
 XX This invention relates to a method for the production of tripeptides. The  
 CC method comprises treating material containing milk casein with a

CC proteinase to produce intermediate peptide containing ValProPro or  
 CC IleProPro with no proline residue any where else in the peptide. Use of  
 CC the peptides may result in hypotensive and tranquiliser activity. The  
 CC peptide can be used in treatments to lower blood pressure and in the  
 CC treatment of stress. The present sequence represents an intermediate  
 CC peptide of the invention.

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 5; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVPPP 9  
 Db 1 VVPPP 5

# RESULT 30

ABBB4004  
 ID ABBB4004 standard; peptide; 5 AA.

XX AC ABBB4004;

XX DT 21-AUG-2002 (first entry)

XX DE Transglutaminase inhibitory peptide ap type #4.

XX KW Transglutaminase inhibitor; Factor XIII inhibitor; XIIIa inhibitor;  
 KW ophthalmological; antiinflammatory; antirheumatic; antiarthritic;  
 KW thrombolytic; neuroprotective; nootropic; antiseborrheic; dermatological;  
 KW cytostatic; anti-HIV; antipsoriatic; Cataract; inflammatory disease;  
 KW arthritis; thrombosis; Alzheimer's disease; Huntington's chorea;  
 KW acne; cancer; HIV infection; psoriasis.

XX OS Unidentified.

XX PN WO200236798-A2.

XX PD 10-MAY-2002.

XX PF 02-NOV-2001; 2001WO-EP12727.

XX PR 03-NOV-2000; 2000DE-1054687. \*

XX PA (NZYM-) N ZYME BIOTEC GMBH.

XX PI Fuchsbaauer H, Pasternack R, Zotzel J;

XX DR WPI; 2002-444364/47.

XX PT New amino acid or peptide derivatives or analogs, are selective  
 PT transglutaminase inhibitors useful e.g. for treating cataract,  
 PT inflammatory diseases, rheumatoid arthritis, thrombosis, Alzheimer's  
 PT disease and cancer -

XX PS Disclosure; Page 13; 44pp; German.

XX CC This invention describes novel amino acid or peptide derivatives or  
 CC analogues (I), containing a modified side-chain (e.g. containing a formyl  
 CC group) which are transglutaminase inhibitors and Factor XIII/XIIIa  
 CC inhibitors. The products of the invention have ophthalmological,  
 CC antiinflammatory, antirheumatic, antiarthritic, thrombolytic,  
 CC neuroprotective, nootropic, antiseborrheic, dermatological, cytostatic,  
 CC anti-HIV and antipsoriatic activity. (I) are transglutaminase inhibitors,  
 CC especially inhibitors of crosslinking of proteins or peptides  
 CC (specifically fibrin and/or alpha 2-plasmin inhibitor), incorporation of  
 CC primary amines in proteins and peptides, hydrolysis of the  
 CC gamma-carboxanido group of glutamine residues bound in proteins or  
 CC peptides, blood factor XIII/XIIIa and mammalian, human, tissue, liver,  
 CC brain, eye lens, keratinocyte, epidermal, prostate, plant, parasitic  
 CC and/or bacterial transglutaminases. The products of the invention can be  
 CC used for treating cataract, inflammatory diseases, rheumatoid arthritis,

CC chronic arthritis, thrombosis, Alzheimer's disease, Huntington's chorea,  
 CC acne, cancer (by induction of apoptosis), HIV infections and psoriasis.  
 CC (I) Are targeted and specific transglutaminase inhibitors, which can  
 CC inhibit a specific type of transglutaminase in the human or animal body  
 CC without affecting other transglutaminases. ABBB4001-ABBB4049 represent  
 CC transglutaminase inhibitors described in the method of the invention.

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 5; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVVV 7  
 Db 1 TPVVV 5

# RESULT 31

AAW50303  
 ID AAW50303 standard; peptide; 6 AA.

XX AC AAW50303;

XX DT 08-JUL-1998 (first entry)

XX DE Antineoplastic peptide.

XX KW Antineoplastic; antitumour agent; Dolastatin; tumour; cancer;  
 KW Dolastatin 10.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N,N-dimethylvaline"

FT Modified-site 3 /note= "N-methylvaline"

FT Modified-site 6 /note= "N-substituted isoleucine amide"

XX FN WO9722621-A2.

XX PD 26-JUN-1997.

XX PF 11-DEC-1996; 96WO-EP05518.

XX PR 15-DEC-1995; 95US-0573422.

XX PA (BADI ) BASF AG.

XX PI Amberg W, Barlozzari T, Bernard H, Buschmann E;  
 PI Haupt A, Hege H, Janssenb, Kling A, Lietz H, Ritter K;  
 PI Ullrich M, Weymann J, Zierke T;  
 XX WPI; 1997-341627/31.

XX PT New peptide(s) with anti-neoplastic activity - useful for treating  
 PT solid tumours and haematological malignancies

XX PS Example 2; Page 16; 54pp; English.

XX CC This sequence represents an antineoplastic peptide of the formula  
 CC R1R2N-CHX-CO-A-B-D-E-(G)s-K (I), in which R1 = H, Me or Et; R2 = Me or  
 CC Et; or R1R2N = a pyrrolidine ring; A = valyl, isoleucyl, allo-isoleucyl,  
 CC 2-tert-butylglycyl, 2-ethylglycyl, norleucyl or norvalyl residue; B =  
 CC N-methyl-valyl, N-methyl-norvalyl, N-methylleucyl, N-methylisoleucyl, N-  
 CC methyl-2-tert-butylglycyl, N-methyl-2-ethylglycyl or N-methyl-norleucyl  
 CC residue; D = prolyl, homoprolyl, hydroxyprolyl or thiazolidine-4-  
 CC carbonyl residue; E = prolyl, homoprolyl, hydroxyprolyl, thiazolidine-4-  
 CC carbonyl, trans- or cis-4-fluoro-L-prolyl, or trans- or cis-4-chloro-L-  
 CC prolyl residue; X = Et, propyl, butyl, isopropyl, sec-butyl, tert-butyl,  
 CC cyclopropyl or cyclopentyl; G = L- or D-2-tert-butylglycyl, D-valyl,

CC D-isoleucyl, D-leucyl, D-norvalyl, 1-aminopentyl-1-carbonyl or 2,2-dimethylglycyl residue; R = 0 or 1; K = -NH-(1-8C alkyl), -NH-(3-8C alkenyl), -NH-(3-8C alkynyl), -NH-(6-8C cycloalkyl), -NH-(1-4C alkenyl)- (3-8C cycloalkyl) or 1-4C alkyl-N(1-6C alkyl)-, in which one CH<sub>2</sub> is optionally replaced by O or S, one H is optionally replaced by Ph or CN, or 1-3 H are optionally replaced by F, except the N-methoxy-N-methylamino, N-benzylamino or N-methyl-N-benzylamino residue; or K is thiazolidino, morpholino, azetidino, bicyclo(3.3.0)octan-1-yl-amino, 4-methyl-tetrahydropyran-4-yl-amino, 2,6-dimethyl-anilino, 1,2,3,4-tetrahydrophthalen-1-yl-amino, indan-1-yl-amino, indan-2-yl-amino, 1-methyl-cyclopropylamino, 1-methyl-cyclobutylamino, 1-methyl-cyclopentylamino, 1-methyl-cyclohexylamino, 1-aminocarbonyl-1-methyl-ethylamino, fluoren-9-yl-amino, tetrahydrofuran-2-ylmethyl-amino, isocindolino or adamantan-1-yl-amino. The peptides are useful for treating neoplastic diseases, particularly solid tumours (e.g. lung, breast, colon, prostate, bladder, rectum or endometrial tumours) or haematological malignancies (e.g. leukaemias, lymphomas). They are resistant to enzymatic degradation and can be administered orally.

XX Sequence 6 AA;

SQ Query Match 50.0%; Score 5; DB 18; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPPP 9  
Db 1 VVPPP 5

RESULT 32  
AAW29043  
ID AAW29043 standard; peptide; 6 AA.  
XX AC AAW29043;  
XX DT 05-MAR-1998 (first entry)  
XX DE Dolastatin analogue peptide.  
XX KW dolastatin; antineoplastic.  
XX OS Synthetic.  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "Me2Val"  
FT Modified-site 3 /note= "MeVal"  
FT Modified-site 4 /note= "MeVal"  
FT Modified-site 6 /note= "4-fluoro-L-Pro"  
FT Modified-site /note= "Leu-propylamide"  
XX W09640751-A1.  
XX PD 19-DEC-1996.  
XX PF 03-JUN-1996; 96WO-EP02392.  
XX PR 07-JUN-1995; 95US-0472453.  
XX PA (BADI ) BASF AG.  
XX EM Emling F, Haupt A, Romerdahl CA;  
XX WI WPI; 1997-099919/09.  
XX New dolastatin derivs. useful as antineoplastic agents - which are more resistant to enzymatic degradation than dolastatin-15  
XX Example 64; Page 19; 38pp; English.

CC New dolastatin derivatives are disclosed having the formula R1R2N-CHX-CO-A-B-D-E-(F)t-K, in which R1 = Me, Et or iPr; R2 = H, Me or Et; or NR1R2 = a pyrrolidine ring; A = a valyl, isoleucyl, leucyl, 2-tert-butylglycyl, 2-ethylglycyl, norleucyl or norvalyl residue; B = a N-methyl-valyl, -leucyl, -isoleucyl, -norvalyl, -norleucyl, -2-tert-butylglycyl, -3-tert-butylalanyl or -2-ethylglycyl residue; D = a 3,4-dehydroprolyl, 4-fluoroprolyl, 4,4-difluoroprolyl, azetidine-2-carbonyl, or 3-, 4- or 5-methylprolyl residue; E = a prolyl, homoprolyl, hydroxyprolyl or thiazolidine-4-carbonyl residue; F = a valyl, 2-tert-butylglycyl, isoleucyl, leucyl, 2-cyclohexylglycyl, norleucyl, norvalyl, neopentylglycyl, alanyl, beta-alanyl or aminoisobutyryl residue; X = alkyl (preferably 2-5C alkyl), cyclopropyl or cyclopentyl; t = 0 or 1; and K = alkoxy (preferably 1-4C alkoxy), benzyl or optionally substituted amino.  
These peptides may be used to treat or inhibit tumours (including tumours of the lung, colon, breast, bladder, rectum or prostate) or haematological malignancies (such as lymphomas and leukaemias). They are more resistant to enzymatic degradation than dolastatin-15.  
The present sequence represents a specific peptide which was prepared in the Examples of the patent.

XX Sequence 6 AA;

SQ Query Match 50.0%; Score 5; DB 18; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPPP 9  
Db 1 VVPPP 5

RESULT 33  
AAW29044  
ID AAW29044 standard; peptide; 6 AA.  
XX AC AAW29044;  
XX DT 05-MAR-1998 (first entry)  
XX DE Dolastatin analogue peptide.  
XX KW dolastatin; antineoplastic.  
XX OS Synthetic.  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "Me2Val"  
FT Modified-site 3 /note= "MeVal"  
FT Modified-site 4 /note= "MeVal"  
FT Modified-site 6 /note= "4-fluoro-L-Pro"  
FT Modified-site /note= "Val-propylamide"  
XX W09640751-A1.  
XX PD 19-DEC-1996.  
XX PF 03-JUN-1996; 96WO-EP02392.  
XX PR 07-JUN-1995; 95US-0472453.  
XX PA (BADI ) BASF AG.  
XX EM Emling F, Haupt A, Romerdahl CA;  
XX WI WPI; 1997-099919/09.  
XX New dolastatin derivs. useful as antineoplastic agents - which are more resistant to enzymatic degradation than dolastatin-15



PT Example 66; Page 19; 38pp; English.

XX New dolastatin derivatives are disclosed having the formula

CC R1R2N-CHX-CO-A-B-D-E-(F)t-K, in which R1 = Me, Et or iPr; R2 = H, Me

CC or Et; or NR1R2 = a pyrrolidine ring; A = a valyl, isoleucyl, leucyl,

CC 2-tert-butylglycyl, 2-ethylglycyl, norleucyl or norvalyl residue; B =

CC a N-methyl-valyl, -leucyl, -isoleucyl, -norleucyl, -norvalyl,

CC 2-tert-butylglycyl, -3-tert-butylalanyl or -2-ethylglycyl residue;

CC D = a 3,4-dehydroprolyl, 4-fluoroprolyl, 4,4-difluoroprolyl,

CC azetidine-2-carbonyl, or 3-, 4- or 5-methylprolyl residue; E = a prolyl,

CC valyl, 2-tert-butylglycyl, isoleucyl, leucyl, 2-cyclohexylglycyl,

CC norleucyl, norvalyl, neopentylglycyl, alanyl, beta-alanyl or

CC aminoisobutyl residue; X = alkyl (preferably 2-5C alkyl), cyclopropyl

CC or cyclopentyl; t = 0 or 1; and K = alkoxy (preferably 1-4C alkoxy),

CC benzoyloxy or optionally substituted amino.

CC These peptides may be used to treat or inhibit tumours (including

CC tumours of the lung, colon, breast, bladder, rectum or prostate) or

CC haematological malignancies (such as lymphomas and leukaemias). They

CC are more resistant to enzymatic degradation than dolastatin-15.

CC The present sequence represents a specific peptide which was

CC prepared in the Examples of the patent.

XX Sequence 6 AA;

SQ Query Match 50.0%; Score 5; DB 18; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVPPP 9

DB 1 VVPPP 5

RESULT 34

AAW29045

ID AAW29045 standard; peptide; 6 AA.

XX AAW29045;

AC AAW29045;

XX 05-MAR-1998 (first entry)

DT Dolastatin analogue peptide.

XX dolastatin; antineoplastic.

DE dolastatin; antineoplastic.

KW dolastatin; antineoplastic.

XX dolastatin; antineoplastic.

OS Synthetic.

XX Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1 /note= "Me2Val"

FT Modified-site 3 /note= "MeVal"

FT Modified-site 4 /note= "4-fluoro-L-Pro"

FT Modified-site 6 /note= "Ile-propylamide"

XX WO9640751-A1.

PN 19-DEC-1996.

XX 03-JUN-1996; 96WO-EP02392.

PF 07-JUN-1995; 95US-0472453.

PR (BADI ) BASF AG.

XX Emling F, Haupt A, Romerdahl CA;

PI WPI; 1997-099919/09.

XX New dolastatin deriva. useful as antineoplastic agents - which are

PT more resistant to enzymatic degradation than dolastatin-15

XX Example 67; Page 19; 38pp; English.

XX New dolastatin derivatives are disclosed having the formula

CC R1R2N-CHX-CO-A-B-D-E-(F)t-K, in which R1 = Me, Et or iPr; R2 = H, Me

CC or Et; or NR1R2 = a pyrrolidine ring; A = a valyl, isoleucyl, leucyl,

CC 2-tert-butylglycyl, 2-ethylglycyl, norleucyl or norvalyl residue; B =

CC a N-methyl-valyl, -leucyl, -isoleucyl, -norleucyl, -norvalyl,

CC 2-tert-butylglycyl, -3-tert-butylalanyl or -2-ethylglycyl residue;

CC D = a 3,4-dehydroprolyl, 4-fluoroprolyl, 4,4-difluoroprolyl,

CC azetidine-2-carbonyl, or 3-, 4- or 5-methylprolyl residue; E = a prolyl,

CC valyl, 2-tert-butylglycyl, isoleucyl, leucyl, 2-cyclohexylglycyl,

CC norleucyl, norvalyl, neopentylglycyl, alanyl, beta-alanyl or

CC aminoisobutyl residue; X = alkyl (preferably 2-5C alkyl), cyclopropyl

CC or cyclopentyl; t = 0 or 1; and K = alkoxy (preferably 1-4C alkoxy),

CC benzoyloxy or optionally substituted amino.

CC These peptides may be used to treat or inhibit tumours (including

CC tumours of the lung, colon, breast, bladder, rectum or prostate) or

CC haematological malignancies (such as lymphomas and leukaemias). They

CC are more resistant to enzymatic degradation than dolastatin-15.

CC The present sequence represents a specific peptide which was

CC prepared in the Examples of the patent.

XX Sequence 6 AA;

SQ Query Match 50.0%; Score 5; DB 18; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVPPP 9

DB 1 VVPPP 5

RESULT 35

AAW66746

ID AAW66746 standard; peptide; 6 AA.

XX AAW66746;

AC AAW66746;

XX 02-DEC-1998 (first entry)

DT Dolastatin-15 derivative in composition for treatment of cancer.

DE dolastatin-15; cancer; paclitaxel; taxane; taxotere.

KW dolastatin-15; cancer; paclitaxel; taxane; taxotere.

XX dolastatin-15; cancer; paclitaxel; taxane; taxotere.

OS Synthetic.

XX Dolabella auricularia.

FH Key Location/Qualifiers

FT Modified-site 1 /note= "N,N-dimethyl-Val"

FT Modified-site 3 /label= MeVal

FT Modified-site 6 /note= "N-methyl-valine"

XX WO9840092-A1.

PN 17-SEP-1998.

XX 09-MAR-1998; 98WO-US04594.

PF 13-MAR-1997; 97US-0819101.

PR (BADI ) BASF AG.

XX (BADI ) BASF BIORESEARCH CORP.

PI Barlozzari T, Haupt A;



DE Casein-related peptide SEQ ID 20.  
KW Tripeptide; casein; hypotensive; tranquilliser; blood pressure; stress.  
OS Synthetic.  
XX WO200134828-A1.  
PN  
XX  
XX PD 17-MAY-2001.  
XX  
XX PF 10-NOV-2000; 2000WO-JP07930.  
XX  
XX PR 11-NOV-1999; 99JP-0321084.  
XX  
XX PA (CALV ) CALPIS CO LTD.  
XX  
XX PI Yamamoto N, Ueno K, Ejiri M;  
XX WPI; 2001-343606/36.  
XX  
XX PT Production of tripeptides for treating hypertension and stress by  
XX processing casein with proteinase and peptidase -  
XX  
XX PS Claim 3; Page 26; 32pp; Japanese.  
XX  
XX CC This invention relates to a method for the production of tripeptides. The  
XX method comprises treating material containing milk casein with a  
XX proteinase to produce intermediate peptide containing Valpropro or  
XX Ilepropro with no proline residue any where else in the peptide. Use of  
XX the peptides may result in hypotensive and tranquilliser activity. The  
XX peptide can be used in treatments to lower blood pressure and in the  
XX treatment of stress. The present sequence represents an intermediate  
XX peptide of the invention.  
XX  
XX SQ Sequence 6 AA;  
Query Match 50.0%; Score 5; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 VVPPF 10  
DB 1 VVPPF 5  
RESULT 38  
AAW93991  
ID AAW93991 standard; peptide; 7 AA.  
XX  
XX AC AAW93991;  
XX  
XX DT 01-JUL-1999 (first entry)  
XX  
XX DE Antineoplastic peptide 12.  
XX Tetrapeptide; tumour; dolastatin; antineoplastic activity; lung; breast;  
KW intestine; bladder; rectum; uterus; prostate; leukaemia; lymphoma;  
KW neoplastic disease.  
XX  
XX OS Synthetic.  
XX  
XX FH Key Location/Qualifiers  
FT Modified-site 1 /note= "Me2-Val"  
FT Modified-site 3 /note= "Me-Val"  
FT Modified-site 7 /note= "Me-Val"  
XX  
XX PN DE4415998-A1.  
XX  
XX PD 09-NOV-1995.  
XX  
XX PF 06-MAY-1994; 94DE-4415998.  
XX

PR 06-MAY-1994; 94DE-4415998.  
XX  
XX PA (BADI ) BASF AG.  
XX  
XX PI Amberg W, Bernard H, Buschmann E, De Potzoli B;  
PI Haupt A, Janitschke L, Janssen B, Karl U, Kling A;  
PI Mueller S, Ritter K, Thyes M, Zierke T;  
XX  
XX DR WPI; 1995-393582/51.  
XX  
XX PT Prepn. of proline contg. tetra:peptide derivs. - comprises  
XX condensing tri:peptide with protected amino acid, deprotection, and  
XX N-di:methylation, useful as e.g. intermediates for dolastatin  
XX  
XX PS Example 4; Page 7; 8pp; German.  
XX  
XX CC This invention describes a method for the production of tetrapeptides  
XX which comprises reacting a tripeptide with an amino acid, removing Z and  
XX methylating the free amino group twice. R1-R4 = 1-6C alkyl; and Z =  
XX optional ring substituted benzoyloxycarbonyl. The products of the  
XX invention are intermediates for dolastatin 15 which have high  
XX antineoplastic activity. The peptides of the invention are active against  
XX solid tumours (of lung, breast, intestine, bladder, rectum, uterus and  
XX prostate), leukaemia, lymphoma and other neoplastic diseases. The  
XX peptides can now be produced from material available in large quantities,  
XX without racemisation and without requiring very expensive or hazardous  
XX reagents.  
XX  
XX SQ Sequence 7 AA;  
Query Match 50.0%; Score 5; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 VVPPP 9  
DB 1 VVPPP 5  
RESULT 39  
AAW11170  
ID AAW11170 standard; peptide; 7 AA.  
XX  
XX AC AAW11170;  
XX  
XX DT 27-NOV-1997 (first entry)  
XX  
XX DE Heptapeptide compound.  
XX  
XX KW dolastatin; antineoplastic.  
XX  
XX OS Synthetic.  
XX  
XX FH Key Location/Qualifiers  
FT Modified-site 1 /note= "Me2Val"  
FT Modified-site 3 /note= "MeVal"  
FT Modified-site 7 /note= "Phe-NH2"  
XX  
XX PN DE19527575-A1.  
XX  
XX PD 30-JAN-1997.  
XX  
XX PF 28-JUL-1995; 95DE-1027575.  
XX  
XX PR 28-JUL-1995; 95DE-1027575.  
XX  
XX PA (BADI ) BASF AG.  
XX  
XX PI Amberg W, Bernard H, Buschmann E, Haupt A, Janssen B;  
PI Kling A, Ritter K, Zierke T, Karl U, Mueller S;

XX WPI; 1997-100961/10.

XX Prodn. of penta-peptide anti:neoplastic cpds. and dolastatin

PT precursor - from prolinamide by stepwise amino acid coupling and

PT optionally terminal enzymatic hydrolysis

XX Disclosure; Page 4; 10pp; German.

XX The patent relates to a new process for preparing pentapeptides

CC having -Pro-Pro at the C-terminal, starting from a prolinamide and

CC proceeding stepwise via a dipeptide, a tripeptide and a tetra-peptide,

CC optionally followed by hydrolysis of the C-terminal amide with a

CC prolyl endopeptidase. The preferred pentapeptide prepared is

CC Me2Val-Val-MeVal-Pro-Pro-OH (or its amide form) (see GENSESEQ AAW11169)

CC which is an antineoplastic compound and also an intermediate for

CC Dolastatin 15 and other peptides disclosed in WO9323424, for example

CC the present heptapeptide.

SQ Sequence 7 AA;

Query Match 50.0%; Score 5; DB 18; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPPP 9

Db 1 VVPPP 5

RESULT 40

AAW66747

ID AAW66747 standard; peptide; 7 AA.

AC AAW66747;

DT 02-DEC-1998 (first entry)

DE Dolastatin-15 derivative in composition for treatment of cancer.

KW dolastatin-15; cancer; paclitaxel; taxane; taxoid; taxotere.

OS Synthetic.

OS Dolabella auricularia.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N,N-dimethyl-Val"

FT Modified-site 3 /label= MeVal

FT Modified-site 7 /note= "N-methyl-valine"

FT /note= "Phe-NH2"

PN WO9840092-A1.

PD 17-SEP-1998.

PF 09-MAR-1998; 98WO-US04594.

PR 13-MAR-1997; 97US-0819101.

XX (BADI ) BASF AG.

PA (BADI ) BASF BIORESEARCH CORP.

XX Barlozzari T, Haupt A;

XX WPI; 1998-520790/44.

XX Composition used for treating cancer - comprises paclitaxel,

PT taxotere or modified taxane or taxoid analogs and tetra- to hepta-

PT peptide(s).

XX

PS Example 189; Page 57; 114pp; English.

XX The invention relates to a composition for the treatment of cancer. The

CC composition comprises: (a) paclitaxel, taxotere or modified taxane or

CC taxoid analogs; (b) tetra- to hepta- peptides of formula

CC R1R2N-CHX-CO-A-B-D-(E)s-(F)-t-(G)u-K (I) or their salts and optionally (c)

CC a carrier. R1 = alkyl, cycloalkyl, alkylsulphonyl, fluoroalkyl or

CC aminosulphonyl; R2 = H, alkyl, fluoroalkyl, or cycloalkyl or NR1R2 =

CC pyrrolidino or piperidino; A = valyl, isoleucyl, leucyl, alloisoleucyl,

CC 2,2-dimethylglycyl, 2-cyclopropylglycyl, 2-cyclopentylglycyl,

CC 3-tert-butylalanyl, 2-tert-butylglycyl, 3-cyclohexylalanyl,

CC 2-ethylglycyl, 2-cyclohexylglycyl, norleucyl or norvalyl; B = an N-alkyl

CC derivative of A except alloisoleucyl or cyclohexylalanyl; D, E = prolyl,

CC homoprolyl, hydroxyprolyl, 3,4-dehydroprolyl, 4-fluoroprolyl, 3-, 4- or

CC 5-methylprolyl, azetidine-2-carboxyl, 3,3-dimethylprolyl,

CC 4,4-difluoroprolyl, oxazolidine-4-carboxyl, or thiazolidine-4-carboxyl;

CC F, G = prolyl, homoprolyl, hydroxyprolyl, thiazolidine-4-carboxyl,

CC 1-aminoprolyl-1-carboxyl, valyl, 2-tert-butylglycyl, isoleucyl, leucyl,

CC 3-cyclohexylalanyl, phenylalanyl, N-methyl-phenylalanyl, 3-pyridylalanyl,

CC tetrahydroisquinolyl-2-histidyl, 1-aminoindyl-1-carboxyl,

CC 2-cyclohexylglycyl, norleucyl, norvalyl, neopentylglycyl, tryptophanyl,

CC glycyl, 2,2-dimethylglycyl, alanyl, beta-alanyl or 3-naphthylalanyl; X =

CC H, alkyl, cycloalkyl, methylcyclohexyl or arylalkyl; s, t, u = 0 or 1 and

CC K = hydroxy, alkoxy, phenoxy, benzyloxy or amino (optionally

CC substituted). The composition is used for treating lung, breast, colon,

CC prostate, bladder, rectal, endometrial and haematological cancers e.g.

CC leukaemias and lymphomas. The present sequence represents a specific

CC example of a heptapeptide disclosed in the specification.

XX SQ Sequence 7 AA;

Query Match 50.0%; Score 5; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPPP 9

Db 1 VVPPP 5

RESULT 41

AAW66748

ID AAW66748 standard; peptide; 7 AA.

AC AAW66748;

DT 02-DEC-1998 (first entry)

DE Dolastatin-15 derivative in composition for treatment of cancer.

KW dolastatin-15; cancer; paclitaxel; taxane; taxoid; taxotere.

OS Synthetic.

OS Dolabella auricularia.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N,N-dimethyl-Val"

FT Modified-site 3 /label= MeVal

FT Modified-site 7 /note= "N-methyl-valine"

FT /note= "Phe-NH2"

PN WO9840092-A1.

PD 17-SEP-1998.

PF 09-MAR-1998; 98WO-US04594.

PR 13-MAR-1997; 97US-0819101.

XX (BADI ) BASF AG.

PA (BADI ) BASF AG.

XX Barlozzari T, Haupt A;

XX WPI; 1998-520790/44.

XX Composition used for treating cancer - comprises paclitaxel,

PT taxotere or modified taxane or taxoid analogs and tetra- to hepta-

PT peptide(s).

XX

PA (BADI ) BASF BIORESEARCH CORP.  
 XX Barlozzari T, Haupt A;  
 XX WPI; 1998-520790/44.  
 XX Composition used for treating cancer - comprises paclitaxel,  
 PT taxotere or modified taxane or taxoid analogs and tetra- to hepta-  
 XX peptide(s)  
 XX Example 190; Page 57; 114pp; English.  
 XX The invention relates to a composition for the treatment of cancer. The  
 CC composition comprises: (a) paclitaxel, taxotere or modified taxane or  
 CC taxoid analogs; (b) tetra- to hepta- peptides of formula  
 CC R1R2N-CHX-CO-A-B-D-(E)s-(F)t-(G)u-K (I) or their salts and optionally (c)  
 CC a carrier. R1 = alkyl, cycloalkyl, alkylsulphonyl, fluoroalkyl or  
 CC aminosulphonyl; R2 = H, alkyl, fluoroalkyl, or cycloalkyl or NR1R2 =  
 CC pyrrolidino or piperidino; A = valyl, isoleucyl, leucyl, alioisoleucyl,  
 CC 2,2-dimethylglycyl, 2-cyclopropylglycyl, 2-cyclopentylglycyl,  
 CC 3-tert-butylalanyl, 2-tert-butylglycyl, 3-cyclohexylalanyl,  
 CC 4,4-difluoropropyl, oxazolidine-4-carbonyl, or thiazolidine-4-carbonyl;  
 CC F, G = prolyl, homopropyl, hydroxypropyl, thiazolidine-4-carbonyl,  
 CC 1-aminopentyl-1-carbonyl, valyl, 2-tert-butylglycyl, isoleucyl, leucyl,  
 CC 3-cyclohexylalanyl, phenylalanyl, N-methyl-phenylalanyl, 3-pyridylalanyl,  
 CC tetrahydroisquinolyl-2-histidyl, 1-aminoindyl-1-carbonyl,  
 CC 2-cyclohexylglycyl, norleucyl, norvalyl, neopentylglycyl, tryptophanyl,  
 CC glycyl, 2,2-dimethylglycyl, alanyl, beta-alanyl or 3-naphthylalanyl; X =  
 CC H, alkyl, cycloalkyl, methylcyclohexyl or arylalkyl; s, t, u = 0 or 1 and  
 CC K = hydroxy, alkoxy, phenoxy, benzoyloxy or amino (optionally  
 CC substituted). The composition is used for treating lung, breast, colon,  
 CC prostate, bladder, rectal, endometrial and haematological cancers e.g.  
 CC leukaemias and lymphomas. The present sequence represents a specific  
 CC example of a heptapeptide disclosed in the specification.  
 XX Sequence 7 AA;

Query Match 50.0%; Score 5; DB 19; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 VVPPP 9  
 DB 1 VVPPP 5

RESULT 42  
 AA066734  
 ID AA066734 standard; peptide; 7 AA.  
 XX AA066734;  
 XX 02-DEC-1998 (first entry)  
 XX Dolastatin-15 derivative in composition for treatment of cancer.  
 XX dolastatin-15; cancer; paclitaxel; taxane; taxoid; taxotere.  
 XX Synthetic.  
 XX Dolabella auricularia.  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "N,N-dimethyl-Val"  
 FT Modified-site 3 /label= MeVal  
 FT Modified-site 7 /note= "N-methyl-valine"  
 FT Modified-site /note= "C-terminal amide"

XX WO9840092-A1.  
 XX 17-SEP-1998.  
 XX 09-MAR-1998; 98WO-US04594.  
 XX 13-MAR-1997; 97US-0819101.  
 XX (BADI ) BASF AG.  
 XX (BADI ) BASF BIORESEARCH CORP.  
 XX Barlozzari T, Haupt A;  
 XX WPI; 1998-520790/44.  
 XX Composition used for treating cancer - comprises paclitaxel,  
 PT taxotere or modified taxane or taxoid analogs and tetra- to hepta-  
 XX peptide(s)  
 XX Example 1A; Page 33; 114pp; English.  
 XX The invention relates to a composition for the treatment of cancer. The  
 CC composition comprises: (a) paclitaxel, taxotere or modified taxane or  
 CC taxoid analogs; (b) tetra- to hepta- peptides of formula  
 CC R1R2N-CHX-CO-A-B-D-(E)s-(F)t-(G)u-K (I) or their salts and optionally (c)  
 CC a carrier. R1 = alkyl, cycloalkyl, alkylsulphonyl, fluoroalkyl or  
 CC aminosulphonyl; R2 = H, alkyl, fluoroalkyl, or cycloalkyl or NR1R2 =  
 CC pyrrolidino or piperidino; A = valyl, isoleucyl, leucyl, alioisoleucyl,  
 CC 2,2-dimethylglycyl, 2-cyclopropylglycyl, 2-cyclopentylglycyl,  
 CC 3-tert-butylalanyl, 2-tert-butylglycyl, 3-cyclohexylalanyl,  
 CC 4,4-difluoropropyl, oxazolidine-4-carbonyl, or thiazolidine-4-carbonyl;  
 CC F, G = prolyl, homopropyl, hydroxypropyl, thiazolidine-4-carbonyl,  
 CC 1-aminopentyl-1-carbonyl, valyl, 2-tert-butylglycyl, isoleucyl, leucyl,  
 CC 3-cyclohexylalanyl, phenylalanyl, N-methyl-phenylalanyl, 3-pyridylalanyl,  
 CC tetrahydroisquinolyl-2-histidyl, 1-aminoindyl-1-carbonyl,  
 CC 2-cyclohexylglycyl, norleucyl, norvalyl, neopentylglycyl, tryptophanyl,  
 CC glycyl, 2,2-dimethylglycyl, alanyl, beta-alanyl or 3-naphthylalanyl; X =  
 CC H, alkyl, cycloalkyl, methylcyclohexyl or arylalkyl; s, t, u = 0 or 1 and  
 CC K = hydroxy, alkoxy, phenoxy, benzoyloxy or amino (optionally  
 CC substituted). The composition is used for treating lung, breast, colon,  
 CC prostate, bladder, rectal, endometrial and haematological cancers e.g.  
 CC leukaemias and lymphomas. The present sequence represents a specific  
 CC example of a heptapeptide disclosed in the specification.  
 XX Sequence 7 AA;

Query Match 50.0%; Score 5; DB 19; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 VVPPP 9  
 DB 1 VVPPP 5

RESULT 43  
 AA008847  
 ID AA008847 standard; peptide; 7 AA.  
 XX AA008847;  
 XX 06-JUL-1999 (first entry)  
 XX Dolastatin-15 derivative for treatment of rheumatoid arthritis.  
 XX Dolastatin; antiarthritic; rheumatoid arthritis.  
 XX Synthetic.

```

XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT Modified-site 3 /note= "N,N-dimethyl-Val"
XX FT Modified-site 3
XX FT Modified-site 7 /note= "N-methyl-Val"
XX FT Modified-site 7 /note= "Phe-NH2"
XX PN WO9917792-A1.
XX PD 15-APR-1999.
XX PF 24-SEP-1998; 98WO-US19841.
XX PR 06-OCT-1997; 97US-0944479.
XX PA (BADI ) BASF AG.
XX PI Banerjee S, Barlozzari T, Haupt A;
XX DR WPI; 1999-277207/23.
XX PT Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,
XX PT alone or in combination with other antiarthritic drugs
XX PS Example 189; Page 52; 106pp; English.
XX CC The invention relates to a method for treating rheumatoid arthritis
XX CC using dolastatin-15 derivatives. The present peptide is a specific
XX CC example of a dolastatin compound which was prepared for use in the
XX CC method.
XX SQ Sequence 7 AA;

Query Match 50.0%; Score 5; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVPPP 9
DB 1 VVPPP 5

RESULT 44
AAW08848
ID AAW08848 standard; peptide; 7 AA.
XX AC AAW08848;
XX DT 06-JUL-1999 (first entry)
XX DE Dolastatin-15 derivative for treatment of rheumatoid arthritis.
XX KW Dolastatin; antiarthritic; rheumatoid arthritis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "N,N-dimethyl-Val"
XX FT Modified-site 3 /note= "N-methyl-Val"
XX FT Modified-site 7 /note= "Phe-NH2"
XX PN WO9917792-A1.
XX PD 15-APR-1999.
XX PF 24-SEP-1998; 98WO-US19841.
XX PR 06-OCT-1997; 97US-0944479.
XX PA (BADI ) BASF AG.
XX PI Banerjee S, Barlozzari T, Haupt A;
XX DR WPI; 1999-277207/23.
XX PT Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,
XX PT alone or in combination with other antiarthritic drugs
XX PS Disclosure; Page 34; 106pp; English.
XX CC The invention relates to a method for treating rheumatoid arthritis
XX CC using dolastatin-15 derivatives. The present peptide is a specific
XX CC example of a dolastatin compound which was prepared for use in the
XX CC method.

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XX PA (BADI ) BASF AG.
XX PI Banerjee S, Barlozzari T, Haupt A;
XX DR WPI; 1999-277207/23.
XX PT Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,
XX PT alone or in combination with other antiarthritic drugs
XX PS Example 190; Page 52; 106pp; English.
XX CC The invention relates to a method for treating rheumatoid arthritis
XX CC using dolastatin-15 derivatives. The present peptide is a specific
XX CC example of a dolastatin compound which was prepared for use in the
XX CC method.
XX SQ Sequence 7 AA;

Query Match 50.0%; Score 5; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVPPP 9
DB 1 VVPPP 5

RESULT 45
AAW08840
ID AAW08840 standard; peptide; 7 AA.
XX AC AAW08840;
XX DT 06-JUL-1999 (first entry)
XX DE Dolastatin-15 derivative for treatment of rheumatoid arthritis.
XX KW Dolastatin; antiarthritic; rheumatoid arthritis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "N,N-dimethyl-Val"
XX FT Modified-site 3 /note= "N-methyl-Val"
XX FT Modified-site 7 /note= "Phe-NH2"
XX PN WO9917792-A1.
XX PD 15-APR-1999.
XX PF 24-SEP-1998; 98WO-US19841.
XX PR 06-OCT-1997; 97US-0944479.
XX PA (BADI ) BASF AG.
XX PI Banerjee S, Barlozzari T, Haupt A;
XX DR WPI; 1999-277207/23.
XX PT Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,
XX PT alone or in combination with other antiarthritic drugs
XX PS Disclosure; Page 34; 106pp; English.
XX CC The invention relates to a method for treating rheumatoid arthritis
XX CC using dolastatin-15 derivatives. The present peptide is a specific
XX CC example of a dolastatin compound which was prepared for use in the
XX CC method.

```

AC	AAW08838;	
XX		
DT	06-JUL-1999 (first entry)	
XX		
DE	Dolastatin-15 derivative for treating rheumatoid arthritis.	
XX		
KW	Dolastatin; antiarthritic; rheumatoid arthritis.	
XX		
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	Modified-site 1	/note= "N,N-dimethyl-Val"
FT	Modified-site 3	/note= "N-methyl-Val"
FT	Modified-site 7	/note= "Phe-NH2"
FT		
XX		
PN	W09917709-A2.	
XX		
PD	15-APR-1999.	
XX		
PF	30-SEP-1998; 98WO-US20465.	
XX		
PR	06-OCT-1997; 97US-0944479.	
XX		
PA	(BADI ) BASF AG.	
XX		
PI	Banerjee S, Barlozzari T, Haupt A;	
XX		
DR	WPI; 1999-277175/23.	
XX		
PT	Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,	
PT	alone or in combination with other antiarthritic drugs	
XX		
PS	Example 189; Page 52; 103pp; English.	
XX		
CC	The invention relates to a method for treating rheumatoid arthritis	
CC	using dolastatin-15 derivatives. The present peptide is a specific	
CC	example of a dolastatin compound which was prepared for use in the	
CC	method.	
XX		
SQ	Sequence 7 AA;	
	Query Match 50.0%; Score 5; DB 20; Length 7;	
	Best Local Similarity 100.0%; Pred.No. 9.3e+05;	
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	5 VVVPP 9	
Db	1 VVVPP 5	
RESULT 48		
AAW08839		
ID	AAW08839 standard; peptide; 7 AA.	
XX		
AC	AAW08839;	
XX		
DT	06-JUL-1999 (first entry)	
XX		
DE	Dolastatin-15 derivative for treating rheumatoid arthritis.	
XX		
KW	Dolastatin; antiarthritic; rheumatoid arthritis.	
XX		
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	Modified-site 1	/note= "N,N-dimethyl-Val"
FT	Modified-site 3	/note= "N-methyl-Val"
FT	Modified-site 7	/note= "Phe-NH2"
FT		

PT /note= "Phe-NH2"  
 XX WO9917709-A2.  
 XX 15-APR-1999.  
 XX 30-SEP-1998; 98WO-US20465.  
 XX 06-OCT-1997; 97US-0944479.  
 XX (BADI ) BASF AG.  
 XX Banerjee S, Barlozzari T, Haupt A;  
 XX WPI; 1999-277175/23.  
 XX Treatment of rheumatoid arthritis using Dolastatin-15 derivatives,  
 PT alone or in combination with other antiarthritic drugs  
 XX Example 190; Page 52; 103pp; English.  
 XX The invention relates to a method for treating rheumatoid arthritis  
 CC using dolastatin-15 derivatives. The present peptide is a specific  
 CC example of a dolastatin compound which was prepared for use in the  
 CC method.  
 XX Sequence 7 AA;  
 SQ Query Match 50.0%; Score 5; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 VVPPP 9  
 Db 1 VVPPP 5

RESULT 49  
 AAG62318  
 ID AAG62318 standard; peptide; 7 AA.  
 XX AC AAG62318;  
 XX 24-AUG-2001 (first entry)  
 XX Casein-related peptide SEQ ID 17.  
 XX Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.  
 XX Synthetic.  
 XX WO200134828-A1.  
 XX 17-MAY-2001.  
 XX 10-NOV-2000; 2000WO-JP07930.  
 XX 11-NOV-1999; 99JP-0321084.  
 XX (CALV ) CALPIS CO LTD.  
 XX Yanamoto N, Ueno K, Ejiri M;  
 XX WPI; 2001-343606/36.  
 XX Production of tripeptides for treating hypertension and stress by  
 PT processing casein with proteinase and peptidase -  
 XX Claim 3; Page 25; 32pp; Japanese.  
 XX This invention relates to a method for the production of tripeptides. The  
 CC method comprises treating material containing milk casein with a  
 CC proteinase to produce intermediate peptide containing ValproPro or

CC IleProPro with no proline residue any where else in the peptide. Use of  
 CC the peptides may result in hypotensive and tranquiliser activity. The  
 CC peptide can be used in treatments to lower blood pressure and in the  
 CC treatment of stress. The present sequence represents an intermediate  
 CC peptide of the invention.  
 XX Sequence 7 AA;  
 SQ Query Match 50.0%; Score 5; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 VVPPP 10  
 Db 1 VVPPP 5

RESULT 50  
 ABJ19910  
 ID ABJ19910 standard; Peptide; 9 AA.  
 XX AC ABJ19910;  
 XX 10-APR-2003 (first entry)  
 XX MHC binding peptide SEQ ID No 75.  
 XX Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;  
 KW antiinflammatory; major histocompatibility complex; MHC;  
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;  
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;  
 KW inflammation; gene therapy; MHC binding peptide.  
 XX Synthetic.  
 OS WO200294981-A2.  
 XX 28-NOV-2002.  
 XX 16-MAY-2002; 2002WO-IL00383.  
 XX 16-MAY-2001; 2001US-290958P.  
 XX 29-MAY-2001; 2001US-0865548.  
 XX (TECR ) TECHNION RES & DEV FOUND LTD.  
 XX Barnea E, Beer I, Ziv T, Admon A, Daseau L, Buchsbaum S;  
 XX WPI; 2003-210043/20.  
 XX Identifying peptides that are capable of binding to major  
 PT histocompatibility complex (MHC) molecules of a particular haplotype by  
 PT analyzing peptides bound to the soluble and secreted form of the MHC  
 PT molecules of the particular haplotype -  
 XX Claim 37; Page 65; 238pp; English.  
 XX The invention relates to a novel method for identifying peptides  
 CC originating from a particular cell type, which are capable of binding to  
 CC major histocompatibility complex (MHC) molecules of a particular  
 CC haplotype. The method comprises analysing peptides bound to the soluble  
 CC and secreted form of the MHC molecules of the particular haplotype. The  
 CC method is useful for identifying peptides for treating an autoimmune  
 CC disease, such as T or B cell and/or allergic disease or condition,  
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,  
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The  
 CC sequences of the invention may be used in a gene therapy application.  
 CC This sequence represents a peptide relating to the method for identifying  
 CC MHC binding peptides of the invention.  
 XX Sequence 9 AA;  
 SQ Query Match 50.0%; Score 5; DB 24; Length 9;



Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVVV 7  
| | | | |  
Db 3 TPVVV 7

RESULT 51  
ABB84044  
ID ABB84044 standard; peptide; 10 AA.  
XX AC ABB84044;  
XX DT 21-AUG-2002 (first entry)  
XX XX Transglutaminase inhibitory peptide cr type #14.  
XX XX Transglutaminase inhibitor; Factor XIII inhibitor; XIIIa inhibitor;  
KW ophthalmological; antiinflammatory; anti-rheumatic; antiarthritic;  
KW thrombolytic; neuroprotective; neurotropic; antiseborrheic; dermatological;  
KW cytosolic; anti-HIV; antipsoriatic; cataract; inflammatory disease;  
KW arthritis; thrombosis; Alzheimer's disease; Huntington's chorea;  
KW acne; cancer; HIV infection; psoriasis.  
XX Unidentified.  
OS XX  
XX WO200236798-A2.  
PN XX  
XX 10-MAY-2002.  
PD XX  
XX 02-NOV-2001; 2001WO-EP12727.  
XX PF  
XX 03-NOV-2000; 2000DE-1054687.  
XX PR  
XX (NZYM-) N ZYME BIOTEC GMBH.  
PA XX  
XX Fuchsbauser H, Pasternack R, Zotzel J;  
PI WPI; 2002-444364/47.  
XX DR  
XX New amino acid or peptide derivatives or analogs, are selective  
PT transglutaminase inhibitors useful e.g. for treating cataract,  
PT inflammatory diseases, rheumatoid arthritis, thrombosis, Alzheimer's  
PT disease and cancer  
XX XX  
PS Disclosure; Page 13; 44pp; German.  
XX XX  
XX This invention describes novel amino acid or peptide derivatives or  
CC analogues (I), containing a modified side-chain (e.g. containing a formyl  
CC group) which are transglutaminase inhibitors and Factor XIII/XIIIa  
CC inhibitors. The products of the invention have ophthalmological,  
CC antiinflammatory, antirheumatic, antiarthritic, thrombolytic,  
CC neuroprotective, neurotropic, antiseborrheic, dermatological, cytosolic,  
CC anti-HIV and antipsoriatic activity. (I) are transglutaminase inhibitors,  
CC especially inhibitors of crosslinking of proteins or peptides  
CC (specifically fibrin and/or alpha 2-plasmin inhibitor), incorporation of  
CC primary amines in proteins and peptides, hydrolysis of the  
CC gamma-carboxamide group of glutamine residues bound in proteins or  
CC peptides, blood factor XIII/XIIIa and mammalian, human, tissue, liver,  
CC brain, eye lens, keratinocyte, epidermal, prostate, plant, parasitic  
CC and/or bacterial transglutaminases. The products of the invention can be  
CC used for treating cataract, inflammatory diseases, rheumatoid arthritis,  
CC chronic arthritis, thrombosis, Alzheimer's disease, Huntington's chorea,  
CC acne, cancer (by induction of apoptosis), HIV infections and psoriasis.  
CC (I) Are targeted and specific transglutaminase inhibitors, which can  
CC inhibit a specific type of transglutaminase in the human or animal body  
CC without affecting other transglutaminases. ABB84001-ABB84049 represent  
CC transglutaminase inhibitors described in the method of the invention.  
XX XX  
SQ Sequence 10 AA;

Query Match 50.0%; Score 5; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TPVVV 7  
| | | | |  
Db 1 TPVVV 5

RESULT 52  
AAM97801  
ID AAM97801 standard; Peptide; 14 AA.  
XX AC AAM97801;  
XX DT 24-JAN-2002 (first entry)  
XX XX Human peptide #1076 encoded by a SNP oligonucleotide.  
XX DE  
XX XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease.  
XX XX  
OS Homo sapiens.  
XX XX  
PN WO200147944-A2.  
XX XX  
XX 05-JUL-2001.  
XX PD  
XX 28-DEC-2000; 2000WO-US35498.  
XX PF  
XX 28-DEC-1999; 99US-0173419.  
PR 27-DEC-2000; 2000US-0173419.  
XX PR  
XX (CURA-) CURAGEN CORP.  
XX PA  
XX Shimketa RA, Leach M;  
PI WPI; 2001-465210/50.  
XX DR  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX XX  
PS Disclosure; Page 3903; 4143pp; English.  
XX XX  
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
CC encoding polymorphic variants of proteins related to amylases, amyloid  
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
CC complement related proteins, cytochromes, kinesins, cytokines,  
CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
CC The present sequence is a peptide encoded by one such oligonucleotide.  
CC The oligonucleotides and the peptides encoded by them may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the proteins listed above. Disorders that may  
CC be prevented, diagnosed and/or treated include multifactorial diseases  
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
CC system and an infection of pathogenic organisms.  
XX XX  
SQ Sequence 14 AA;

Query Match 50.0%; Score 5; DB 22; Length 14;

Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      5 VVVP 9
      |||||
Db      5 VVVP 9

RESULT 53
AAB00054
ID AAB00054 standard; peptide; 15 AA.
XX
AC AAB00054;
XX
XX 08-NOV-2000 (first entry)
XX
DE Angiostatin peptide fragment.
XX
KW Angiostatin; plasminogen; kringle domain; angiogenesis; inhibition;
KW arthritis; macular degeneration; diabetic retinopathy.
XX
OS Mus musculus.
XX
PN WO200004391-A2.
XX
XX 03-AUG-2000.
XX
XX 26-JAN-2000; 2000WO-US02091.
XX
XX 28-JAN-1999; 99US-0117617.
XX
PR 09-AUG-1999; 99US-0370719.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Shing YW, O'reilly MS, Folkman MJ;
XX
XX WPI; 2000-505907/45.
XX
XX Inhibiting angiogenesis for the treatment of cancers, arthritis,
XX macular degeneration and diabetic retinopathy by administering a
XX Kringle 4 region fragment derived from human plasminogen
XX
XX Example 1; Fig 5; 44pp; English.
XX
XX Angiostatin is a protein which has significant homology with a
XX fragment of murine plasminogen beginning at amino acid 98 of the
XX intact murine plasminogen molecule. Angiostatin comprises kringle
XX regions 1 to 4 of a plasminogen molecule. Angiogenesis can be
XX inhibited in an individual by administering a Kringle 4 region
XX cell inhibitor and reversibly inhibits the proliferation of these
XX cells. The mechanism by which the protein inhibits endothelial cell
XX growth remains uncharacterized. The method may be used to treat
XX diseases and disorders characterized by angiogenesis such as
XX arthritis, macular degeneration and/or diabetic retinopathy.
XX Three variants of the kringle 4 domain were found in murine
XX angiostatin due to variable cleavage sites between the kringle 3
XX and kringle 4 domains. See GENESEQ records AAB00054-B00057. This
XX sequence corresponds to amino acids 370-384 of angiostatin.
XX
SQ      Sequence 15 AA;
      Query Match 50.0%; Score 5; DB 21; Length 15;
      Best Local Similarity 100.0%; Pred. No. 90;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QTPV 6
      |||||
Db      1 QTPV 5

RESULT 54
AAY84247
ID AAY84247 standard; peptide; 16 AA.
XX
XX AAY84247;
AC

```

```

XX      12-JUL-2000 (first entry)
XX
XX Consensus site for MAPK phosphorylation.
DE
XX
XX Antibody; MAPK phosphorylation; combinatorial peptide library;
KW enzyme substrate; drug screen; enzymatic modification;
KW protein phosphorylation.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 10
FT /note= "phosphothreonine"
XX
XX WO2000014536-A1.
XX
XX 16-MAR-2000.
XX
XX 26-AUG-1999; 99WO-US19597.
XX
XX 04-SEP-1998; 98US-0148712.
XX
XX (NEW ) NEW ENGLAND BIOLABS INC.
XX
XX Tan Y, Comb MJ;
XX
XX WPI; 2000-257066/22.
XX
XX Novel methods for the production of motif-specific, context-independent
XX antibodies using peptide libraries as antigens -
XX
XX Example 2; Fig 2A; 75pp; English.
XX
XX The present sequence represents a consensus site for MAPK
XX phosphorylation. The peptide was used to produce polyclonal antibodies
XX using the method of the invention. The specification describes methods
XX for the production of antibodies that selectively recognize short amino
XX acid motifs independent of the surrounding sequences. The method
XX comprises constructing a combinatorial peptide library comprising at
XX least one fixed amino acid and variable surrounding amino acids, and
XX immunizing a host with the peptide library. The methods allows the
XX production of antibodies that recognize single amino acids and motifs,
XX e.g. phosphorylated serine, threonine and tyrosine, or acetylated lysine,
XX as well as other unmodified or modified amino acids. The antibodies may
XX be used to identify an unknown substrate of an enzymes, e.g. to detect
XX new substrates in a variety of cascades which involve conserved
XX substrate motifs. The antibodies may also be used to identify an enzyme
XX which modifies a known substrate, e.g. to detect new proteins which act
XX on known classes of substrates. The antibodies may also be used in vitro
XX as reagents in high-throughput assays, e.g. drug screens, to detect the
XX enzymatic modification of certain substrates containing a conserved
XX motif. The antibodies may also be used for genome-wide profiling of
XX changes in protein phosphorylation e.g. as a result of drug treatment.
XX They may also be used to detect protein kinase or acetyltransferase
XX activity.
XX
SQ      Sequence 16 AA;
      Query Match 50.0%; Score 5; DB 21; Length 16;
      Best Local Similarity 100.0%; Pred. No. 95;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TPVV 7
      |||||
Db      10 TPVV 14

RESULT 55
ABU64607
ID ABU64607 standard; Peptide; 16 AA.
XX
XX ABU64607;
AC

```

```

XX 13-MAY-2003 (first entry)
XX Motif-specific and context-independent antibody peptide antigen #30.
XX
XX Motif-specific antibody; context-independent antibody.
XX enzyme substrate identification; modification state detection;
XX enzyme inhibition; enzyme activation; protein level profile;
XX post-translation modification; phosphothreonine; phosphoserine;
XX phosphotyrosine; acetyl-lysine; nitrotyrosine;
XX kinase consensus substrate motif; protein binding motif.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX US2002168684-A1.
XX
XX 14-NOV-2002.
XX
XX 13-NOV-2001; 2001US-0014485.
XX
XX 04-SEP-1998; 98US-0148712.
XX 24-MAR-2000; 2000US-0535364.
XX
XX (COMB/) COMB M J.
XX (TANY/) TAN Y.
XX (ZHAN/) ZHANG H.
XX
XX Comb MJ, Tan Y, Zhang H;
XX
XX WPI; 2003-298726/29.
XX
XX Producing motif-specific, context-independent antibody recognizing
XX motif-containing proteins, using a degenerate peptide library having
XX target motifs with invariant amino acids flanked by degenerate amino
XX acids, as antigens -
XX
XX Example 2; Fig 2A; 86pp; English.
XX
XX The invention describes a method of producing a motif-specific,
XX context-independent antibody (I) that recognises several peptides or
XX proteins within the genome that contain motifs. The method is useful
XX for: (1) identifying an unknown substrate of an enzyme, which involves
XX generating at least one (I) which recognizes a motif common to several
XX substrate of the enzyme with a genome; (2) detecting the modification
XX state of a target substrate that contains a motif common to several
XX substrates of an enzyme within a genome; (3) screening a drug for the
XX inhibition or activation of enzyme activity on at least one substrate
XX that contains a motif common to several substrates of the enzyme within
XX a genome; (4) identifying an enzyme which modifies a known substrate
XX that contains a motif common to several substrates of the enzyme within
XX a genome; (5) profiling protein levels or post-translation modifications
XX in a cell or tissue on a genome wide scale; (6) profiling drug-induced
XX changes in protein levels or post-translation modifications in a cell or
XX tissue on a genome wide scale. The motif is selected from single
XX phosphothreonine, a single phosphoserine, a single phosphotyrosine, a
XX single acetyl-lysine, and a single nitrotyrosine, and comprises all or
XX part of kinase consensus substrate motif or a protein binding motif.
XX This is the amino acid sequence of a peptide used in the creation of
XX a motif-specific, context-independent antibody.
XX
XX Sequence 16 AA;
XX
XX Query Match 50.0%; Score 5; DB 24; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 95;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 3 TPVVV 7
XX |||||
XX Db 10 TPVVV 14
XX
XX RESULT 56

```

```

AAR48289
XX ID AAR48289 standard; peptide; 4 AA.
XX AC AAR48289;
XX
XX 25-MAR-2003 (updated)
XX 08-JUL-1994 (first entry)
XX
XX ACE inhibitor peptide.
XX
XX ACE inhibitor; angiotensin converting enzyme inhibitor; hypotensive;
XX hypertension; high blood pressure; lactic acid bacterium; yeast.
XX
XX Synthetic.
XX
XX EP583074-A2.
XX
XX 16-FEB-1994.
XX
XX 14-JUL-1993; 93EP-0305507.
XX
XX 23-JUL-1992; 92JP-0197239.
XX
XX (CALV ) CALPIS FOOD IND CO LTD.
XX (CALV ) CALPIS SHOKUHIN KOGYO KK.
XX
XX Nakamura Y, Takano T;
XX
XX WPI; 1994-050387/07.
XX
XX New angiotensin converting enzyme inhibitor peptide(s) - contg.
XX 3-10 amino acids and the amino acid residue sequence
XX Valine-Proline-Proline
XX
XX Example 3; Page 7; 8pp; English.
XX
XX ACE inhibitors having the sequences given in AAR48287-95 are prepared
XX by solid phase synthesis or by fermentation of e.g. milk, casein,
XX corn, wheat or soybean products using lactic acid bacteria or yeast.
XX They exhibit high safety and effective hypotensive activity when
XX administered orally at low doses.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 4 AA;
XX
XX Query Match 40.0%; Score 4; DB 15; Length 4;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 6 WVPP 9
XX |||||
XX Db 1 WVPP 4
XX
XX RESULT 57
XX AAW93980
XX ID AAW93980 standard; peptide; 4 AA.
XX AC AAW93980;
XX
XX 01-JUL-1999 (first entry)
XX
XX Antineoplastic peptide 1.
XX
XX Tetrapeptide; tumour; dolastatin; antineoplastic activity; lung; breast;
XX intestine; bladder; rectum; uterus; prostate; leukaemia; lymphoma;
XX neoplastic disease.
XX
XX Synthetic.
XX
XX Key Modified-site 1 Location/Qualifiers
XX FT /note= "Residue can be Val or Me2-Val"
XX

```

FT Modified-site 3 /note= "Residue can be Val or Me-Val"  
 FT Modified-site 4  
 FT /note= "Pro residue can be modified with OMe, OEt  
 FT or a cyclopentamide group"  
 XX DE4415998-A1.  
 XX  
 XX 09-NOV-1995.  
 XX  
 XX 06-MAY-1994; 94DE-4415998.  
 XX  
 XX 06-MAY-1994; 94DE-4415998.  
 XX  
 XX (BADI ) BASF AG.  
 XX  
 XX Amberg W, Bernard H, Buschmann E, De Potzoll B;  
 PI Haupt A, Janitschke L, Janssen B, Karl U, Kling A;  
 PI Mueller S, Ritter K, Thyse M, Zierke T;  
 XX WPI; 1995-393582/51.  
 XX  
 XX Prepn. of proline contg. tetra:peptide derivs. - comprises  
 PT condensing tri:peptide with protected amino acid, deprotection, and  
 PT N-di:methylation, useful as e.g. intermediates for dolastatin  
 XX  
 XX Example 1; Page 4; 8pp; German.  
 XX  
 XX This invention describes a method for the production of tetrapeptides  
 CC which comprises reacting a tripeptide with an amino acid, removing Z and  
 CC methylating the free amino group twice. R1-R4 = 1-6C alkyl; and Z =  
 CC optional ring substituted benzyloxycarbonyl. The products of the  
 CC invention are intermediates for dolastatin 15 which have high  
 CC antineoplastic activity. The peptides of the invention are active against  
 CC solid tumours (of lung, breast, intestine, bladder, rectum, uterus and  
 CC prostate), leukaemia, lymphoma and other neoplastic diseases. The  
 CC peptides can now be produced from material available in large quantities,  
 CC without racemisation and without requiring very expensive or hazardous  
 CC reagents.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 40.0%; Score 4; DB 16; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 VVVP 8  
 Db 1 VVVP 4  
 RESULT 58  
 ID AAR88264  
 XX AAR88264 standard; peptide; 4 AA.  
 XX  
 XX AAR88264;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 13-JUN-1996 (first entry)  
 DE Intermediate X for prepn. of Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl.  
 XX  
 XX Anti-neoplastic agent; solid tumour; leukaemia; lymphoma; treatment;  
 KW crystalline; non-racemic; intermediate; benzylamide hydrochloride salt.  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note= "protected Z-Val, where Z is benzyloxy-  
 FT carbonyl, opt. ring substd."  
 FT Modified-site 3  
 FT /label= OTHER

FT Modified-site /note= "MeVal"  
 FT 4  
 FT /note= "Pro-O-CO-R2, where R2 is tert.butyl,  
 FT 2-ethylhexyl or 1-4C alkoxy"  
 XX DE4415997-A1.  
 XX  
 XX 09-NOV-1995.  
 XX  
 XX 06-MAY-1994; 94DE-4415997.  
 XX  
 XX 06-MAY-1994; 94DE-4415997.  
 XX  
 XX (BADI ) BASF AG.  
 XX  
 XX Amberg W, Bernard H, Buschmann E, Haupt A, Janitschke L;  
 PI Janssen B, Karl U, Kling A, Mueller S, Potzoll B, Ritter K;  
 PI Zierke T, Thyse M;  
 XX WPI; 1995-393581/51.  
 XX  
 XX Benzyl:amide hydrochloride salt of anti:neoplastic penta:peptide -  
 PT can be produced without racemisation and in easily crystallisable  
 PT form  
 XX  
 XX Claim 5; Page 8; 8pp; German.  
 XX  
 XX The salt Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl is prepared by one of  
 CC the following methods:  
 CC (1). claimed intermediate II (AAR88260) is deprotected by removal of Z  
 CC to give claimed intermediate III (AAR88261) which is methylated twice  
 CC and the product is hydrolysed to give intermediate (V) (AAR88266).  
 CC This cpd. is pref. converted to the claimed mixed anhydride VII  
 CC (AAR88262) before reaction with proline benzylamide and conversion to  
 CC the hydrochloride salt; or  
 CC (2). intermediate II is hydrolysed to claimed intermediate IX  
 CC (AAR88263), which is pref. converted to the claimed mixed anhydride  
 CC X (AAR88264) before reaction with proline benzylamide; then Z is  
 CC removed, N-methyl introduced as above and product converted to  
 CC hydrochloride. The free base form of the pentapeptide is known as an  
 CC anti-neoplastic agent suitable for treatment of solid tumours, leukaemia,  
 CC lymphoma and other neoplastic diseases. The benzylamide hydrochloride  
 CC salt is easily crystallisable and can be produced in high yield without  
 CC racemisation or the use of expensive or dangerous reagents.  
 CC The present sequence is that of intermediate X.  
 CC (Updated on 25-MAR-2003 to correct FI field.)  
 XX  
 SQ Sequence 4 AA;  
 Query Match 40.0%; Score 4; DB 16; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 VVVP 8  
 Db 1 VVVP 4  
 RESULT 59  
 ID AAR88266  
 XX AAR88266 standard; peptide; 4 AA.  
 XX  
 XX AAR88266;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 13-JUN-1996 (first entry)  
 DE Intermediate V for prepn. of Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl.  
 XX  
 XX Anti-neoplastic agent; solid tumour; leukaemia; lymphoma; treatment;  
 KW crystalline; non-racemic; intermediate; benzylamide hydrochloride salt.  
 XX Synthetic.  
 OS

```

XX PH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "Me2Val"
FT Modified-site 3
FT /label= OTHER
FT /note= "MeVal"
XX DE4415997-A1.
XX 09-NOV-1995.
XX 06-MAY-1994; 94DE-4415997.
XX 06-MAY-1994; 94DE-4415997.
XX (BADI ) BASF AG.
XX Amberg W, Bernard H, Buschmann E, Haupt A, Janitschke L;
PI Janssen B, Karl U, Kling A, Mueller S, Potzolli B, Ritter K;
PI Zierke T, Thyse M;
XX WPI; 1995-393581/51.
XX Benzyl:amide hydrochloride salt of anti:neoplastic penta:peptide -
PT can be produced without racemisation and in easily crystallisable
PT form
XX Claim 3; Page 8; 8pp; German.
XX The salt Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl is prepared by one of
CC the following methods:
CC (1). Claimed intermediate II (AAR88260) is deprotected by removal of Z
CC to give claimed intermediate III (AAR88261) which is methylated twice
CC and the product is hydrolysed to give intermediate (V) (AAR88266).
CC This cpd. is pref. converted to the claimed mixed anhydride VII
CC (AAR88262) before reaction with proline benzylamide and conversion to
CC the hydrochloride salt; or
CC (2). intermediate II is hydrolysed to claimed intermediate IX
CC (AAR88263), which is pref. converted to the claimed mixed anhydride
CC X (AAR88264) before reaction with proline benzylamide; then Z is
CC removed, N-methyl introduced as above and product converted to
CC hydrochloride. The free base form of the pentapeptide is known as an
CC anti-neoplastic agent suitable for treatment of solid tumours, leukaemia,
CC lymphoma and other neoplastic diseases. The benzylamide hydrochloride
CC salt is easily crystallisable and can be produced in high yield without
CC racemisation or the use of expensive or dangerous reagents.
CC The present sequence is that of intermediate V; this is the only
CC intermediate which is not claimed per se.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 4 AA;
Query Match 40.0%; Score 4; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 VVVP 8
DB 1 VVVP 4
RESULT 60
AAR88260
ID AAR88260 standard; peptide; 4 AA.
XX AC AAR88260;
XX 25-MAR-2003 (updated)
DT 13-JUN-1996 (first entry)
XX DE Intermediate II for prepn. of Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl.

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XX Anti-neoplastic agent; solid tumour; leukaemia; lymphoma; treatment;
KW crystalline; non-racemic; intermediate; benzylamide hydrochloride salt.
XX Synthetic.
XX Key Location/Qualifiers
FT Modified-site 1
FT /note= "protected Z-Val, where Z is benzyloxy/-
FT carbonyl, opt. ring subst."
FT Modified-site 3
FT /label= OTHER
FT /note= "MeVal"
FT Modified-site 4
FT /note= "Pro-OR1, where R1 is 1-5C alkyl"
XX DE4415997-A1.
XX 09-NOV-1995.
XX 06-MAY-1994; 94DE-4415997.
XX 06-MAY-1994; 94DE-4415997.
XX (BADI ) BASF AG.
XX Amberg W, Bernard H, Buschmann E, Haupt A, Janitschke L;
PI Janssen B, Karl U, Kling A, Mueller S, Potzolli B, Ritter K;
PI Zierke T, Thyse M;
XX WPI; 1995-393581/51.
XX Benzyl:amide hydrochloride salt of anti:neoplastic penta:peptide -
PT can be produced without racemisation and in easily crystallisable
PT form
XX Claim 5; Page 8; 8pp; German.
XX The salt Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl is prepared by one of
CC the following methods:
CC (1). Claimed intermediate II (AAR88260) is deprotected by removal of Z
CC to give claimed intermediate III (AAR88261) which is methylated twice
CC and the product is hydrolysed to give intermediate (V) (AAR88266).
CC This cpd. is pref. converted to the claimed mixed anhydride VII
CC (AAR88262) before reaction with proline benzylamide and conversion to
CC the hydrochloride salt; or
CC (2). intermediate II is hydrolysed to claimed intermediate IX
CC (AAR88263), which is pref. converted to the claimed mixed anhydride
CC X (AAR88264) before reaction with proline benzylamide; then Z is
CC removed, N-methyl introduced as above and product converted to
CC hydrochloride. The free base form of the pentapeptide is known as an
CC anti-neoplastic agent suitable for treatment of solid tumours, leukaemia,
CC lymphoma and other neoplastic diseases. The benzylamide hydrochloride
CC salt is easily crystallisable and can be produced in high yield without
CC racemisation or the use of expensive or dangerous reagents.
CC The present sequence is that of intermediate II.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 4 AA;
Query Match 40.0%; Score 4; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 VVVP 8
DB 1 VVVP 4
RESULT 61
AAR88261
ID AAR88261 standard; peptide; 4 AA.
XX

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AC AAR88261;
XX
XX
XX 25-MAR-2003 (updated)
DT 13-JUN-1996 (first entry)
DE
DE Intermediate III for prepn. of Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl.
XX
XX Anti-neoplastic agent; solid tumour; leukaemia; lymphoma; treatment;
KW crystalline; non-racemic; intermediate; benzylamide hydrochloride salt.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 3 /label= OTHER
FT /note= "MeVal"
FT Modified-site 4
FT /note= "Pro-OR1, where R1 is 1-5C alkyl"
XX
XX DE4415997-A1.
XX
XX 09-NOV-1995.
XX
XX 06-MAY-1994; 94DE-4415997.
XX
XX 06-MAY-1994; 94DE-4415997.
XX
XX (BADI ) BASF AG.
XX
XX Amberg W, Bernard H, Buschmann E, Haupt A, Janitschke L;
PI Janssen B, Karl U, Kling A, Mueller S, Potzolli B, Ritter K;
PI Zierke T, Thyges M;
XX
XX WPI; 1995-393581/51.
XX
XX Benzyl:amide hydrochloride salt of anti-neoplastic penta:peptide -
PT can be produced without racemisation and in easily crystallisable
PT form
XX
XX Claim 5; Page 8; 8pp; German.
XX
XX The salt Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl is prepared by one of
XX the following methods:
XX (1). claimed intermediate II (AAR88260) is deprotected by removal of Z
XX to give claimed intermediate III (AAR88261) which is methylated twice
XX and the product is hydrolysed to give intermediate (V) (AAR88266).
XX This cpd. is pref. converted to the claimed mixed anhydride VII
XX (AAR88262) before reaction with proline benzylamide and conversion to
XX the hydrochloride salt; or
XX (2). intermediate II is hydrolysed to claimed intermediate IX
XX (AAR88263), which is pref. converted to the claimed mixed anhydride
XX X (AAR88264) before reaction with proline benzylamide; then Z is
XX removed, N-methyl introduced as above and product converted to
XX hydrochloride. The free base form of the pentapeptide is known as an
XX anti-neoplastic agent suitable for treatment of solid tumours, leukaemia,
XX lymphoma and other neoplastic diseases. The benzylamide hydrochloride
XX salt is easily crystallisable and can be produced in high yield without
XX racemisation or the use of expensive or dangerous reagents.
XX The present sequence is that of intermediate III.
XX (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 4 AA;
XX
XX Query Match 40.0%; Score 4; DB 16; Length 4;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 5 VVVP 8
XX ||||
XX 1 VVVP 4
XX
XX RESULT 62

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AAR88262
ID AAR88262 standard; peptide; 4 AA.
XX
XX AAR88262;
XX
XX 25-MAR-2003 (updated)
DT 13-JUN-1996 (first entry)
DE
DE Intermediate VII for prepn. of Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl.
XX
XX Anti-neoplastic agent; solid tumour; leukaemia; lymphoma; treatment;
KW crystalline; non-racemic; intermediate; benzylamide hydrochloride salt.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /label= OTHER
FT /note= "Me2Val"
FT Modified-site 3 /label= OTHER
FT Modified-site 4 /note= "MeVal"
FT Modified-site 4 /note= "Pro-O-CO-R2, where R2 is tert.butyl,
FT 2-ethylhexyl or 1-4C alkoxy"
XX
XX DE4415997-A1.
XX
XX 09-NOV-1995.
XX
XX 06-MAY-1994; 94DE-4415997.
XX
XX 06-MAY-1994; 94DE-4415997.
XX
XX (BADI ) BASF AG.
XX
XX Amberg W, Bernard H, Buschmann E, Haupt A, Janitschke L;
PI Janssen B, Karl U, Kling A, Mueller S, Potzolli B, Ritter K;
PI Zierke T, Thyges M;
XX
XX WPI; 1995-393581/51.
XX
XX Benzyl:amide hydrochloride salt of anti-neoplastic penta:peptide -
PT can be produced without racemisation and in easily crystallisable
PT form
XX
XX Claim 5; Page 8; 8pp; German.
XX
XX The salt Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl is prepared by one of
XX the following methods:
XX (1). claimed intermediate II (AAR88260) is deprotected by removal of Z
XX to give claimed intermediate III (AAR88261) which is methylated twice
XX and the product is hydrolysed to give intermediate (V) (AAR88266).
XX This cpd. is pref. converted to the claimed mixed anhydride VII
XX (AAR88262) before reaction with proline benzylamide and conversion to
XX the hydrochloride salt; or
XX (2). intermediate II is hydrolysed to claimed intermediate IX
XX (AAR88263), which is pref. converted to the claimed mixed anhydride
XX X (AAR88264) before reaction with proline benzylamide; then Z is
XX removed, N-methyl introduced as above and product converted to
XX hydrochloride. The free base form of the pentapeptide is known as an
XX anti-neoplastic agent suitable for treatment of solid tumours, leukaemia,
XX lymphoma and other neoplastic diseases. The benzylamide hydrochloride
XX salt is easily crystallisable and can be produced in high yield without
XX racemisation or the use of expensive or dangerous reagents.
XX The present sequence is that of intermediate VII.
XX (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 4 AA;
XX
XX Query Match 40.0%; Score 4; DB 16; Length 4;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 VVVP 8  
 ||||  
 Db 1 VVVP 4

RESULT 63  
 AAR88263  
 ID AAR88263 standard; peptide; 4 AA.  
 AC AAR88263;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 13-JUN-1996 (first entry)  
 XX  
 DE Intermediate IX for prepn. of Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl.  
 XX  
 KW Anti-neoplastic agent; solid tumour; leukaemia; lymphoma; treatment;  
 KW crystalline; non-racemic; intermediate; benzylamide hydrochloride salt.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "protected Z-Val, where Z is benzyloxy-  
 FT carbonyl, opt. ring substd."  
 FT Modified-site 3 /label= OTHER  
 FT /note= "MeVal"  
 FT  
 XX DE4415997-Al.  
 XX  
 XX 09-NOV-1995.  
 XX  
 XX 06-MAY-1994; 94DE-4415997.  
 XX  
 XX 06-MAY-1994; 94DE-4415997.  
 XX  
 XX (BADI ) BASF AG.  
 XX  
 XX Amberg W, Bernard H, Buschmann E, Haupt A, Janitschke L;  
 PI Janssen B, Karl U, Kling A, Mueller S, Potzoll B, Ritter K;  
 PI Zierke T, Thyse M;  
 XX  
 XX WPI; 1995-393581/51.  
 DR  
 XX Benzylamide hydrochloride salt of anti-neoplastic penta-peptide -  
 PT can be produced without racemisation and in easily crystallisable  
 PT form  
 PS  
 PS Claim 5; Page 8; 8pp; German.  
 XX  
 XX The salt Me2Val-Val-MeVal-Pro-Pro-NHbenzyl.HCl is prepared by one of  
 CC the following methods:  
 CC (1). Claimed intermediate II (AAR88260) is deprotected by removal of Z  
 CC to give claimed intermediate III (AAR88261) which is methylated twice  
 CC and the product is hydrolysed to give intermediate (V) (AAR88266).  
 CC This cpd. is pref. converted to the claimed mixed anhydride VII  
 CC (AAR88262) before reaction with proline benzylamide and conversion to  
 CC the hydrochloride salt; or  
 CC (2). Intermediate II is hydrolysed to claimed intermediate IX  
 CC (AAR88263), which is pref. converted to the claimed mixed anhydride  
 CC X (AAR88264) before reaction with proline benzylamide; then Z is  
 CC removed, N-methyl introduced as above and product converted to  
 CC hydrochloride. The free base form of the pentapeptide is known as an  
 CC anti-neoplastic agent suitable for treatment of solid tumours, leukaemia,  
 CC lymphoma and other neoplastic diseases. The benzylamide hydrochloride  
 CC salt is easily crystallisable and can be produced in high yield without  
 CC racemisation or the use of expensive or dangerous reagents.  
 CC The present sequence is that of intermediate IX.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 4 AA;

Query Match 40.0%; Score 4; DB 16; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVVP 8  
 ||||  
 Db 1 VVVP 4

RESULT 64  
 AAW66735  
 ID AAW66735 standard; peptide; 4 AA.  
 XX  
 AC AAW66735;  
 XX  
 DT 02-DEC-1998 (first entry)  
 XX  
 DE Dolastatin-15 derivative in composition for treatment of cancer.  
 DE  
 KW dolastatin-15; cancer; paclitaxel; taxane; taxoid; taxotere.  
 XX  
 OS Synthetic.  
 OS Dolabella auricularia.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "N,N-dimethyl-Val"  
 FT Modified-site 3 /label= MeVal  
 FT /note= "N-methyl-valine"  
 FT Modified-site 4 /note= "Pro-[1-(thiazol-(2)-yl)-2-phenyl]-ethylamide"  
 FT  
 XX  
 XX WO9840092-Al.  
 PN  
 XX 17-SEP-1998.  
 PD  
 XX 09-MAR-1998; 98WO-US04594.  
 PF  
 XX 13-MAR-1997; 97US-0819101.  
 PR  
 XX (BADI ) BASF AG.  
 PA (BADI ) BASF BIORESEARCH CORP.  
 XX  
 XX Barlozzari T, Haupt A;  
 PI  
 XX WPI; 1998-520790/44.  
 DR  
 XX Composition used for treating cancer - comprises paclitaxel,  
 PT taxotere or modified taxane or taxoid analogs and tetra- to hepta-  
 PT peptide(s)  
 XX  
 XX Example 2A; Page 37; 114pp; English.  
 PS  
 XX The invention relates to a composition for the treatment of cancer. The  
 CC composition comprises: (a) paclitaxel, taxotere or modified taxane or  
 CC taxoid analogs; (b) tetra- to hepta- peptides of formula  
 CC R1R2N-CHX-CO-A-B-D-(E)-S-(Ft)-(G)U-K (I) or their salts and optionally (c)  
 CC a carrier. R1 = alkyl, cycloalkyl, alkylsulphonyl, fluoroalkyl or  
 CC aminoalkyl; R2 = H, alkyl, fluoroalkyl, or cycloalkyl or NR1R2 =  
 CC pyrrolidino or piperidino; A = valyl, isoleucyl, leucyl, alloisoleucyl,  
 CC 2,4-dimethylglycyl, 2-cyclopropylglycyl, 2-cyclopentylglycyl,  
 CC 3-tert-butylalanyl, 2-tert-butylglycyl, 3-cyclohexylalanyl,  
 CC 2-ethylglycyl, 2-cyclohexylglycyl, norleucyl or norvalyl; B = an N-alkyl  
 CC derivative of A except alloisoleucyl or cyclohexylalanyl; D, E = prolyl,  
 CC homoprolyl, hydroxyprolyl, 3,4-dehydroprolyl, 4-fluoroprolyl, 3-, 4- or  
 CC 5-methylprolyl, azetidine-2-carbonyl, 3,3-dimethylprolyl,  
 CC 4,4-difluoroprolyl, oxazolidine-4-carbonyl, or thiazolidine-4-carbonyl;  
 CC F, G = prolyl, homoprolyl, hydroxyprolyl, thiazolidine-4-carbonyl,  
 CC 1-aminopentyl-1-carbonyl, valyl, 2-tert-butylglycyl, isoleucyl, leucyl,  
 CC 3-cyclohexylalanyl, phenylalanyl, N-methyl-phenylalanyl, 3-pyridylalanyl,  
 CC tetrahydroisoquinolyl-2-histidyl, 1-aminoindolyl-1-carbonyl,

CC 2-cyclohexylglycyl, norleucyl, norvalyl, neopentylglycyl, tryptophanyl,  
 CC glycyl, 2,2-dimethylglycyl, alanyl, beta-alanyl or 3-naphthylalanyl; X =  
 CC H, alkyl, cycloalkyl, methoxycyclohexyl or arylalkyl; S, t, u = 0 or 1 and  
 CC K = hydroxy, alkoxy, phenoxy, benzyloxy or amino (optionally  
 CC substituted). The composition is used for treating lung, breast, colon,  
 CC prostate, bladder, rectal, endometrial and haematological cancers e.g.  
 CC leukaemias and lymphomas. The present sequence represents a specific  
 CC example of a tetrapeptide disclosed in the specification.

XX Sequence 4 AA;  
 SQ Query Match 40.0%; Score 4; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VVVP 8  
 DB 1 VVVP 4

RESULT 65  
 AAWE6566  
 ID AAWE6566 standard; peptide; 4 AA.

AC AAWE6566;

XX 30-NOV-1998 (first entry)

XX Peptide useful as anti-cancer agent.

XX Dolastatin; anti-cancer agent; solid tumour; lymphoma; leukemia;  
 KW haematological malignancy.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "Me2Val"  
 FT Modified-site 3 /label= MeVal  
 FT Modified-site 4 /note= "Pro-2-benzoylpyrrolidine amide"  
 FT WO9840400-A1.

XX 17-SEP-1998.

XX 05-MAR-1998; 98WO-US04317.

XX 10-MAR-1997; 97US-0814577.

XX (BADI ) BASF AG.

XX (BADI ) BASF BIORESEARCH CORP.

XX Amberg W, Barlozzari T, Haupt A, Janssen B, Kling A;  
 PI Ritter K;

XX WPI; 1998-520799/44.

XX New peptide(s) are anti-cancer agents - useful in treatment of solid  
 PT tumours and haematological malignancies

XX Example 4; Page 47; 110pp; English.

XX The present invention relates to peptides of formula A-B-D-E-F-G.  
 CC A, B, D, E = amino acid residue; F = azacycloalkane carboxylic acid  
 CC residue; G = H, alkyl, aryl, cycloalkyl, cycloalkylalkyl, aminocarboxyl-  
 CC alkyl, arylalkyl, alkoxy-carboxylalkyl, aryloxy-carboxylalkyl, alkyl-  
 CC sulphonylalkyl, alkylsulphonylalkyl, arylsulphonylalkyl, arylsulphonyl-  
 CC alkyl, alkyl- or aryl-sulphonyl or alkyl- or aryl-sulphonyl; or F =  
 CC azacycloalkyl and G = heteroaryl. The compounds are useful in the  
 CC treatment of solid tumours (e.g. of the lung, breast, colon, prostate,  
 CC bladder, or rectum or endometrial tumours) or haematological malignancies

CC (e.g. leukaemias or lymphomas). The present sequence represents an  
 CC example of an anti-cancer agent disclosed in the specification.

XX Sequence 4 AA;

XX Query Match 40.0%; Score 4; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VVVP 8  
 DB 1 VVVP 4

RESULT 66  
 AAU07306  
 ID AAU07306 standard; Peptide; 4 AA.

XX AAU07306;

XX 17-DEC-2001 (first entry)

XX Antineoplastic peptide #2.

XX Antineoplastic; tumour; cytostatic; therapeutic; lung; breast;  
 KW colon; prostate; bladder; rectum; endometrial tumour; leukaemia;  
 KW haematological malignancy; lymphoma.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "Benzoyloxyl carbonyl protected"  
 FT Modified-site 3 /label= MeVal  
 FT Modified-site 5 /note= "N-methyl valine"  
 FT Modified-site 5 /note= "Pro-OME, Pro-OH"

XX US2001009901-A1.

XX 26-JUL-2001.

XX 09-JAN-2001; 2001US-0757142.

XX 12-JUN-1998; 98US-0097184.

XX 11-DEC-1996; 96WO-EP05518.

XX (BADI ) BASF AG.

XX Amberg W, Barlozzari T, Bernard H, Buschmann E, Haupt A, Hege H;  
 PI Janssen B, Kling A, Lietz H, Ritter K, Ullrich M, Weymann J;  
 PI Zierke T;

XX WPI; 2001-529023/58.

XX New penta- and hexapeptides, which are resistant to enzymatic  
 PT degradation, are used to inhibit or treat solid tumours e.g. of the  
 PT lung, colon, prostate, bladder and rectum, and leukaemias and lymphomas

XX Example 1; Page 5; 22pp; English.

XX The invention relates to novel antineoplastic peptides of formula (I):  
 CC (N(R1)(R2)-CHX-C(O)-A-B-D-E-(G)S-K. Where R1 = H, CH3 or C2H5;  
 CC R2 = CH3 or C2H5; or NR1R2 = pyrrolidine; A = valyl, isoleucyl, allo-  
 CC isoleucyl, 2-tert-butylglycyl, 2-ethylglycyl, norleucyl or norvalyl  
 CC residue; B = N-methyl-valyl, N-methyl-norvalyl, N-methyl-leucyl,  
 CC N-methyl-isoleucyl, N-methyl-2-tertbutylglycyl, N-methyl-2-ethylglycyl  
 CC or N-methyl-norleucyl; D = prolyl, homoprolyl, hydroxyprolyl or  
 CC thiazolidine-4-carboxyl residue; E = prolyl, homoprolyl, thiazolidine-4-  
 CC carbonyl, trans-4-fluoro-L-prolyl, cis-4-fluoro-L-prolyl, trans-4-chloro-  
 CC L-prolyl or cis-4-chloro-L-prolyl; X = C2H5, C3H7, C4H9, isopropyl, sec-



CC butyl, tert-butyl, cyclopropyl or cyclopentyl; G = L-2-tert-butylglycyl,  
 CC D-2-tert-butylglycyl, D-valyl, D-isoleucyl, D-leucyl, D-norvalyl,  
 CC 1-aminopentyl-1-carboxyl or 2,2-dimethylglycyl; s = 0 or 1; K' = NH-1-8C  
 CC alkyl, NH-3-8C alkanyl, -NH-3-8C alkanyl, -NH-6-8C cycloalkyl, -NH-4C  
 CC alkene-3-8C cycloalkyl, 1-4C alkyl-N-1-6C alkyl (one CH<sub>2</sub> group may be  
 CC replaced by O or S, one H by phenyl or CW, or mono, di or tri-H by F,  
 CC except for N-methoxy-N-methylamino, N-benzylamino or N-methyl-N-  
 CC benzylamino residue), morpholine, azetidine, thiazolidine, hexahydro-  
 CC pentalen-3a-ylamine, methyl-(4-methyl-tetrahydro-pyran-4-yl) amine,  
 CC 2,6-dimethyl-phenylamine, 1,2,3,4-tetrahydro-naphthalen-1-ylamine,  
 CC indan-1-ylamine, indan-2-ylamine, 1-methyl-cyclopropylamine,  
 CC 1-methyl-cyclobutylamine, 1-methyl-cyclopentylamine,  
 CC 1-methyl-cyclohexylamine, tetrahydro-furan-2-yl methylamine,  
 CC 2,3-dihydro-1H-isoindole, adamantan-1-yl amine, NH-C(CH<sub>3</sub>)<sub>2</sub>(CONH<sub>2</sub>) or  
 CC 9-fluorenylamine. The peptides are used to inhibit or otherwise treat  
 CC solid tumours (e.g. tumours of the lungs, breast, colon, prostate,  
 CC bladder, rectum or endometrial tumours) or haematological malignancies  
 CC (e.g. leukaemias, lymphomas). The peptide is resistant to enzymatic  
 CC degradation and can also be administered orally. The present sequence  
 CC represents antineoplastic peptide #2 used in an example of the invention.  
 XX  
 XX Sequence 4 AA;

Query Match 40.0%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8  
 ||||  
 Db 1 VVVP 4

RESULT 67  
 AAG65279  
 ID AAG65279 standard; peptide; 4 AA.

XX AC AAG65279;

XX DT 20-NOV-2001 (first entry)

XX DE Cell growth inhibitor peptide.

XX KW Cell growth inhibition; cancer; dolastatin.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

FT /note= "optionally Me2 or Z"

FT Modified-site 3 /label= OTHER

FT /note= "methylvaline"

FT Modified-site 4 /label= OTHER

FT /note= "optionally modified by NH-C6H4-CON(CH<sub>3</sub>)<sub>2</sub>,

FT NH-C6H4-CON(CH<sub>3</sub>) (OCH<sub>3</sub>) or

FT cis-2-aminocyclopentanecarboxylic acid-NH<sub>2</sub>N"

XX US2001018422-A1.

XX PD 30-AUG-2001.

XX PF 08-JAN-2001; 2001US-0756593.

XX PR 23-JUN-1999; 99WO-US14099.

XX PA (BADI ) BASF AG.

XX PI Ritter K, Janssen B, Haupt A, Kling A, Barlozzari T, Amberg W;

XX DR WPI; 2001-595752/67.

XX

PT New dolastatin derivatives, useful for treating cancer  
 XX Claim 18; Page 42; 43pp; English.

XX The present invention provides derivatives of dolastatin which are  
 CC capable of acting as cell growth inhibitors. They are useful in the  
 CC treatment of cancer. The present sequence is the peptide of the  
 CC invention.

XX Sequence 4 AA;

Query Match 40.0%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8  
 ||||  
 Db 1 VVVP 4

RESULT 68

AAG62325

ID AAG62325 standard; peptide; 4 AA.

XX AC AAG62325;

XX DT 24-AUG-2001 (first entry)

XX DE Casein-related peptide SEQ ID 24.

XX KW Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.

XX OS Synthetic.

XX FN WO200134828-A1.

XX PD 17-MAY-2001.

XX PF 10-NOV-2000; 2000WO-JP07930.

XX PR 11-NOV-1999; 99JP-0321084.

XX PA (CALV ) CALPIS CO LTD.

XX PI Yamamoto N, Ueno K, Ejiri M;

XX DR WPI; 2001-343606/36.

XX Production of tripeptides for treating hypertension and stress by  
 processing casein with proteinase and peptidase -

XX Claim 3; Page 27; 32pp; Japanese.

XX This invention relates to a method for the production of tripeptides. The  
 method comprises treating material containing milk casein with a  
 CC proteinase to produce intermediate peptide containing Valpropro or  
 CC IleproPro with no proline residue any where else in the peptide. Use of  
 CC the peptides may result in hypotensive and tranquilliser activity. The  
 CC peptide can be used in treatments to lower blood pressure and in the  
 CC treatment of stress. The present sequence represents an intermediate  
 CC peptide of the invention.

XX Sequence 4 AA;

Query Match 40.0%; Score 4; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10  
 ||||  
 Db 1 VPPF 4

RESULT 69  
AAW50302 standard; peptide; 4 AA.  
XX AC AAW50302;  
XX DT 24-AUG-2001 (first entry)  
XX DE Casein-related peptide SEQ ID 26.  
XX KW Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.  
XX OS Synthetic.  
XX PN WO200134828-A1.  
XX PD 17-MAY-2001.  
XX PF 10-NOV-2000; 2000WO-JP07930.  
XX PR 11-NOV-1999; 99JP-0321084.  
XX PA (CALV ) CALPIS CO LTD.  
XX PI Yamamoto N, Ueno K, Ejiri M;  
XX WPI; 2001-343606/36.  
XX Production of tripeptides for treating hypertension and stress by processing casein with proteinase and peptidase -  
XX Claim 3; Page 27; 32pp; Japanese.  
XX This invention relates to a method for the production of tripeptides. The method comprises treating material containing milk casein with a proteinase to produce intermediate peptide containing Valpropro or Ilepropro with no proline residue any where else in the peptide. Use of the peptides may result in hypotensive and tranquiliser activity. The peptide can be used in treatments to lower blood pressure and in the treatment of stress. The present sequence represents an intermediate peptide of the invention.

Query Match 40.0%; Score 4; DB 22; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VVPP 9  
|||  
DB 1 VVPP 4

RESULT 70  
AAW50302 standard; peptide; 5 AA.  
XX AC AAW50302;  
XX DT 08-JUL-1998 (first entry)  
XX DE Antineoplastic peptide.  
XX KW Antineoplastic; antitumour agent; Dolastatin; tumour; cancer;  
XX OS Synthetic.  
XX Key Location/Qualifiers  
XX Modified-site 1 /note= "N,N-dimethylvaline"  
XX Modified-site 3 /note= "N-methylvaline"

Modified-site 5 /note= "Amide substituted thiaproline"

FT FT WO9722621-A2.  
XX PN 26-JUN-1997.  
XX PD 11-DEC-1996; 96WO-EP05518.  
XX PF 15-DEC-1995; 95US-0573422.  
XX PR (BADI ) BASF AG.  
XX PA Amberg W, Barlozzari T, Bernard H, Buschmann E;  
XX PI Haupt A, Hege H, Janssenb, Kling A, Lietz H, Ritter K;  
XX PI Ullrich M, Weymann J, Zierke T;  
XX DR WPI; 1997-341627/31.  
XX New peptide(s) with anti-neoplastic activity - useful for treating solid tumours and haematological malignancies

Example 2; Page 15; 54pp; English.

This sequence represents an antineoplastic peptide of the formula R1R2N-CHX-CO-A-B-D-E-(G)s-K (I), in which R1 = H, Me or Et; R2 = Me or Et; or R1R2N = a pyrrolidine ring; A = valyl, isoleucyl, allo-isoleucyl, 2-tert-butylglycyl, 2-ethylglycyl, norleucyl or norvalyl residue; B = N-methyl-2-tert-butylglycyl, N-methyl-norvalyl, N-methylisoleucyl, N-methyl-2-valyl, N-methylglycyl, N-methyl-2-ethylglycyl or N-methyl-norleucyl residue; D = prolyl, homoprolyl, hydroxyprolyl or thiazolidine-4-carboxyl residue; E = prolyl, homoprolyl, hydroxyprolyl, thiazolidine-4-carboxyl, trans- or cis-4-fluoro-L-prolyl, or trans- or cis-4-chloro-L-prolyl residue; X = Et, propyl, butyl, isopropyl, sec-butyl, tert-butyl, cyclopropyl or cyclopentyl; G = L- or D-2-tert-butylglycyl, D-valyl, D-isoleucyl, D-leucyl, D-norvalyl, 1-aminopentyl-1-carboxyl or 2,2-dimethylglycyl residue; s = 0 or 1; K = -NH-(1-8C alkyl), -NH-(3-8C alkyl), -NH-(3-8C alkyl), -NH-(6-8C cycloalkyl), -NH-(1-4C alkenyl)- (3-8C cycloalkyl) or 1-4C alkyl-N(1-6C alkyl), in which one CH2 is optionally replaced by O or S, one H is optionally replaced by Ph or CN, or 1-3 H are optionally replaced by F, except the N-methoxy-N-methylamino, N-benzylamino or N-methyl-N-benzylamino residue; or K is thiazolidino, morpholino, azetidino, bicyclo(3,3,0)octan-1-yl-amino, 4-methyl-tetrahydroxyran-4-yl-amino, 2,6-dimethyl-anilino, 1,2,3,4-tetrahydronaphthalen-1-yl-amino, indan-1-yl-amino, indan-2-yl-amino, 1-methyl-cyclopropylamino, 1-methyl-cyclobutylamino, 1-methyl-cyclopentylamino, 1-methyl-cyclohexylamino, 1-aminocarbonyl-1-methyl-ethylamino, fluoren-9-yl-amino, tetrahydrofuran-2-ylmethyl-amino, isoindolino or adamantan-1-yl-amino. The peptides are useful for treating neoplastic diseases, particularly solid tumours (e.g. lung, breast, colon, prostate, bladder, rectum or endometrial tumours) or haematological malignancies (e.g. leukaemias, lymphomas). They are resistant to enzymatic degradation and can be administered orally.

Sequence 5 AA;

Query Match 40.0%; Score 4; DB 18; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VVPP 8  
|||  
DB 1 VVPP 4

RESULT 71  
AAW29046 standard; peptide; 5 AA.  
XX ID AAW29046  
XX AC AAW29046;  
XX DT 05-MAR-1998 (first entry)  
XX

DE	Dolastatin analogue peptide.	
XX	dolastatin; antineoplastic.	
XX	Synthetic.	
OS		
XX	Key	Location/Qualifiers
FH	Modified-site 1	/note= "Me2Val"
FT	Modified-site 3	/note= "MeVal"
FT	Misc-difference 5	/note= "L-azetidiny-2-carboxamide or 3,4-dehydroprolyl benzylamide"
FT		
FT		
XX	WO9640752-A1.	
XX	19-DEC-1996.	
XX	03-JUN-1996;	96WO-EP02393.
XX	07-JUN-1995;	95US-0472453.
XX	(BADI ) BASF AG.	
XX	Emling F, Haupt A, Romerdahl CA;	
XX	WPI; 1997-077262/07.	
XX	New dolastatin derivs. useful as antineoplastic agents - which exhibit improved resistance to enzymatic degradation	
XX	Examples 1, 2; Pages 18, 19; 47pp; English.	
XX	New dolastatin derivatives are disclosed having the formula	
CC	R1R2N-CHX-CO-A-B-D-E-(F)-K, in which: R1 = Me, Et or iPr; R2 = H, Me or Et; or NR1R2 = a pyrrolidine ring; A = a valyl, isoleucyl, leucyl, 2-tert-butylglycyl, 2-ethylglycyl, norleucyl or norvalyl residue;	
CC	B = a N-methyl-valyl, -leucyl, -isoleucyl, -norvalyl, -norleucyl, -2-tert-butylglycyl, -3-tert-butylalanyl or -2-ethylglycyl residue;	
CC	D = a prolyl, 3,4-dehydroprolyl, 4-fluoroprolyl, 4,4-difluoroprolyl, azetidine-2-carbonyl, homoprolyl, thiazolidine-4-carbonyl or 3-, 4- or 5-methylprolyl residue; E = a 3,4-dehydroprolyl, 4-fluoroprolyl, 3- or 4-methylprolyl, 4,4-difluoroprolyl or azetidine-2-carbonyl residue; F = a valyl, 2-tert-butylglycyl, isoleucyl, leucyl, 2-cyclohexylglycyl, norleucyl, norvalyl, neopentylglycyl, alanyl, beta-alanyl or aminoisobutyryl residue; X = alkyl (preferably 2-5C alkyl), cyclopropyl or cyclopentyl; t = 0 or 1; and K = alkoxy (preferably 1-4C alkoxy), benzyl or optionally substituted amino.	
CC	The peptides may be used to treat or inhibit tumours (including tumours of the lung, colon, breast, bladder, rectum or prostate) or haematological malignancies (such as lymphomas and leukaemias). They are more resistant to enzymatic degradation than dolastatin-15.	
CC	The present sequence represents two specific peptides which were prepared in the Examples of the patent.	
XX		
SQ	Sequence 5 AA;	
Query Match	40.0%;	Score 4; DB 18; Length 5;
Best Local Similarity	100.0%;	Pred. No. 9.3e+05;
Matches	4; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	5 VVVP 8	
Db	1 VVVP 4	
RESULT 72		
AAW66739		
ID	AAW66739 standard; peptide; 5 AA.	
XX	AC	
XX	AAW66739;	
XX		
DT	02-DEC-1998 (first entry)	
XX	Dolastatin-15 derivative in composition for treatment of cancer.	
XX	dolastatin-15; cancer; paclitaxel; taxane; taxoid; taxotere.	
XX	Synthetic.	
OS	Dolabella auricularia.	
XX	Key	Location/Qualifiers
FH	Modified-site 1	/note= "N,N-dimethyl-Ile"
FT	Modified-site 3	/label= MeVal
FT		/note= "N-methyl-valine"
FT	Modified-site 5	/note= "Pro-NHCH (CH3)CH2CH3"
FT		
XX	WO9840092-A1.	
XX	17-SEP-1998.	
XX	09-MAR-1998;	98WO-US04594.
XX	13-MAR-1997;	97US-0819101.
XX	(BADI ) BASF AG.	
XX	(BADI ) BASF BIORESEARCH CORP.	
XX	Barlozzari T, Haupt A;	
PI	WPI; 1998-520790/44.	
XX	Composition used for treating cancer - comprises paclitaxel, taxotere or modified taxane or taxoid analogs and tetra- to hepta-peptide(s)	
XX	Example 105; Page 55; 114pp; English.	
XX	The invention relates to a composition for the treatment of cancer. The composition comprises: (a) paclitaxel, taxotere or modified taxane or taxoid analogs; (b) tetra- to hepta- peptides of formula R1R2N-CHX-CO-A-B-D-(E)-F)-t-(G)-K (I) or their salts and optionally a carrier. R1 = alkyl, cycloalkyl, alkylsulphonyl, fluoroalkyl or aminoalkyl; R2 = H, alkyl, fluoroalkyl, or cycloalkyl or NR1R2 = pyrrolidino or piperidino; A = valyl, isoleucyl, leucyl, alioisoleucyl, 2,2-dimethylglycyl, 2-cyclopropylglycyl, 2-cyclopentylglycyl, 3-tert-butylalanyl, 2-tert-butylglycyl, 3-cyclohexylalanyl, 2-ethylglycyl, 2-cyclohexylglycyl, norleucyl or norvalyl; B = an N-alkyl derivative of A except alioisoleucyl or cyclohexylalanyl; D, E = prolyl, homoprolyl, hydroxyprolyl, 3,4-dehydroprolyl, 4-fluoroprolyl, 3-, 4- or 5-methylprolyl, azetidine-2-carbonyl, 3,3-dimethylprolyl, 4,4-difluoroprolyl, oxazolidine-4-carbonyl, or thiazolidine-4-carbonyl; F, G = prolyl, homoprolyl, hydroxyprolyl, thiazolidine-4-carbonyl, 1-amino-2-ethyl-1-carbonyl, valyl, 2-tert-butylglycyl, isoleucyl, leucyl, 3-cyclohexylalanyl, phenylalanyl, N-methyl-phenylalanyl, 3-pyridylalanyl, tetrahydroisoquinolyl-2-histidyl, 1-aminoindyl-1-carbonyl, 2-cyclohexylglycyl, norleucyl, norvalyl, neopentylglycyl, tryptophanyl, glycyl, 2,2-dimethylglycyl, alanyl, beta-alanyl or 3-naphthylalanyl; X = H, alkyl, cycloalkyl, methylcyclohexyl or arylalkyl; s, t, u = 0 or 1 and K = hydroxy, alkoxy, phenoxy, benzyl or amino (optionally substituted). The composition is used for treating lung, breast, colon, prostate, bladder, rectal, endometrial and haematological cancers e.g. leukaemias and lymphomas. The present sequence represents a specific example of a peptide disclosed in the specification.	
XX	Sequence 5 AA;	
Query Match	40.0%;	Score 4; DB 19; Length 5;
Best Local Similarity	100.0%;	Pred. No. 9.3e+05;
Matches	4; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	6 VVVP 9	

```

Db          |||||
            2 VVPP 5

RESULT 73
AAY69982
ID AAY69982 standard; peptide; 5 AA.
XX
AC AAY69982;
XX
DT 17-APR-2000 (first entry)
XX
DE ACE inhibitor peptide.
XX
KW ACE inhibitor; angiotensin converting enzyme; hypertension; therapy.
XX
OS Synthetic.
XX
PN JP11343298-A.
XX
PD 14-DEC-1999.
XX
PF 27-MAY-1998; 98JP-0185530.
XX
PR 27-MAY-1998; 98JP-0185530.
XX
PA (SUET/) SUETSUNA Y.
XX
XX WPI; 2000-129318/12.
XX
PT New pentapeptide useful as angiotensin converting enzyme inhibitor for
PT treating hypertension - consists of defined amino acid sequence
XX
PS Claim 1; Page 2; 6pp; Japanese.
XX
XX This sequence represents the angiotensin converting enzyme (ACE)
CC inhibitory peptide of the invention. The pentapeptide is useful for
CC preventing and treating hypertension. The pentapeptide does not have any
CC adverse side effect.
XX
SQ Sequence 5 AA;
    Query Match 40.0%; Score 4; DB 21; Length 5;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 VVPP 9
Db      |||||
        1 VVPP 4

RESULT 74
AAG62322
ID AAG62322 standard; peptide; 5 AA.
XX
AC AAG62322;
XX
DT 24-AUG-2001 (first entry)
XX
DE Casein-related peptide SEQ ID 21.
XX
KW Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.
XX
OS Synthetic.
XX
PN WO200134828-A1.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-JP07930.
XX
PR 11-NOV-1999; 99JP-0321084.
XX

(PALV ) CALPIS CO LTD.
Yamamoto N, Ueno K, Ejiri M;
WPI; 2001-343606/36.
Production of tripeptides for treating hypertension and stress by
processing casein with proteinase and peptidase -
Claim 3; Page 26; 32pp; Japanese.
This invention relates to a method for the production of tripeptides. The
method comprises treating material containing milk casein with a
proteinase to produce intermediate peptide containing ValProPro or
IleProPro with no proline residue any where else in the peptide. Use of
the peptides may result in hypotensive and tranquiliser activity. The
peptide can be used in treatments to lower blood pressure and in the
treatment of stress. The present sequence represents an intermediate
peptide of the invention.
SQ Sequence 5 AA;
    Query Match 40.0%; Score 4; DB 22; Length 5;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 VVPP 10
Db      |||||
        1 VVPP 4

RESULT 75
AAE33698
ID AAE33698 standard; peptide; 5 AA.
XX
AC AAE33698;
XX
DT 16-APR-2003 (first entry)
XX
DE Genome derived antigen 33 (GNA33) peptide #1.
XX
KW Genome derived antigen 33; GNA33; Neisseria meningitidis serogroup B;
KW MenB; immune response; infection; vaccine; antibacterial.
XX
OS Unidentified.
XX
PN WO200283711-A2.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US11501.
XX
PR 17-APR-2001; 2001US-284554P.
PR 03-OCT-2001; 2001US-326838P.
XX
PA (CHIR ) CHIRON CORP.
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
XX
PI Granoff D, Moe G, Rappuoli R;
XX
DR WPI; 2003-120415/11.
XX
XX New GNA33 peptides that elicit production of antibodies exhibiting
PT complement-mediated bactericidal activity against a Neisseria
PT meningitidis serogroup B (MenB), useful for diagnosing or preventing
PT (as vaccine) MenB infection -
XX
PS Claim 2; Page 60; 70pp; English.
XX
XX The invention relates to novel genome derived antigen 33 (GNA33) peptides
CC which are capable of eliciting the production of antibodies that exhibit
CC complement-mediated bactericidal activity and/or opsonic activity against
CC a surface-exposed epitope on loop 4 of PorA of Neisseria meningitidis

```

CC serogroup B (MenB) Fl.2 serosubtype. GNA33 sequences are useful for  
CC eliciting an immune response against MenB bacterium in a mammalian  
CC subject. They are useful for detecting MenB antibodies in a biological  
CC sample. GNA33 sequences are useful to prevent or diagnose MenB bacterium  
CC infection. Sequences of the invention are used as vaccines. The present  
CC sequence is GNA33 peptide.

XX  
SQ Sequence 5 AA;

Query Match 40.0%; Score 4; DB 24; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
| | | |  
Db 2 QTPV 5

Search completed: November 25, 2003, 18:16:07  
Job time : 33.3936 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 19.8936 Seconds  
(without alignments)  
92.715 Million cell updates/sec

Title: US-09-641-801-20

Perfect score: 10

Sequence: 1 TQTPVVPVPF 10

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 18443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	15	US-10-281-652-20
2	5	50.0	8	15	US-10-264-480-29
3	5	50.0	8	15	US-10-264-480-30
4	5	50.0	9	11	US-09-865-548A-75
5	5	50.0	16	12	US-10-224-999A-3099
6	5	50.0	16	14	US-10-139-841-32
7	5	50.0	16	14	US-10-014-485A-32
8	5	50.0	16	15	US-10-174-105A-32
9	5	50.0	17	12	US-10-224-999A-3112
10	5	50.0	17	12	US-10-224-999A-3113
11	5	50.0	18	12	US-10-224-999A-3126
12	5	50.0	18	12	US-10-224-999A-3127
13	5	50.0	18	12	US-10-224-999A-3128
14	5	50.0	19	12	US-10-224-999A-3141
15	5	50.0	19	12	US-10-224-999A-3142

16	5	50.0	19	12	US-10-224-999A-3143	Sequence 3143, Ap
17	5	50.0	19	12	US-10-224-999A-3144	Sequence 3144, Ap
18	5	50.0	20	12	US-10-224-999A-3157	Sequence 3157, Ap
19	5	50.0	20	12	US-10-224-999A-3158	Sequence 3158, Ap
20	5	50.0	20	12	US-10-224-999A-3159	Sequence 3159, Ap
21	5	50.0	20	12	US-10-224-999A-3160	Sequence 3160, Ap
22	5	50.0	20	12	US-10-224-999A-3161	Sequence 3161, Ap
23	4	40.0	8	15	US-10-264-480-27	Sequence 27, Appl
24	4	40.0	8	15	US-10-264-480-28	Sequence 28, Appl
25	4	40.0	9	10	US-09-780-053-63	Sequence 63, Appl
26	4	40.0	9	10	US-09-780-053-146	Sequence 146, App
27	4	40.0	9	10	US-09-780-053-561	Sequence 561, App
28	4	40.0	9	12	US-09-932-165-433	Sequence 433, App
29	4	40.0	9	12	US-09-932-165-611	Sequence 611, App
30	4	40.0	9	12	US-09-932-165-1014	Sequence 1014, App
31	4	40.0	9	12	US-09-932-165-1033	Sequence 1033, Ap
32	4	40.0	9	12	US-09-932-165-1219	Sequence 1219, Ap
33	4	40.0	9	12	US-10-353-929-109	Sequence 109, App
34	4	40.0	9	12	US-10-119-536A-57	Sequence 57, Appl
35	4	40.0	9	12	US-10-119-536A-163	Sequence 163, App
36	4	40.0	9	12	US-10-277-292-146	Sequence 146, App
37	4	40.0	9	12	US-10-277-292-332	Sequence 332, App
38	4	40.0	9	12	US-10-280-340-146	Sequence 146, App
39	4	40.0	9	12	US-10-280-340-332	Sequence 332, App
40	4	40.0	10	9	US-09-767-460-53	Sequence 53, Appl
41	4	40.0	10	9	US-09-860-276-15	Sequence 15, Appl
42	4	40.0	10	9	US-09-860-276-16	Sequence 16, Appl
43	4	40.0	10	9	US-09-860-276-17	Sequence 17, Appl
44	4	40.0	10	10	US-09-780-053-514	Sequence 514, App
45	4	40.0	10	10	US-09-780-053-673	Sequence 673, App
46	4	40.0	10	11	US-09-860-395-15	Sequence 15, Appl
47	4	40.0	10	11	US-09-860-395-16	Sequence 16, Appl
48	4	40.0	10	11	US-09-860-395-17	Sequence 17, Appl
49	4	40.0	10	12	US-09-932-165-146	Sequence 146, App
50	4	40.0	10	12	US-09-932-165-329	Sequence 329, App
51	4	40.0	10	12	US-09-932-165-546	Sequence 546, App
52	4	40.0	10	12	US-09-932-165-702	Sequence 702, App
53	4	40.0	10	12	US-09-932-165-947	Sequence 947, App
54	4	40.0	10	12	US-09-932-165-1095	Sequence 1095, Ap
55	4	40.0	10	12	US-09-932-165-1379	Sequence 1379, Ap
56	4	40.0	10	12	US-10-147-140-7	Sequence 7, Appl
57	4	40.0	10	12	US-10-277-292-199	Sequence 199, App
58	4	40.0	10	12	US-10-277-292-535	Sequence 535, App
59	4	40.0	10	12	US-10-277-292-637	Sequence 637, App
60	4	40.0	10	12	US-10-280-340-199	Sequence 199, App
61	4	40.0	10	12	US-10-280-340-535	Sequence 535, App
62	4	40.0	10	12	US-10-280-340-637	Sequence 637, App
63	4	40.0	10	15	US-10-201-386-14	Sequence 14, Appl
64	4	40.0	11	9	US-09-811-672-14	Sequence 14, Appl
65	4	40.0	11	12	US-10-161-660-17	Sequence 17, Appl
66	4	40.0	11	15	US-10-104-755-14	Sequence 14, Appl
67	4	40.0	11	15	US-10-104-755-17	Sequence 17, Appl
68	4	40.0	12	9	US-09-804-733A-29	Sequence 29, Appl
69	4	40.0	12	10	US-09-912-787-51	Sequence 51, Appl
70	4	40.0	12	11	US-09-954-385-294	Sequence 294, App
71	4	40.0	12	12	US-09-990-832C-62	Sequence 62, Appl
72	4	40.0	12	14	US-10-014-326-37	Sequence 37, Appl
73	4	40.0	13	15	US-10-272-601-10	Sequence 10, Appl
74	4	40.0	14	9	US-09-880-713A-25	Sequence 25, Appl
75	4	40.0	14	9	US-09-873-637-46	Sequence 46, Appl
76	4	40.0	15	9	US-09-732-411-5	Sequence 5, Appl
77	4	40.0	15	11	US-09-880-505-15	Sequence 15, Appl
78	4	40.0	15	12	US-10-224-999A-3087	Sequence 3087, Ap
79	4	40.0	15	12	US-10-239-555A-46	Sequence 46, Appl
80	4	40.0	15	12	US-10-239-555A-47	Sequence 47, Appl
81	4	40.0	15	12	US-10-360-202-16	Sequence 16, Appl
82	4	40.0	15	14	US-10-051-643-15	Sequence 15, Appl
83	4	40.0	15	15	US-10-091-724-17	Sequence 17, Appl
84	4	40.0	16	9	US-09-860-276-3	Sequence 3, Appl
85	4	40.0	16	10	US-09-822-698A-55	Sequence 55, Appl
86	4	40.0	16	11	US-09-860-395-3	Sequence 3, Appl
87	4	40.0	16	11	US-09-880-748-2930	Sequence 2930, Ap
88	4	40.0	16	12	US-10-224-999A-3100	Sequence 3100, Ap

89 4 40.0 16 12 US-10-161-791-449 Sequence 449, Appl  
90 4 40.0 17 12 US-10-231-894-8 Sequence 8, Appl  
91 4 40.0 17 12 US-10-224-999A-3114 Sequence 3114, Ap  
92 4 40.0 17 12 US-10-231-889-8 Sequence 8, Appl  
93 4 40.0 17 15 US-10-225-567A-2016 Sequence 2016, Ap  
94 4 40.0 18 12 US-10-224-999A-3129 Sequence 3129, Ap  
95 4 40.0 19 9 US-09-732-411-4 Sequence 4, Appl  
96 4 40.0 19 12 US-10-224-999A-3145 Sequence 3145, Ap  
97 4 40.0 19 15 US-10-091-724-27 Sequence 27, Appl  
98 4 40.0 20 9 US-09-864-761-35406 Sequence 35406, A  
99 4 40.0 20 10 US-09-731-449-27 Sequence 27, Appl  
100 4 40.0 20 10 US-09-973-025-80 Sequence 80, Appl

## ALIGNMENTS

RESULT 1  
US-10-281-652-20  
; Sequence 20, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: BOLDGOUGH, Ietvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-20  
; OTHER INFORMATION: peptide

Query Match 100.0%; Score 10; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00054;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPVVVPFF 10  
Db 1 TQTPVVVPFF 10

RESULT 2  
US-10-264-480-29  
; Sequence 29, Application US/10264480  
; Publication No. US20030113892A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammock, Bruce D.  
; APPLICANT: Inceoglu, Bora  
; TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS  
; FILE REFERENCE: UCAL256  
; CURRENT APPLICATION NUMBER: US/10/264,480  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/393,070  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/327,602  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29

; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Parabuthus transvaalicus  
US-10-264-480-29  
Query Match 50.0%; Score 5; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVPPF 10  
Db 3 VVPPF 7

RESULT 3  
US-10-264-480-30  
; Sequence 30, Application US/10264480  
; Publication No. US20030113892A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammock, Bruce D.  
; APPLICANT: Inceoglu, Bora  
; TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS  
; FILE REFERENCE: UCAL256  
; CURRENT APPLICATION NUMBER: US/10/264,480  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/393,070  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/327,602  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Parabuthus transvaalicus  
; FEATURE:  
; NAME/KEY: METHYLATION  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: N-terminal Proline is modified.  
US-10-264-480-30

Query Match 50.0%; Score 5; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVPPF 10  
Db 3 VVPPF 7

RESULT 4  
US-09-865-548A-75  
; Sequence 75, Application US/09865548A  
; Publication No. US20030096298A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnea, Eilon  
; APPLICANT: Beer, Ilan  
; APPLICANT: Ziv, Tamar  
; APPLICANT: Admon, Arie  
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE  
; FILE REFERENCE: 01/22080  
; CURRENT APPLICATION NUMBER: US/09/865,548A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: US 60/290,958  
; PRIOR FILING DATE: 2001-05-16  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 75  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence



; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-865-548A-75

Query Match 50.0%; Score 5; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPVVV 7  
|||||  
Db 3 TPVVV 7

## RESULT 5

US-10-224-999A-3099  
; Sequence 3099, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3099  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 5  
US-10-224-999A-3099

Query Match 50.0%; Score 5; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPV 5  
|||||  
Db 1 TQTPV 5

## RESULT 6

US-10-139-841-32  
; Sequence 32, Application US/10139841  
; Publication No. US20020132988A1  
; GENERAL INFORMATION:  
; APPLICANT: Cell Signaling Technology, Inc.  
; APPLICANT: COMB, Michael J.  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES U  
; FILE REFERENCE: CST-138 CON  
; CURRENT APPLICATION NUMBER: US/10/139,841  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 10 is phosphorylated  
US-10-139-841-32

Query Match 50.0%; Score 5; DB 14; Length 16;

Best Local Similarity 100.0%; Pred. No. 71;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPVVV 7  
|||||  
Db 10 TPVVV 14

## RESULT 7

US-10-014-485A-32  
; Sequence 32, Application US/10014485A  
; Publication No. US20020168684A1  
; GENERAL INFORMATION:  
; APPLICANT: Cell Signaling Technology, Inc.  
; APPLICANT: COMB, Michael J.  
; APPLICANT: ZHANG, Hui  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES U  
; FILE REFERENCE: CST-138 CIP2  
; CURRENT APPLICATION NUMBER: US/10/014,485A  
; CURRENT FILING DATE: 2002-03-18  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/535,364  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 10 is phosphorylated  
US-10-014-485A-32

Query Match 50.0%; Score 5; DB 14; Length 16;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPVVV 7  
|||||  
Db 10 TPVVV 14

## RESULT 8

US-10-174-105A-32  
; Sequence 32, Application US/10174105A  
; Publication No. US20030068652A1  
; GENERAL INFORMATION:  
; APPLICANT: Cell Signaling Technology, Inc.  
; APPLICANT: ZHANG, Hui  
; APPLICANT: COMB, Michael J.  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,  
; FILE REFERENCE: CST-138 CIP3  
; CURRENT APPLICATION NUMBER: US/10/174,105A  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/535,364  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 193  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide

; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (10)- (10)  
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 10 is phosphorylated  
US-10-174-105A-32

Query Match 50.0%; Score 5; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPVVV 7  
Db 10 TPVVV 14

RESULT 9  
US-10-224-999A-3112  
; Sequence 3112, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3112  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 5  
US-10-224-999A-3112

Query Match 50.0%; Score 5; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 5  
Db 2 TOTPV 6

RESULT 10  
US-10-224-999A-3113  
; Sequence 3113, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3113  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 5  
US-10-224-999A-3113

Query Match 50.0%; Score 5; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 5  
Db 1 TOTPV 5

RESULT 11  
US-10-224-999A-3126  
; Sequence 3126, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3126  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 5  
US-10-224-999A-3126

Query Match 50.0%; Score 5; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 5  
Db 3 TOTPV 7

RESULT 12  
US-10-224-999A-3127  
; Sequence 3127, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3127  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 5  
US-10-224-999A-3127

Query Match 50.0%; Score 5; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 5  
Db 2 TOTPV 6

RESULT 13  
US-10-224-999A-3128  
; Sequence 3128, Application US/10224999A

```
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3128
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human herpesvirus 5
US-10-224-999A-3128

Query Match          50.0%; Score 5; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 5
Db 1 TOTPV 5

RESULT 14
US-10-224-999A-3141
; Sequence 3141, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3141
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human herpesvirus 5
US-10-224-999A-3141

Query Match          50.0%; Score 5; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 5
Db 4 TOTPV 8

RESULT 15
US-10-224-999A-3142
; Sequence 3142, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A

; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3142
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human herpesvirus 5
US-10-224-999A-3142

Query Match          50.0%; Score 5; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 5
Db 3 TOTPV 7

RESULT 16
US-10-224-999A-3143
; Sequence 3143, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3143
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human herpesvirus 5
US-10-224-999A-3143

Query Match          50.0%; Score 5; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 5
Db 2 TOTPV 6

RESULT 17
US-10-224-999A-3144
; Sequence 3144, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3144
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human herpesvirus 5
US-10-224-999A-3144
```

## US-10-224-999A-3144

Query Match 50.0%; Score 5; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPV 5  
Db 1 TQTPV 5

## RESULT 18

US-10-224-999A-3157  
Sequence 3157, Application US/10224999A  
Publication No. US20030171318A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
FILE REFERENCE: 5004.01  
CURRENT APPLICATION NUMBER: US/10/224,999A  
CURRENT FILING DATE: 2003-03-03  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 3484  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3157  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Human herpesvirus 5  
US-10-224-999A-3157

Query Match 50.0%; Score 5; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPV 5  
Db 5 TQTPV 9

## RESULT 19

US-10-224-999A-3158  
Sequence 3158, Application US/10224999A  
Publication No. US20030171318A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
FILE REFERENCE: 5004.01  
CURRENT APPLICATION NUMBER: US/10/224,999A  
CURRENT FILING DATE: 2003-03-03  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 3484  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3158  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Human herpesvirus 5  
US-10-224-999A-3158

Query Match 50.0%; Score 5; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPV 5  
Db 4 TQTPV 8

## RESULT 20

US-10-224-999A-3159  
Sequence 3159, Application US/10224999A  
Publication No. US20030171318A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
FILE REFERENCE: 5004.01  
CURRENT APPLICATION NUMBER: US/10/224,999A  
CURRENT FILING DATE: 2003-03-03  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 3484  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3159  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Human herpesvirus 5  
US-10-224-999A-3159

Query Match 50.0%; Score 5; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPV 5  
Db 3 TQTPV 7

## RESULT 21

US-10-224-999A-3160  
Sequence 3160, Application US/10224999A  
Publication No. US20030171318A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
FILE REFERENCE: 5004.01  
CURRENT APPLICATION NUMBER: US/10/224,999A  
CURRENT FILING DATE: 2003-03-03  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 3484  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3160  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Human herpesvirus 5  
US-10-224-999A-3160

Query Match 50.0%; Score 5; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPV 5  
Db 2 TQTPV 6

## RESULT 22

US-10-224-999A-3161  
Sequence 3161, Application US/10224999A  
Publication No. US20030171318A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3161  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 5  
US-10-224-999A-3161

Query Match 50.0%; Score 5; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPV 5  
Db 1 TQTPV 5

RESULT 23  
US-10-264-480-27  
; Sequence 27, Application US/10264480  
; Publication No. US20030113892A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammock, Bruce D.  
; APPLICANT: Inceoglu, Bora  
; TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS  
; FILE REFERENCE: UCAL256  
; CURRENT APPLICATION NUMBER: US/10/264,480  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/393,070  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/327,602  
; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Parabuthus transvaalicus  
US-10-264-480-27

Query Match 40.0%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10  
Db 4 VPPF 7

RESULT 24  
US-10-264-480-28  
; Sequence 28, Application US/10264480  
; Publication No. US20030113892A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammock, Bruce D.  
; APPLICANT: Inceoglu, Bora  
; TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS  
; FILE REFERENCE: UCAL256  
; CURRENT APPLICATION NUMBER: US/10/264,480  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/393,070  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/327,602

; PRIOR FILING DATE: 2001-10-04  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Parabuthus transvaalicus  
; FEATURE:  
; NAME/KEY: METHYLATION  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: N-terminal proline is modified.  
US-10-264-480-28

Query Match 40.0%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10  
Db 4 VPPF 7

RESULT 25  
US-09-780-053-63  
; Sequence 63, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-63

Query Match 40.0%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10  
Db 6 VPPF 9

RESULT 26  
US-09-780-053-146  
; Sequence 146, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1

; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 146  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-146

Query Match 40.0%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10  
Db 4 VPPF 7

## RESULT 27

US-09-780-053-561  
; Sequence 561, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Paris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 561  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-561

Query Match 40.0%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10  
Db 3 VPPF 6

## RESULT 28

US-09-932-165-433  
; Sequence 433, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND

; TITLE OF INVENTION: DETECTION OF CANCER  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 433  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-433

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
Db 5 QTPV 8

## RESULT 29

US-09-932-165-611  
; Sequence 611, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 611  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-611

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
Db 5 QTPV 8

## RESULT 30

US-09-932-165-1014  
; Sequence 1014, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.

; APPLICANT: PARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1014  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-1014

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8  
Db 5 VVVP 8

RESULT 31  
US-09-932-165-1033  
; Sequence 1033, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: PARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1033  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-1033

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8  
Db 2 VVVP 5

RESULT 32  
US-09-932-165-1219  
; Sequence 1219, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: PARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1219  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-1219

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8  
Db 5 VVVP 8

RESULT 33  
US-10-353-929-109  
; Sequence 109, Application US/10353929  
; Publication No. US20030175288A1  
; GENERAL INFORMATION:  
; APPLICANT: ITOH, KYOGO  
; TITLE OF INVENTION: Tumor antigen  
; FILE REFERENCE: GP01-1024  
; CURRENT APPLICATION NUMBER: US/10/353,929  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: JP P2000-231814  
; PRIOR FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 109  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Designed peptide based on the amino acid sequence of SEQ ID NO.47  
US-10-353-929-109

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTP 4  
Db 1 TQTP 4

RESULT 34  
US-10-119-536A-57  
; Sequence 57, Application US/10119536A  
; Publication No. US20030199438A1  
; GENERAL INFORMATION:  
; APPLICANT: Shaw, Allan Christian  
; APPLICANT: Vandahl, Brian Berg  
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria  
; FILE REFERENCE: 4305/1J091US1  
; CURRENT APPLICATION NUMBER: US/10/119,536A  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: DK PA 200100581  
; PRIOR FILING DATE: 2001-04-09  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (1)..(9)  
; OTHER INFORMATION: CPN0619 immunogenic peptide  
US-10-119-536A-57

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVVY 7  
Db 6 PVVY 9

RESULT 35  
US-10-119-536A-163  
; Sequence 163, Application US/10119536A  
; Publication No. US20030199438A1  
; GENERAL INFORMATION:  
; APPLICANT: Shaw, Allan Christian  
; APPLICANT: Vandahl, Brian Berg  
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria  
; FILE REFERENCE: 4305/1J091US1  
; CURRENT APPLICATION NUMBER: US/10/119,536A  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: DK PA 200100581  
; PRIOR FILING DATE: 2001-04-09  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 163  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Chlamydia trachomatis  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (1)..(9)  
; OTHER INFORMATION: CT500 immunogenic peptide  
US-10-119-536A-163

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVVY 7  
Db 6 PVVY 9

RESULT 36  
US-10-277-292-146  
; Sequence 146, Application US/10277292  
; Publication No. US20030199470A1

GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 146  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-146

Query Match 40.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
Db 5 QTPV 8

RESULT 37  
US-10-277-292-332  
; Sequence 332, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 332  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-10-277-292-332



```
Query Match      40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QTPV 5
Db      2 QTPV 5
      |||||

RESULT 38
US-10-280-340-146
; Sequence 146, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PD7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-146

Query Match      40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QTPV 5
Db      5 QTPV 8
      |||||

RESULT 39
US-10-280-340-332
; Sequence 332, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PD7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
```

```
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-332

Query Match      40.0%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QTPV 5
Db      2 QTPV 5
      |||||

RESULT 40
US-09-767-460-53
; Sequence 53, Application US/09767460
; Patent No. US20020009756A1
; GENERAL INFORMATION:
; APPLICANT: Mandell, Arnold
; APPLICANT: Seitz, Karen
; APPLICANT: Shiesinger, Michael
; TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or Modulation of
; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins
; FILE REFERENCE: 01561-0002-CPUS01
; CURRENT APPLICATION NUMBER: US/09/767,460
; CURRENT FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-767-460-53

Query Match      40.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 VPPF 10
Db      1 VPPF 4
      |||||

RESULT 41
US-09-860-276-15
; Sequence 15, Application US/09860276
; Patent No. US20020090609A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Juergen
; APPLICANT: Kremmer, Elisabeth
; APPLICANT: Kliche, Stefanie
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with
; TITLE OF INVENTION: HHV-8 Infections
; FILE REFERENCE: 080318-000000US
; CURRENT APPLICATION NUMBER: US/09/860,276
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/291,803
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: DE 198 16 732.6
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 25
```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 8
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: K12D3
US-09-860-276-15

Query Match          40.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred.No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VPPP 9
Db 7 VPPP 10

RESULT 42
US-09-860-276-16
; Sequence 16, Application US/09860276
; Patent No. US20020090609A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Juergen
; APPLICANT: Kremmer, Elisabeth
; APPLICANT: Kliche, Stefanie
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with
; TITLE OF INVENTION: HHV-8 Infections
; FILE REFERENCE: 080318-000000US
; CURRENT APPLICATION NUMBER: US/09/860,276
; CURRENT FILING DATE: 2001-05-16
; PRIOR FILING DATE: 1999-04-14
; PRIOR FILING DATE: 1999-04-14
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 8
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: K12D4
US-09-860-276-16

Query Match          40.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred.No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VPPP 9
Db 4 VPPP 7

RESULT 43
US-09-860-276-17
; Sequence 17, Application US/09860276
; Patent No. US20020090609A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Juergen
; APPLICANT: Kremmer, Elisabeth
; APPLICANT: Kliche, Stefanie
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with
; TITLE OF INVENTION: HHV-8 Infections
; FILE REFERENCE: 080318-000000US
; CURRENT APPLICATION NUMBER: US/09/860,276
; CURRENT FILING DATE: 2001-05-16

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; PRIOR APPLICATION NUMBER: 09/291,803
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: DE 198 16 732.6
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 8
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: K12D5
US-09-860-276-17

Query Match          40.0%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred.No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VPPP 9
Db 1 VPPP 4

RESULT 44
US-09-780-053-514
; Sequence 514, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: 83PG4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.SUSUI
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 514
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-514

Query Match          40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred.No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPP 10
Db 3 VPPP 6

RESULT 45
US-09-780-053-673
; Sequence 673, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits

```

```

; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: HIGHLY EXPRESSED IN PROSTATE CANCER
; CURRENT APPLICATION NUMBER: 129.5USU1
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US/09/780,053
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 673
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-780-053-673

```

```

Query Match      40.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 7 VPPF 10
    ||||
Db 3 VPPF 6

```

## RESULT 46

```

US-09-860-395-15
; Sequence 15, Application US/09860395
; Publication No. US20030013077A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Juergen
; APPLICANT: Kremmer, Elisabeth
; APPLICANT: Kliche, Stefanie
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with
; TITLE OF INVENTION: HHV-8 Infections
; FILE REFERENCE: 080318-000000US
; CURRENT APPLICATION NUMBER: US/09/860,395
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/291,803
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: DE 198 16 732.6
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 8
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: K12D3
; US-09-860-395-15

```

```

Query Match      40.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 VVPP 9
    ||||
Db 7 VVPP 10

```

## RESULT 47

```

US-09-860-395-16
; Sequence 16, Application US/09860395
; Publication No. US20030013077A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Juergen
; APPLICANT: Kremmer, Elisabeth
; APPLICANT: Kliche, Stefanie
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with

```

```

; TITLE OF INVENTION: HHV-8 Infections
; FILE REFERENCE: 080318-000000US
; CURRENT APPLICATION NUMBER: US/09/860,395
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/291,803
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: DE 198 16 732.6
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 8
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: K12D4
; US-09-860-395-16

```

```

Query Match      40.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 VVPP 9
    ||||
Db 4 VVPP 7

```

## RESULT 48

```

US-09-860-395-17
; Sequence 17, Application US/09860395
; Publication No. US20030013077A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Juergen
; APPLICANT: Kremmer, Elisabeth
; APPLICANT: Kliche, Stefanie
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with
; TITLE OF INVENTION: HHV-8 Infections
; FILE REFERENCE: 080318-000000US
; CURRENT APPLICATION NUMBER: US/09/860,395
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/291,803
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: DE 198 16 732.6
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 8
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: K12D5
; US-09-860-395-17

```

```

Query Match      40.0%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 VVPP 9
    ||||
Db 1 VVPP 4

```

## RESULT 49

```

US-09-932-165-146
; Sequence 146, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:

```

APPLICANT: RAITANO, ARTHUR  
APPLICANT: CHALLITA-EID, PIA M.  
APPLICANT: FARIS, MARY  
APPLICANT: SAFFRAN, DOUGLAS  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: HUBERT, RENE  
APPLICANT: GE, WANGMAO  
APPLICANT: JAKOBOVITS, AYA  
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
TITLE OF INVENTION: DETECTION OF CANCER  
FILE REFERENCE: 51158-20014.00  
CURRENT APPLICATION NUMBER: US/09/932,165  
CURRENT FILING DATE: 2001-08-17  
PRIOR FILING DATE: 2000-08-17  
NUMBER OF SEQ ID NOS: 1508  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 146  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-146

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
Db 4 QTPV 7

RESULT 50  
US-09-932-165-329  
; Sequence 329, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
; TITLE OF INVENTION: DETECTION OF CANCER  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 329  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-329

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
Db 4 QTPV 7

RESULT 51  
US-09-932-165-546  
; Sequence 546, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
; TITLE OF INVENTION: DETECTION OF CANCER  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 546  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-546

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
Db 4 QTPV 7

RESULT 52  
US-09-932-165-702  
; Sequence 702, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
; TITLE OF INVENTION: DETECTION OF CANCER  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 702  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-702

Query Match      40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QTPV 5
Db      6 QTPV 9
      ||||
      ||||

RESULT 53
US-09-932-165-947
; Sequence 947, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 947
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-947

Query Match      40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QTPV 5
Db      1 QTPV 4
      ||||
      ||||

RESULT 54
US-09-932-165-1095
; Sequence 1095, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
```

```
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1095
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1095

Query Match      40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QTPV 5
Db      1 QTPV 4
      ||||
      ||||

RESULT 55
US-09-932-165-1379
; Sequence 1379, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1379
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1379

Query Match      40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 WVP 8
Db      6 WVP 9
      ||||
      ||||

RESULT 56
US-10-147-140-7
; Sequence 7, Application US/10147140
; Publication No. US20030153730A1
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY
; APPLICANT: LIOTTA, LANCE
; APPLICANT: SCHIFFMANN, ELLIOTT
; APPLICANT: KRUTZCH, HENRY
; APPLICANT: MURATA, JUN
```

; TITLE OF INVENTION: AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN  
; FILE OF INVENTION: CANCER DIAGNOSIS AND THERAPY  
; FILE REFERENCE: 2026-4149US4  
; CURRENT APPLICATION NUMBER: US/10/147,140  
; PRIOR FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: 07/822,043  
; PRIOR FILING DATE: 1992-01-17  
; PRIOR APPLICATION NUMBER: 08/249,182  
; PRIOR FILING DATE: 1994-05-25  
; PRIOR APPLICATION NUMBER: 08/346,455  
; PRIOR FILING DATE: 1994-11-28  
; PRIOR APPLICATION NUMBER: 08/977,221  
; PRIOR FILING DATE: 1997-11-24  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; US-10-147-140-7

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10  
|  
|  
|  
|  
Db 1 VPPF 4

RESULT 57  
US-10-277-292-199  
; Sequence 199, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 199  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
; US-10-277-292-199

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
|  
|  
|  
|  
Db 6 QTPV 9

RESULT 58  
US-10-277-292-535  
; Sequence 535, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 535  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
; US-10-277-292-535

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
|  
|  
|  
|  
Db 6 QTPV 9

RESULT 59  
US-10-277-292-637  
; Sequence 637, Application US/10277292  
; Publication No. US20030199470A1  
; GENERAL INFORMATION:  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; FILE REFERENCE: 51158-20050.00  
; CURRENT APPLICATION NUMBER: US/10/277,292  
; CURRENT FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US/09/935,430  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/282,739  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 700  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 637  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
; US-10-277-292-199

Query Match 40.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
|  
|  
|  
|

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-637

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QTPV 5
Db      6 QTPV 9

RESULT 60
US-10-280-340-199
; Sequence 199, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 199
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-199

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QTPV 5
Db      7 QTPV 10

RESULT 61
US-10-280-340-535
; Sequence 535, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
```

```
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 535
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-535

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QTPV 5
Db      6 QTPV 9

RESULT 62
US-10-280-340-637
; Sequence 637, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 637
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-637

Query Match          40.0%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QTPV 5
Db      6 QTPV 9

RESULT 63
US-10-280-340-637
; Sequence 637, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
```

US-10-201-386-14  
; Sequence 14, Application US/10201386  
; Publication No. US20030091567A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Karl  
; APPLICANT: Joukov, Vladimir  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN  
; TITLE OF INVENTION: AND GENE, MUTANTS THEREOF, AND USES THEREOF  
; FILE REFERENCE: 28967/34140A  
; CURRENT APPLICATION NUMBER: US/10/201,386  
; CURRENT FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: US/09/534,376  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 09/355,700  
; PRIOR FILING DATE: 1999-11-05  
; PRIOR APPLICATION NUMBER: PCT/US98/01973  
; PRIOR FILING DATE: 1998-02-02  
; PRIOR APPLICATION NUMBER: 08/795,430  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: PCT/FI96/00427  
; PRIOR FILING DATE: 1996-08-01  
; PRIOR APPLICATION NUMBER: 08/671,573  
; PRIOR FILING DATE: 1996-06-28  
; PRIOR APPLICATION NUMBER: 08/601,132  
; PRIOR FILING DATE: 1996-02-14  
; PRIOR APPLICATION NUMBER: 08/585,895  
; PRIOR FILING DATE: 1996-01-12  
; PRIOR APPLICATION NUMBER: 08/510,133  
; PRIOR FILING DATE: 1995-08-01  
; PRIOR APPLICATION NUMBER: 08/340,011  
; PRIOR FILING DATE: 1994-11-14  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
; OTHER INFORMATION: Igg-Kappa sequence  
US-10-201-386-14  
Query Match 40.0%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TQTP 4  
Db 5 TQTP 8  
|||||

RESULT 64  
US-09-811-672-14  
; Sequence 14, Application US/09811672  
; Patent No. US20020052490A1  
; GENERAL INFORMATION:  
; APPLICANT: BALL, Tanja  
; APPLICANT: VRTALA, Susanne  
; APPLICANT: SPERR, Wolfgang  
; APPLICANT: VALENT, Peter  
; APPLICANT: SUSANI, Markus  
; APPLICANT: KRAFT, Dietrich  
; APPLICANT: KRAFT, Dietrich  
; APPLICANT: VALENTA, Rudolf  
; APPLICANT: LAFFER, Sylvia  
; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, CORRESPONDING RECOMBINANT  
; TITLE OF INVENTION: MOLECULES, VECTORS AND HOSTS CONTAINING THE DNA MOLECULES, DIAGN  
; TITLE OF INVENTION: THERAPEUTIC USES OF SAID ALLERGENS AND FRAGMENTS  
; FILE REFERENCE: 1614-0247P  
; CURRENT APPLICATION NUMBER: US/09/811,672  
; CURRENT FILING DATE: 2001-03-20  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14

; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Timothy Grass  
US-09-811-672-14  
Query Match 40.0%; Score 4; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 PVVV 7  
Db 1 PVVV 4  
|||||

RESULT 65  
US-10-161-660-17  
; Sequence 17, Application US/10161660  
; Publication No. US20030171567A1  
; GENERAL INFORMATION:  
; APPLICANT: BALL, TANJA  
; APPLICANT: VRTALA, SUSANNE  
; APPLICANT: SPERR, WOLFGANG  
; APPLICANT: VALENT, PETER  
; APPLICANT: SUSANI, MARKUS  
; APPLICANT: KRAFT, DIETRICH  
; APPLICANT: LAFFER, SYLVIA  
; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF,  
; TITLE OF INVENTION: CORRESPONDING RECOMBINANT DNA MOLECULES, VECTORS AND HOSTS  
; TITLE OF INVENTION: CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC  
; TITLE OF INVENTION: USES OF SAID ALLERGENS AND FRAGMENTS  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,660  
; FILING DATE: 05-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/750,419  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1614-175  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: No. US20030171567A1 Relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-161-660-17  
Query Match 40.0%; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 PVVV 7  
Db 1 PVVV 4  
|||||



```
Db          1  TPVV 4

RESULT 66
US-10-104-755-14
; Sequence 14, Application US/10104755
; Publication No. US20030031645A1
; GENERAL INFORMATION:
; APPLICANT: Strieter, Robert M.
;              Polverini, Peter J.
;              Kunkel, Steven L.
; TITLE OF INVENTION: CXc Chemokines as Regulators of
;                   Angiogenesis
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/104,755
; FILING DATE: 21-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/213,383
; FILING DATE: 09-Dec-1998
; APPLICATION NUMBER: 08/468,819
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UMIC:003/HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-104-755-14
Query Match          40.0%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          3  TPVV 6
           ||||
Db          1  TPVV 4

RESULT 67
US-10-104-755-17
; Sequence 17, Application US/10104755
; Publication No. US20030031645A1
; GENERAL INFORMATION:
; APPLICANT: Strieter, Robert M.
;              Polverini, Peter J.
;              Kunkel, Steven L.
; TITLE OF INVENTION: CXc Chemokines as Regulators of
;                   Angiogenesis
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/104,755
; FILING DATE: 21-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/213,383
; FILING DATE: 09-Dec-1998
; APPLICATION NUMBER: 08/468,819
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UMIC:003/HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-104-755-14
Query Match          40.0%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          3  TPVV 6
           ||||
Db          1  TPVV 4

RESULT 68
US-09-804-733A-29
; Sequence 29, Application US/09804733A
; Patent No. US20020059656A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: RECOMBINANT PROTEINS CONTAINING REPEATING UNITS
; FILE REFERENCE: MTC6614.2
; CURRENT APPLICATION NUMBER: US/09/804,733A
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/188,990
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 29
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(12)
; OTHER INFORMATION: Fusion protein
; US-09-804-733A-29
Query Match          40.0%; Score 4; DB 9; Length 12;
```



Qy 1 TOTP 4  
|  
|  
|  
|  
Db 6 TOTP 9

## RESULT 73

US-10-272-601-10  
; Sequence 10, Application US/10272601  
; Publication No. US20030082171A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomasi, Jean-Paul  
; APPLICANT: Gersdorff, Michel  
; APPLICANT: Rousseau, Guy  
; TITLE OF INVENTION: VACCINES  
; FILE REFERENCE: B45084  
; CURRENT APPLICATION NUMBER: US/10/272,601  
; CURRENT FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US/09/611,908  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 09/125,754  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: GB 9604595.0  
; PRIOR FILING DATE: 1996-03-04  
; PRIOR APPLICATION NUMBER: GB 9605229.5  
; PRIOR FILING DATE: 1996-03-12  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Guinea Pig  
US-10-272-601-10

Query Match 40.0%; Score 4; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
|  
|  
|  
|  
Db 1 QTPV 4

## RESULT 74

US-09-880-713A-25  
; Sequence 25, Application US/09880713A  
; Patent No. US20020049307A1  
; GENERAL INFORMATION:  
; APPLICANT: Aebersold, Ruedi  
; APPLICANT: Zhou, Huilin  
; TITLE OF INVENTION: Selective Labeling and Isolation of Phosphopeptides and  
; FILE REFERENCE: 39-00  
; CURRENT APPLICATION NUMBER: US/09/880,713A  
; CURRENT FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: US 60/210,972  
; PRIOR FILING DATE: 2000-06-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-880-713A-25

Query Match 40.0%; Score 4; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5  
|  
|  
|  
|  
Db 8 QTPV 11

## RESULT 75

US-09-873-637-46  
; Sequence 46, Application US/09873637  
; Patent No. US20020061543A1  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Jeffrey  
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
; FILE REFERENCE: 960296.95131  
; CURRENT APPLICATION NUMBER: US/09/873,637  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-873-637-46

Query Match 40.0%; Score 4; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8  
|  
|  
|  
|  
Db 11 VVVP 14

Search completed: November 25, 2003, 20:25:46  
Job time : 20.8936 secs

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## ALIGNMENTS

## RESULT 1

US-09-641-803-20  
; Sequence 20, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-20

Query Match 100.0%; Score 10; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPVVPPF 10  
|||  
Db 1 TOTPVVPPF 10

## RESULT 2

US-08-384-618-5  
; Sequence 5, Application US/08384618  
; Patent No. 5449661  
; GENERAL INFORMATION:  
; APPLICANT: Nakamura, Yasunori  
; APPLICANT: Takano, Toshiaki  
; TITLE OF INVENTION: Angiotensin Convertin Enzyme Inhibitor  
; TITLE OF INVENTION: and Method for Preparing Same  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby  
; STREET: 805 Third Ave.  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/384,618  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER: US/08/090,530  
; FILING DATE:  
; APPLICATION NUMBER: JP 4/197239  
; FILING DATE: 23-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: 'Ludwig, S. Peter'  
US-08-384-618-5

Query Match 60.0%; Score 6; DB 1; Length 6;

; REGISTRATION NUMBER: 25,351  
; REFERENCE/DOCKET NUMBER: 4703/08827  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)527-7700  
; TELEFAX: (212)753-7513  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-384-618-5

Query Match 90.0%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00092;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPVVPP 9  
|||  
Db 2 TOTPVVPP 10

## RESULT 3

US-08-384-618-4  
; Sequence 4, Application US/08384618  
; Patent No. 5449661  
; GENERAL INFORMATION:  
; APPLICANT: Nakamura, Yasunori  
; APPLICANT: Takano, Toshiaki  
; TITLE OF INVENTION: Angiotensin Convertin Enzyme Inhibitor  
; TITLE OF INVENTION: and Method for Preparing Same  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby  
; STREET: 805 Third Ave.  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/384,618  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER: US/08/090,530  
; FILING DATE:  
; APPLICATION NUMBER: JP 4/197239  
; FILING DATE: 23-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, S. Peter  
US-08-384-618-4

; REGISTRATION NUMBER: 25,351  
; REFERENCE/DOCKET NUMBER: 4703/08827  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)527-7700  
; TELEFAX: (212)753-7513  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-384-618-4

Query Match 60.0%; Score 6; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVVPP 9  
Db 1 PVVPP 6

## RESULT 4

US-08-384-618-3  
; Sequence 3, Application US/08384618  
; Patent No. 549661  
; GENERAL INFORMATION:  
; APPLICANT: Nakamura, Yasunori  
; APPLICANT: Takano, Toshiaki  
; TITLE OF INVENTION: Angiotensin Convertin Enzyme Inhibitor  
; TITLE OF INVENTION: and Method for Preparing Same  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby  
; STREET: 805 Third Ave.  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/384,618  
; FILING DATE:  
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/090,530  
; FILING DATE:  
; APPLICATION NUMBER: JP 4/197239  
; FILING DATE: 23-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, S. Peter

; REGISTRATION NUMBER: 25,351  
; REFERENCE/DOCKET NUMBER: 4703/08827  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)527-7700  
; TELEFAX: (212)753-7513  
; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-384-618-3

Query Match 50.0%; Score 5; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPPP 9  
Db 1 VVPPP 5

## RESULT 5

US-08-814-577-3  
; Sequence 3, Application US/08814577  
; Patent No. 5965537  
; GENERAL INFORMATION:  
; APPLICANT: Ritter, Kurt  
; APPLICANT: Amberg, Wilhelm  
; APPLICANT: Barlozzari, Teresa

; APPLICANT: Haupt, Andreas  
; APPLICANT: Janssen, Bernd  
; APPLICANT: Kling, Andreas  
; TITLE OF INVENTION: Dolastatin 15 Derivatives with Carbonyl  
; TITLE OF INVENTION: and Heterocyclic Functionalities at the C-Terminus  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/814,577  
; FILING DATE: 10-MAR-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: BBC-024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781) 861-6240  
; TELEFAX: (781) 861-9540

; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-814-577-3

Query Match 50.0%; Score 5; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPPP 9  
Db 1 VVPPP 5

## RESULT 6

US-08-460-874A-38  
; Sequence 38, Application US/08460874A  
; Patent No. 5744298  
; GENERAL INFORMATION:  
; APPLICANT: Stuber, Werner  
; APPLICANT: Wiczorek, Leszek  
; APPLICANT: Ziegelmaier, Robert  
; TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
; TITLE OF INVENTION: and the Use Thereof  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington,  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,874A

;; FILING DATE: 06-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/936,219  
;; FILING DATE: 27-AUG-1992  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: DE P4128684.7  
;; FILING DATE: 29-AUG-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Forman, David S.  
;; REGISTRATION NUMBER: 33,694  
;; REFERENCE/DOCKET NUMBER: 05552-1210-04000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-408-4400  
;; TELEFAX: 202-408-4400  
;; INFORMATION FOR SEQ ID NO: 38:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-460-874A-38

Query Match 50.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 5  
Db 2 TOTPV 6

RESULT 7  
US-08-388-883B-38  
; Sequence 38, Application US/08388883B  
; Patent No. 5859185  
; GENERAL INFORMATION:  
; APPLICANT: ST BER, Werner  
; APPLICANT: WIECZOREK, Leszek  
; APPLICANT: ZIEGELMAIER, Robert  
; TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
; TITLE OF INVENTION: and the Use Thereof  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner L.L.P.  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington,  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,883B  
; FILING DATE: 13-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/300,305  
; FILING DATE: 23-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/936,219  
; FILING DATE: 27-AUG-1992  
; APPLICATION NUMBER: DE P4128684.7  
; FILING DATE: 29-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Forman, David S.  
; REGISTRATION NUMBER: 33,694

;; REFERENCE/DOCKET NUMBER: 5552-1210-02000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-408-4000  
;; TELEFAX: 202-408-4400  
;; INFORMATION FOR SEQ ID NO: 38:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-388-883B-38

Query Match 50.0%; Score 5; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TOTPV 5  
Db 2 TOTPV 6

RESULT 8  
US-08-462-211A-38  
; Sequence 38, Application US/08462211A  
; Patent No. 6143493  
; GENERAL INFORMATION:  
; APPLICANT: Stuber, Werner  
; APPLICANT: WIECZOREK, Leszek  
; APPLICANT: ZIEGELMAIER, Robert  
; TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor  
; TITLE OF INVENTION: and the Use Thereof  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner L.L.P.  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington,  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,211A  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/388,883  
; FILING DATE: 13-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/300,305  
; FILING DATE: 23-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/936,219  
; FILING DATE: 27-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P4128684.7  
; FILING DATE: 29-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Forman, David S.  
; REGISTRATION NUMBER: 33,694  
; REFERENCE/DOCKET NUMBER: 5552-1210-03000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-408-4000  
;; TELEFAX: 202-408-4400  
;; INFORMATION FOR SEQ ID NO: 38:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide



## US-08-463-211A-38

Query Match 50.0%; Score 5; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTPV 5  
|  
|  
|  
|  
Db 2 TQTPV 6

## RESULT 9

US-09-148-712-15

; Sequence 15, Application US/09148712A

; Patent No. 6441140

; GENERAL INFORMATION:

; APPLICANT: COMB, MICHAEL J.

; APPLICANT: TAN, YI

; TITLE OF INVENTION: Production Of Motif-Specific And Context-Independent

; FILE OF INVENTION: Antibodies Using Peptide Libraries As Antigens

; FILE REFERENCE: NEB-138

; CURRENT APPLICATION NUMBER: US/09/148,712A

; CURRENT FILING DATE: 1998-09-04

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 15

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (10)

; OTHER INFORMATION: phosphorylated threonine

US-09-148-712-15

Query Match

Best Local Similarity 50.0%; Score 5; DB 4; Length 16;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPVVV 7  
|  
|  
|  
|  
Db 10 TPVVV 14

## RESULT 10

US-08-384-618-2

; Sequence 2, Application US/08384618

; Patent No. 5449661

; GENERAL INFORMATION:

; APPLICANT: Nakamura, Yasunori

; APPLICANT: Takano, Toshiaki

; TITLE OF INVENTION: Angiotensin Convertin Enzyme Inhibitor

; TITLE OF INVENTION: and Method for Preparing Same

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Darby &amp; Darby

; STREET: 805 Third Ave.

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/384,618

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/090,530

; FILING DATE:

US-08-814-577-2

; APPLICATION NUMBER: JP 4/197239

; FILING DATE: 23-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, S. Peter

; REGISTRATION NUMBER: 25,351

; REFERENCE/DOCKET NUMBER: 4703/08827

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)527-7700

; TELEFAX: (212)753-7513

; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-384-618-2

Query Match

Best Local Similarity 40.0%; Score 4; DB 1; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVPP 9  
|  
|  
|  
|  
Db 1 VVPP 4

## RESULT 11

US-08-814-577-2

; Sequence 2, Application US/08814577

; Patent No. 5965537

; GENERAL INFORMATION:

; APPLICANT: Ritter, Kurt

; APPLICANT: Amberg, Wilhelm

; APPLICANT: Barlozzari, Teresa

; APPLICANT: Haupt, Andreas

; APPLICANT: Janssen, Bernd

; APPLICANT: Kling, Andreas

; TITLE OF INVENTION: Dolastatin 15 Derivatives with Carbonyl

; TITLE OF INVENTION: and Heterocyclic Functionalities at the C-Terminus

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith &amp; Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/814,577

; FILING DATE: 10-MAR-1997

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: BBC-024

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781) 861-6240

; TELEFAX: (781) 861-9540

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-814-577-2

Query Match 40.0%; Score 4; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8  
Db 1 VVVP 4

RESULT 12  
US-08-814-577-1  
; Sequence 1, Application US/08814577  
; Patent No. 5965537  
; GENERAL INFORMATION:  
; APPLICANT: Ritter, Kurt  
; APPLICANT: Amberg, Wilhelm  
; APPLICANT: Barlozzari, Teresa  
; APPLICANT: Haupt, Andreas  
; APPLICANT: Janssen, Bernd  
; APPLICANT: Kling, Andreas  
; TITLE OF INVENTION: Dolastatin 15 Derivatives with Carbonyl  
; and Heterocyclic Functionalities at the C-Terminus  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/814,577  
; FILING DATE: 10-MAR-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: BBC-024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781) 861-6240  
; TELEFAX: (781) 861-9540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-814-577-1

Query Match 40.0%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8  
Db 1 VVVP 4

RESULT 13  
US-08-896-394-1  
; Sequence 1, Application US/08896394  
; Patent No. 6143721  
; GENERAL INFORMATION:  
; APPLICANT: Janssen, Bernd  
; APPLICANT: Barlozzari, Teresa  
; APPLICANT: Haupt, Andreas

; APPLICANT: Zierke, Thomas  
; TITLE OF INVENTION: Dolastatin 15 Derivatives  
; FILE REFERENCE: BBC-023  
; CURRENT APPLICATION NUMBER: US/08/896,394  
; CURRENT FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; OTHER INFORMATION: Contains Xaa at position 1. Xaa represents  
; OTHER INFORMATION: several possible nonnatural amino acids as  
; OTHER INFORMATION: described in the specification.  
US-08-896-394-1

Query Match 40.0%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVVP 9  
Db 2 VVVP 5

RESULT 14  
US-08-896-394-3  
; Sequence 3, Application US/08896394  
; Patent No. 6143721  
; GENERAL INFORMATION:  
; APPLICANT: Janssen, Bernd  
; APPLICANT: Barlozzari, Teresa  
; APPLICANT: Haupt, Andreas  
; APPLICANT: Zierke, Thomas  
; APPLICANT: Kling, Andreas  
; TITLE OF INVENTION: Dolastatin 15 Derivatives  
; FILE REFERENCE: BBC-023  
; CURRENT APPLICATION NUMBER: US/08/896,394  
; CURRENT FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-08-896-394-3

Query Match 40.0%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVVP 9  
Db 2 VVVP 5

RESULT 15  
US-08-896-394-5  
; Sequence 5, Application US/08896394  
; Patent No. 6143721  
; GENERAL INFORMATION:  
; APPLICANT: Janssen, Bernd  
; APPLICANT: Barlozzari, Teresa  
; APPLICANT: Haupt, Andreas  
; APPLICANT: Zierke, Thomas  
; APPLICANT: Kling, Andreas  
; TITLE OF INVENTION: Dolastatin 15 Derivatives  
; FILE REFERENCE: BBC-023

; CURRENT APPLICATION NUMBER: US/08/896,394  
; CURRENT FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-08-896-394-5

Query Match 40.0%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVPP 9  
Db 2 VVPP 5

RESULT 16  
US-09-618-694-1  
; Sequence 1, Application US/09618694  
; Patent No. 6458765  
; GENERAL INFORMATION:  
; APPLICANT: Janssen, Bernd  
; APPLICANT: Barlozzari, Teresa  
; APPLICANT: Haupt, Andreas  
; APPLICANT: Zierke, Thomas  
; APPLICANT: Kling, Andreas  
; TITLE OF INVENTION: DOLASTATIN 15 DERIVATIVES  
; FILE REFERENCE: 2079.1004-036  
; CURRENT APPLICATION NUMBER: US/09/618,694  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: US/08/896,394  
; PRIOR FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; OTHER INFORMATION: Contains Xaa at position 1. Xaa represents  
; OTHER INFORMATION: several possible nonnatural amino acids as  
; OTHER INFORMATION: described in the specification.  
US-09-618-694-1

Query Match 40.0%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVPP 9  
Db 2 VVPP 5

RESULT 17  
US-09-618-694-3  
; Sequence 3, Application US/09618694  
; Patent No. 6458765  
; GENERAL INFORMATION:  
; APPLICANT: Janssen, Bernd  
; APPLICANT: Barlozzari, Teresa  
; APPLICANT: Haupt, Andreas  
; APPLICANT: Zierke, Thomas  
; APPLICANT: Kling, Andreas  
; TITLE OF INVENTION: DOLASTATIN 15 DERIVATIVES  
; FILE REFERENCE: 2079.1004-036  
; CURRENT APPLICATION NUMBER: US/09/618,694  
; CURRENT FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: US/08/896,394  
; PRIOR FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-618-694-3

Query Match 40.0%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVPP 9  
Db 2 VVPP 5

RESULT 18  
US-09-618-694-5  
; Sequence 5, Application US/09618694  
; Patent No. 6458765  
; GENERAL INFORMATION:  
; APPLICANT: Janssen, Bernd  
; APPLICANT: Barlozzari, Teresa  
; APPLICANT: Haupt, Andreas  
; APPLICANT: Zierke, Thomas  
; APPLICANT: Kling, Andreas  
; TITLE OF INVENTION: DOLASTATIN 15 DERIVATIVES  
; FILE REFERENCE: 2079.1004-036  
; CURRENT APPLICATION NUMBER: US/09/618,694  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: US/08/896,394  
; PRIOR FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-618-694-5

Query Match 40.0%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVPP 9  
Db 2 VVPP 5

RESULT 19  
US-08-093-741-76  
; Sequence 76, Application US/08093741  
; Patent No. 5681721  
; GENERAL INFORMATION:  
; APPLICANT: STEFFENS, GERT J.  
; APPLICANT: WENNDT, STEPHAN  
; APPLICANT: SCHNEIDER, JOHANNES  
; APPLICANT: HEINZEL-WIELAND, REGINA  
; APPLICANT: SAUNDERS, DEREK J.  
; TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH  
; TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROWBIN  
; TITLE OF INVENTION: INHIBITING EFFECT  
; NUMBER OF SEQUENCES: 83  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan  
; STREET: 1200 G Street, N. W. Suite 700

;; CITY: Washington, D.C.  
;; COUNTRY: U.S.  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/093,741  
;; FILING DATE: 20-JUL-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: DE P43 23 754.1  
;; FILING DATE: 15-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: EVANS, Joseph D.  
;; REGISTRATION NUMBER: 26,269  
;; REFERENCE/DOCKET NUMBER: 148/41345  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)628-8800  
;; TELEFAX: (202)628-8844  
;; INFORMATION FOR SEQ ID NO: 76:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
US-08-093-741-76

Query Match 40.0%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVVV 7  
DB 2 PVVV 5

RESULT 20  
US-08-093-741-78  
;; Sequence 78, Application US/08093741  
;; Patent No. 5681721  
;; GENERAL INFORMATION:  
;; APPLICANT: STEPPENS, Gerd J.  
;; APPLICANT: WENDT, STEPHAN  
;; APPLICANT: SCHNEIDER, JOHANNES  
;; APPLICANT: HEINZEL-WIELAND, REGINA  
;; APPLICANT: SAUNDERS, DEREK J.  
;; TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH  
;; TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN  
;; INHIBITING EFFECT  
;; NUMBER OF SEQUENCES: 83  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSES: Evenson, McKeown, Edwards & Lenahan  
;; STREET: 1200 G Street, N. W. Suite 700  
;; CITY: Washington, D.C.  
;; COUNTRY: U.S.  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/093,741  
;; FILING DATE: 20-JUL-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: DE P43 23 754.1  
;; FILING DATE: 15-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: EVANS, Joseph D.  
;; REGISTRATION NUMBER: 26,269

;; REFERENCE/DOCKET NUMBER: 148/41345  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)628-8800  
;; TELEFAX: (202)628-8844  
;; INFORMATION FOR SEQ ID NO: 78:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
US-08-093-741-78

Query Match 40.0%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVVV 7  
DB 2 PVVV 5

RESULT 21  
US-08-720-012-76  
;; Sequence 76, Application US/08720012  
;; Patent No. 5747291  
;; GENERAL INFORMATION:  
;; APPLICANT: STEPPENS, Gerd J.  
;; APPLICANT: WENDT, STEPHAN  
;; APPLICANT: SCHNEIDER, JOHANNES  
;; APPLICANT: HEINZEL-WIELAND, REGINA  
;; APPLICANT: SAUNDERS, DEREK J.  
;; TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH  
;; TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN  
;; INHIBITING EFFECT  
;; NUMBER OF SEQUENCES: 83  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSES: Evenson, McKeown, Edwards & Lenahan  
;; STREET: 1200 G Street, N. W. Suite 700  
;; CITY: Washington, D.C.  
;; COUNTRY: U.S.  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/720,012  
;; FILING DATE: 27-SEP-1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/093,741  
;; FILING DATE: 20-JUL-1993  
;; APPLICATION NUMBER: DE P43 23 754.1  
;; FILING DATE: 15-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: EVANS, Joseph D.  
;; REGISTRATION NUMBER: 26,269  
;; REFERENCE/DOCKET NUMBER: 148/41345  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)628-8800  
;; TELEFAX: (202)628-8844  
;; INFORMATION FOR SEQ ID NO: 76:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
US-08-720-012-76

Query Match 40.0%; Score 4; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PVVV 7

```
Db          |||||
            2 PVW 5

RESULT 22
US-08-720-012-78
; Sequence 78, Application US/08720012
; Patent No. 5747291
; GENERAL INFORMATION:
; APPLICANT: STEPPENS, Gerd J.
; APPLICANT: WENDT, STEPHAN
; APPLICANT: SCHNEIDER, JOHANNES
; APPLICANT: HEINZEL-WIELAND, REGINA
; APPLICANT: SAUNDERS, DEREK J.
; TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
; TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
; TITLE OF INVENTION: INHIBITING EFFECT
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N. W. Suite 700
; CITY: Washington, D.C.
; COUNTRY: U.S.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720.012
; FILING DATE: 27-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,741
; FILING DATE: 20-JUL-1993
; APPLICATION NUMBER: DE P43 23 754.1
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/41345
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)628-8800
; TELEFAX: (202)628-8844
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-720-012-78

Query Match          40.0%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          4 PVW 7
            |||||
Db          2 PVW 5

RESULT 23
US-08-127-499A-37
; Sequence 37, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-127-499A-37

Query Match          40.0%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 TQTP 4
            |||||
Db          2 TQTP 5

RESULT 24
US-08-127-499A-40
; Sequence 40, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-127-499A-37
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; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-127-499A-40
Query Match 40.0%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTP 4
Db 2 TQTP 5

RESULT 25
US-08-482-847-37
; Sequence 37, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-482-847-40
Query Match 40.0%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTP 4
Db 2 TQTP 5

RESULT 26
US-08-482-847-40
; Sequence 40, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-482-847-37
Query Match 40.0%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTP 4
Db 2 TQTP 5

RESULT 27
US-08-622-720A-17
; Sequence 17, Application US/08622720A
; Patent No. 5814308
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF
; TITLE OF INVENTION: GASTROINTESTINAL TRACT DISORDERS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/622,720A  
;; FILING DATE:  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Winter, Robert B.  
;; REFERENCE/DOCKET NUMBER: A-396  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-622-720A-17

Query Match 40.0%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 VVPP 9  
|||  
Db 2 VVPP 5

RESULT 28  
US-08-350-260A-50  
; Sequence 50, Application US/08350260A  
; Patent No. 5962255  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01134  
; FILING DATE: 10-JUL-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/150,002  
;; FILING DATE: 31-MAR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/307,619  
;; FILING DATE: 16-SEP-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Clough, David W  
;; REGISTRATION NUMBER: 36,107  
;; REFERENCE/DOCKET NUMBER: 28111/32372  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 312-474-6300  
;; INFORMATION FOR SEQ ID NO: 50:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-350-260A-50

Query Match 40.0%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TQTP 4  
|||  
Db 5 TQTP 8

RESULT 29  
US-09-104-337A-50  
; Sequence 50, Application US/09104337A  
; Patent No. 6492160  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 600  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Audrey L. Bartnicki  
; STREET: Marshall, Gerstein & Borun  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/104,337A  
; FILING DATE: 25-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/350,260  
; FILING DATE: 05-DEC-1994  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; APPLICATION NUMBER: US 08/307,619

```
;
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-104-337A-50
;
; Query Match 40.0%; Score 4; DB 4; Length 8;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 TQTP 4
Db 5 TQTP 8
;
; RESULT 30
; US-08-350-260A-373
; Sequence 373, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350.260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-373
;
; Query Match 40.0%; Score 4; DB 2; Length 9;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 2 QTPV 5
Db 5 QTPV 8
;
; RESULT 31
; US-09-171-705-64
; Sequence 64, Application US/09171705
; Patent No. 6184204
; GENERAL INFORMATION:
; APPLICANT: BOOTS, ANNA M.H.
; APPLICANT: VERHEIJDEN, GILBERTUS F.M.
; TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
; FILE REFERENCE: O/96198 US
; CURRENT APPLICATION NUMBER: US/09/171,705
; CURRENT FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
; OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-64
;
; Query Match 40.0%; Score 4; DB 3; Length 9;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 7 VPPF 10
Db 5 VPPF 8
;
; RESULT 32
; US-09-104-337A-373
; Sequence 373, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
```



```
;
; binding pairs
;
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marehall, Gerstein & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
;
; INFORMATION FOR SEQ ID NO: 373:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 373:
US-09-104-337A-373

Query Match 40.0%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QTPV 5
Db 5 QTPV 8

RESULT 33
US-08-346-455B-7
; Sequence 7, Application US/08346455B
; Patent No. 5731167
;
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
```

```
;
;
; COUNTRY: U.S.A.
; ZIP: 10154
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; TOPOLOGY: linear
;
; US-08-346-455B-7

Query Match 40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10
Db 1 VPPF 4

RESULT 34
US-08-434-664-1
; Sequence 1, Application US/08434664
; Patent No. 5879917
;
; GENERAL INFORMATION:
; APPLICANT: ESSIGMANN, JOHN M.
; APPLICANT: CROY, ROBERT G.
; APPLICANT: VAREMA, KEVIN J.
; APPLICANT: TREIBER, DANIEL K.
; APPLICANT: CHEN, ZHENGHUAN
; APPLICANT: MORNINGSTAR, MARSHALL
; TITLE OF INVENTION: PROGRAMMABLE GENOTOXIC AGENTS AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESS: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,664
```

;; FILING DATE: 514  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: FENTON, GILLIAN M.  
;; REGISTRATION NUMBER: 36,508  
;; REFERENCE/DOCKET NUMBER: MIT-018  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 248-7000  
;; TELEFAX: (617) 248-7100  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-434-664-1  
Query Match 40.0%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 VVVP 8  
Db 6 VVVP 9  
|||||  
RESULT 35  
US-08-239-428A-1  
; Sequence 1, Application US/08239428A  
; Patent No. 5882941  
; GENERAL INFORMATION:  
; APPLICANT: ESSIGMANN, JOHN M.  
; APPLICANT: CROY, ROBERT G.  
; APPLICANT: YAREMA, KEVIN J.  
; APPLICANT: TREIBER, DANIEL K.  
; APPLICANT: CHEN, ZHENGHUA  
; APPLICANT: MORNINGSTAR, MARSHALL  
; APPLICANT: ZHAI, XIAOQUAN  
; TITLE OF INVENTION: PROGRAMMABLE GENOTOXIC AGENTS AND USES  
; TITLE OF INVENTION: THEREFOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
; ADDRESSEE: THIBEAULT  
; STREET: 53 STATE STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/239,428A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FENTON, GILLIAN M.  
; REGISTRATION NUMBER: 36,508  
; REFERENCE/DOCKET NUMBER: MIT-018  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-239-428A-1  
Query Match 40.0%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 VVVP 8  
Db 6 VVVP 9  
|||||  
RESULT 36  
US-08-951-923-38  
; Sequence 38, Application US/08951923  
; Patent No. 6048693  
; GENERAL INFORMATION:  
; APPLICANT: Bitter, Grant  
; TITLE OF INVENTION: PHENOTYPIC ASSAYS OF CYCLIN/CYCLIN-DEPENDENT KINASE  
; TITLE OF INVENTION: FUNCTION  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward LLP  
; STREET: 5 Palo Alto Square, 3000 El Camino Real  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/951,923  
; FILING DATE: October 16, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neeley, Richard L.  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: BITT-001/02US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650 843-5000  
; TELEFAX: 650 857-0663  
; TELEX: 380816COOLEYPA  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-951-923-38  
Query Match 40.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 VVVP 9  
Db 2 VVVP 5  
|||||  
RESULT 37  
US-08-977-221-7  
; Sequence 7, Application US/08977221  
; Patent No. 6084069  
; GENERAL INFORMATION:  
; APPLICANT: UNITED STATES OF AMERICA; DEPT.  
; APPLICANT: OF HEALTH AND HUMAN SERVICES  
; TITLE OF INVENTION: MOTILITY STIMULATING  
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND  
; TITLE OF INVENTION: THERAPY

NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/977,221  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/346,455  
FILING DATE: 28-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,182  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/822,043  
FILING DATE: 17-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: DOROTHY R. AUTH  
REGISTRATION NUMBER: 36,434  
REFERENCE/DOCKET NUMBER: 2026-4149US3  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-977-221-7

Query Match 40.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10  
Db 1 VPPF 4

RESULT 38  
US-08-795-430-14  
Sequence 14, Application US/08795430  
Patent No. 6130071  
GENERAL INFORMATION:  
APPLICANT: Alitalo, Kari  
APPLICANT: Joukov, Vladimir  
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,430

FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: PCT/FI96/00427  
FILING DATE: 01-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/671,573  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,895  
FILING DATE: 12-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/340,011  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28967/33691  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-795-430-14

Query Match 40.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTP 4  
Db 5 TQTP 8

RESULT 39  
US-09-291-803-15  
Sequence 15, Application US/09291803  
Patent No. 6319667  
GENERAL INFORMATION:  
APPLICANT: Haas, Juergen  
APPLICANT: Kremmer, Elisabeth  
APPLICANT: Kliche, Stefanie  
APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH  
TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with  
TITLE OF INVENTION: HHV-8 Infections  
FILE REFERENCE: 080318-000000US  
CURRENT APPLICATION NUMBER: US/09/291,803  
CURRENT FILING DATE: 1999-04-14  
EARLIER APPLICATION NUMBER: DE 198 16 732.6  
EARLIER FILING DATE: 1999-04-15  
EARLIER APPLICATION NUMBER: DE 198 16 732.6  
EARLIER FILING DATE: 1998-04-15  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 10  
TYPE: PRT  
ORGANISM: human herpesvirus 8  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(10)

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; OTHER INFORMATION: K12D3
US-09-291-803-15

Query Match      40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      6 VVPP 9
        |||||
Db      7 VVPP 10

RESULT 40
US-09-291-803-16
; Sequence 16, Application US/09291803
; Patent No. 6319667
; GENERAL INFORMATION:
; APPLICANT: Haas, Juergen
; APPLICANT: Kliche, Elisabeth
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with
; FILE REFERENCE: 080318-000000US
; CURRENT APPLICATION NUMBER: US/09/291.803
; CURRENT FILING DATE: 1998-04-14
; EARLIER FILING DATE: 1998-04-15
; EARLIER FILING DATE: 1998-04-15
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 8
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: K12D4
US-09-291-803-16

Query Match      40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      6 VVPP 9
        |||||
Db      4 VVPP 7

RESULT 41
US-09-291-803-17
; Sequence 17, Application US/09291803
; Patent No. 6319667
; GENERAL INFORMATION:
; APPLICANT: Haas, Juergen
; APPLICANT: Kliche, Elisabeth
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with
; FILE REFERENCE: 080318-000000US
; CURRENT APPLICATION NUMBER: US/09/291.803
; CURRENT FILING DATE: 1998-04-14
; EARLIER FILING DATE: 1998-04-15
; EARLIER FILING DATE: 1998-04-15
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 10

; TYPE: PRT
; ORGANISM: human herpesvirus 8
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: K12D5
US-09-291-803-17

Query Match      40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      6 VVPP 9
        |||||
Db      1 VVPP 4

RESULT 42
US-09-355-700-14
; Sequence 14, Application US/09355700
; Patent No. 6361946
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Helsinki University Licensing
; APPLICANT: Alitalo, Kari(U.S. only)
; APPLICANT: Joukov, Vladimir (U.S. only)
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; AND Uses Thereof
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/355,700
; FILING DATE: 05-No. 6361946-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,430
; FILING DATE: 05-FEB-1997
; APPLICATION NUMBER: PCT/F196/00427
; FILING DATE: 01-AUG-1996
; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/34140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
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;
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-355-700-14

Query Match      40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTP 4
   ||||
Db 5 TQTP 8

RESULT 43
US-09-483-831B-7
; Sequence 7, Application US/09483831B
; Patent No. 6417338
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY
; APPLICANT: LIOTTA, LANCE
; APPLICANT: SCHIFFMANN, ELLIOTT
; APPLICANT: KRUTZCH, HENRY
; APPLICANT: MURATA, JUN
; TITLE OF INVENTION: AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
; FILE REFERENCE: 2026-4149US4
; CURRENT APPLICATION NUMBER: US/09/483,831B
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: 07/822,043
; PRIOR FILING DATE: 1992-01-17
; PRIOR APPLICATION NUMBER: 08/249,182
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/346,455
; PRIOR FILING DATE: 1994-11-28
; PRIOR APPLICATION NUMBER: 08/977,221
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-483-831B-7

Query Match      40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10
   ||||
Db 1 VPPF 4

RESULT 44
US-09-103-671-1
; Sequence 1, Application US/09103671
; Patent No. 6500659
; GENERAL INFORMATION:
; APPLICANT: Eeigmann, John
; APPLICANT: Yarema, Kevin
; APPLICANT: Morningstar, Marshall
; APPLICANT: Croy, Robert
; TITLE OF INVENTION: Programmable Genotoxic Agents and Uses Therefor
; FILE REFERENCE: MIT-018CP2
; CURRENT APPLICATION NUMBER: US/09/103,671
; CURRENT FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: US 08/239,428
; PRIOR FILING DATE: 1994-05-04
; PRIOR APPLICATION NUMBER: US 08/434,664
```

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; PRIOR FILING DATE: 1995-05-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: EP240-Cys peptide
US-09-103-671-1

Query Match      40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8
   ||||
Db 6 VVVP 9

RESULT 45
US-09-860-276-15
; Sequence 15, Application US/09860276
; Patent No. 6503513
; GENERAL INFORMATION:
; APPLICANT: Haas, Juergen
; APPLICANT: Kremmer, Elisabeth
; APPLICANT: Kliche, Stefanie
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with
; FILE REFERENCE: HHV-8 Infections
; CURRENT APPLICATION NUMBER: US/09/860,276
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/291,803
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: DE 198 16 732.6
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus 8
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(10)
; OTHER INFORMATION: K12D3
US-09-860-276-15

Query Match      40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVPP 9
   ||||
Db 7 VVPP 10

RESULT 46
US-09-860-276-16
; Sequence 16, Application US/09860276
; Patent No. 6503513
; GENERAL INFORMATION:
; APPLICANT: Haas, Juergen
; APPLICANT: Kremmer, Elisabeth
; APPLICANT: Kliche, Stefanie
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with
; FILE REFERENCE: HHV-8 Infections
; CURRENT APPLICATION NUMBER: US/09/860,276
; CURRENT FILING DATE: 2001-05-16
```

; PRIOR APPLICATION NUMBER: 09/291,803  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: DE 198 16 732.6  
 ; PRIOR FILING DATE: 1998-04-15  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 16  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 8  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(10)  
 ; OTHER INFORMATION: K12D4  
 ; US-09-860-276-16

Query Match 40.0%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VVPP 9  
 Db 4 VVPP 7

RESULT 47  
 US-09-860-276-17  
 ; Sequence 17, Application US/09860276  
 ; Patent No. 6503513  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haas, Juergen  
 ; APPLICANT: Kiemmer, Elisabeth  
 ; APPLICANT: Kliche, Stefanie  
 ; TITLE OF INVENTION: Diagnostica and Therapy of Diseases Associated with  
 ; FILE REFERENCE: 080318-000000US  
 ; CURRENT APPLICATION NUMBER: US/09/860,276  
 ; CURRENT FILING DATE: 2001-05-16  
 ; PRIOR APPLICATION NUMBER: 09/291,803  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: DE 198 16 732.6  
 ; PRIOR FILING DATE: 1998-04-15  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 17  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 8  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(10)  
 ; OTHER INFORMATION: K12D5  
 ; US-09-860-276-17

Query Match 40.0%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VVPP 9  
 Db 1 VVPP 4

RESULT 48  
 US-09-860-395-15  
 ; Sequence 15, Application US/09860395  
 ; Patent No. 6541253  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haas, Juergen  
 ; APPLICANT: Kiemmer, Elisabeth  
 ; APPLICANT: Kliche, Stefanie  
 ; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH

; TITLE OF INVENTION: Diagnostica and Therapy of Diseases Associated with  
 ; FILE REFERENCE: HHV-8 Infections  
 ; CURRENT APPLICATION NUMBER: US/09/860,395  
 ; CURRENT FILING DATE: 2001-05-16  
 ; PRIOR APPLICATION NUMBER: 09/291,803  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: DE 198 16 732.6  
 ; PRIOR FILING DATE: 1998-04-15  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 15  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 8  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(10)  
 ; OTHER INFORMATION: K12D3  
 ; US-09-860-395-15

Query Match 40.0%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VVPP 9  
 Db 7 VVPP 10

RESULT 49  
 US-09-860-395-16  
 ; Sequence 16, Application US/09860395  
 ; Patent No. 6541253  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haas, Juergen  
 ; APPLICANT: Kiemmer, Elisabeth  
 ; APPLICANT: Kliche, Stefanie  
 ; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH  
 ; TITLE OF INVENTION: Diagnostica and Therapy of Diseases Associated with  
 ; FILE REFERENCE: HHV-8 Infections  
 ; CURRENT APPLICATION NUMBER: US/09/860,395  
 ; CURRENT FILING DATE: 2001-05-16  
 ; PRIOR APPLICATION NUMBER: 09/291,803  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: DE 198 16 732.6  
 ; PRIOR FILING DATE: 1998-04-15  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 16  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 8  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(10)  
 ; OTHER INFORMATION: K12D4  
 ; US-09-860-395-16

Query Match 40.0%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VVPP 9  
 Db 4 VVPP 7

RESULT 50  
 US-09-860-395-17  
 ; Sequence 17, Application US/09860395  
 ; Patent No. 6541253

; GENERAL INFORMATION:  
 ; APPLICANT: Haas, Juergen  
 ; APPLICANT: Kremmer, Elisabeth  
 ; APPLICANT: Kliche, Stefanie  
 ; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH  
 ; TITLE OF INVENTION: Diagnostics and Therapy of Diseases Associated with  
 ; TITLE OF INVENTION: HIV-8 Infections  
 ; FILE REFERENCE: 080318-000000US  
 ; CURRENT APPLICATION NUMBER: US/09/860,395  
 ; CURRENT FILING DATE: 2001-05-16  
 ; PRIOR APPLICATION NUMBER: 09/291,803  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: DE 198 16 732.6  
 ; PRIOR FILING DATE: 1998-04-15  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 17  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: human herpesvirus 8  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(10)  
 ; OTHER INFORMATION: K12D5  
 ; OTHER INFORMATION: K12D5  
 ; US-09-860-395-17

Query Match 40.0%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVPP 9  
 Db 1 VVPP 4

RESULT 51  
 US-09-490-702B-53  
 ; Sequence 53, Application US/09490702B  
 ; Patent No. 6560542  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mandell, Arnold  
 ; APPLICANT: Selz, Karen  
 ; APPLICANT: Shlesinger, Michael  
 ; TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or Modulation of  
 ; TITLE OF INVENTION: Functions of Receptors and/or Other Proteins  
 ; FILE REFERENCE: 01561-0002-00US00  
 ; CURRENT APPLICATION NUMBER: US/09/490,702B  
 ; CURRENT FILING DATE: 2000-01-24  
 ; NUMBER OF SEQ ID NOS: 96  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 53  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: synthetic  
 ; US-09-490-702B-53

Query Match 40.0%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVPP 10  
 Db 1 VVPP 4

RESULT 52  
 PCT-US95-05787-1  
 ; Sequence 1, Application PC/TUS9505787  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ESSIGMANN, JOHN M.

; APPLICANT: CROY, ROBERT G.  
 ; APPLICANT: YAREMA, KEVIN J.  
 ; APPLICANT: TREIBER, DANIEL K.  
 ; APPLICANT: CHEN, ZHENGHUAN  
 ; APPLICANT: MORNINGSTAR, MARSHALL  
 ; APPLICANT: ZHAI, XIAOGUAN  
 ; TITLE OF INVENTION: PROGRAMMABLE GENOTOXIC AGENTS AND USES  
 ; TITLE OF INVENTION: THEREFOR  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
 ; ADDRESSEE: THIBEAULT  
 ; STREET: 53 STATE STREET  
 ; CITY: BOSTON  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/05787  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FENTON, GILLIAN M.  
 ; REGISTRATION NUMBER: 36,508  
 ; REFERENCE/DOCKET NUMBER: MIT-018  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 248-7000  
 ; TELEFAX: (617) 248-7100  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; PCT-US95-05787-1

Query Match 40.0%; Score 4; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVPP 8  
 Db 6 VVPP 9

RESULT 53  
 PCT-US95-06613-7  
 ; Sequence 7, Application PC/TUS9506613  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;  
 ; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,  
 ; APPLICANT: HENRY; MURATA, JUN  
 ; TITLE OF INVENTION: MOTILITY STIMULATING  
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND  
 ; TITLE OF INVENTION: THERAPY  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORGAN & FINNEGAN  
 ; STREET: 345 PARK AVENUE  
 ; CITY: NEW YORK  
 ; STATE: NEW YORK  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10154  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy Disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06613  
FILING DATE: 24-MAY-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/346,455  
FILING DATE: 28-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,182  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/822,043  
FILING DATE: 17-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: DOROTHY R. AUTH  
REGISTRATION NUMBER: 36,434  
REFERENCE/DOCKET NUMBER: 2026-4149US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-8849  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: amino acid  
TOPOLOGY: linear  
PCT-US95-06613-7

Query Match 40.0%; Score 4; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VPPF 10  
Db 1 VPPF 4

RESULT 54  
US-08-468-819-14  
Sequence 14, Application US/08468819  
Patent No. 5871723  
GENERAL INFORMATION:  
APPLICANT: Strieter, Robert M.  
APPLICANT: Polverini, Peter J.  
APPLICANT: Kunkel, Steven L.  
TITLE OF INVENTION: CXC Chemokines as Regulators of Angiogenesis  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,819  
FILING DATE: Concurrently herewith  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UMIC:003/HYL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7477  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-468-819-14

Query Match 40.0%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPVV 6  
Db 1 TPVV 4

RESULT 55  
US-08-468-819-17  
Sequence 17, Application US/08468819  
Patent No. 5871723  
GENERAL INFORMATION:  
APPLICANT: Strieter, Robert M.  
APPLICANT: Polverini, Peter J.  
APPLICANT: Kunkel, Steven L.  
TITLE OF INVENTION: CXC Chemokines as Regulators of Angiogenesis  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,819  
FILING DATE: Concurrently herewith  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UMIC:003/HYL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7477  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-468-819-17

Query Match 40.0%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TPVV 6  
Db 1 TPVV 4

RESULT 56  
US-08-456-670B-35  
Sequence 35, Application US/08456670B



Patent No. 5932415  
GENERAL INFORMATION:  
APPLICANT: SCHUBERT, PETER  
APPLICANT: NEUMANN, STEGFRIED  
APPLICANT: PAWELZIK, MARTINA  
APPLICANT: LINKWEILER, WINFRIED  
APPLICANT: BURGER, CHRISTA  
APPLICANT: HOFMANN, GOTTFRIED  
APPLICANT: HUBERT, ANDREAS  
APPLICANT: GOEBEL, WERNER  
APPLICANT: KOHLER, STEFAN  
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING  
TITLE OF INVENTION: LISTERIAS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P.C.  
STREET: 2200 CLARENDON BLVD., SUITE 1400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,670B  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/412,227  
FILING DATE: 27-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/075,248  
FILING DATE: 11-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4239567.4  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 421911.4  
FILING DATE: 11-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1694D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
TELEX: 64191  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Listeria innocua  
US-08-456-670B-35  
Query Match 40.0%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
Oy 3 TPVV 6  
Db 2 TPVV 5  
RESULT 57  
US-08-750-419A-17  
Sequence 17, Application US/08750419A  
Patent No. 6008340

GENERAL INFORMATION:  
APPLICANT: BALL, TANJA  
APPLICANT: VRTALA, SUSANNE  
APPLICANT: SPERR, WOLFGANG  
APPLICANT: VALENT, PETER  
APPLICANT: SUSANI, MARKUS  
APPLICANT: KRAFT, DIETRICH  
APPLICANT: LAFFER, SYLVIA  
TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF,  
TITLE OF INVENTION: CORRESPONDING RECOMBINANT DNA MOLECULES,  
TITLE OF INVENTION: CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: USES OF SAID ALLERGENS AND FRAGMENTS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/750,419A  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR, GERALD M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1614-175  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-750-419A-17  
Query Match 40.0%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
Oy 4 PVVV 7  
Db 1 PVVV 4  
RESULT 58  
US-09-213-383-14  
Sequence 14, Application US/09213383  
Patent No. 649306  
GENERAL INFORMATION:  
APPLICANT: Strieter, Robert M.  
APPLICANT: Polverini, Peter J.  
APPLICANT: Kunkel, Steven L.  
TITLE OF INVENTION: CXc Chemokines as Regulators of  
Angiogenesis  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/213,383  
FILING DATE: 09-Dec-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/468,819  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UMIC:003/HYL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7477  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-213-383-14

Query Match 40.0%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 3 TPVV 6  
Db 1 TPVV 4

RESULT 59  
US-09-213-383-17  
Sequence 17, Application US/09213383  
Patent No. 6491906  
GENERAL INFORMATION:  
APPLICANT: Strieter, Robert M.  
Polverini, Peter J.  
Kunkel, Steven L.  
TITLE OF INVENTION: CXG Chemokines as Regulators of Angiogenesis  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/213,383  
FILING DATE: 09-Dec-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/468,819  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UMIC:003/HYL  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7477  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-213-383-17

Query Match 40.0%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 3 TPVV 6  
Db 1 TPVV 4

## RESULT 60

US-09-811-672-14  
Sequence 14, Application US/09811672  
Patent No. 6559120  
GENERAL INFORMATION:  
APPLICANT: BALL, Tanja  
APPLICANT: VRTALA, Susanne  
APPLICANT: SPERR, Wolfgang  
APPLICANT: VALENT, Peter  
APPLICANT: SUSANI, Markus  
APPLICANT: KRAFT, Dietrich  
APPLICANT: VALENTA, Rudolf  
APPLICANT: LAFFER, Sylvia  
TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, CORRESPONDING RECOMBINANT MOLECULES, VECTORS AND HOSTS CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC USES OF SAID ALLERGENS AND FRAGMENTS  
FILE REFERENCE: 1614-0247P  
CURRENT APPLICATION NUMBER: US/09/811.672  
CURRENT FILING DATE: 2001-03-20  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 14  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Timothy Grass  
US-09-811-672-14

Query Match 40.0%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 4 PVVV 7  
Db 1 PVVV 4

## RESULT 61

US-07-927-391-1  
Sequence 1, Application US/07927391  
Patent No. 6001649  
GENERAL INFORMATION:  
APPLICANT: CAPUT, Daniel  
APPLICANT: FERRARA, Pascual  
APPLICANT: MILOUX, Brigitte  
APPLICANT: MINTY, Adrian  
APPLICANT: VITA, Natalio  
TITLE OF INVENTION: Protein having a cytokin type activity, and recombinant DNA, expression vector and hosts for its preparation.  
TITLE OF INVENTION: for its preparation.  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER  
STREET: King Street Station, Suite 500, 1800 Diagonal  
CITY: ALEXANDRIA  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 19920929  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 16781/369  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-927-391-1

Query Match 40.0%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTP 4  
Db 8 TQTP 11

RESULT 62  
US-08-127-499A-36  
; Sequence 36, Application US/08127499A  
; Patent No. 5510264  
; GENERAL INFORMATION:  
; APPLICANT: VAN ALSTYNE, Diane  
; APPLICANT: SHARMA, Lawrence Rajendra  
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/127,499A  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399

TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
US-08-127-499A-36

Query Match 40.0%; Score 4; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTP 4  
Db 9 TQTP 12

RESULT 63  
US-08-127-499A-39  
; Sequence 39, Application US/08127499A  
; Patent No. 5510264  
; GENERAL INFORMATION:  
; APPLICANT: VAN ALSTYNE, Diane  
; APPLICANT: SHARMA, Lawrence Rajendra  
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/127,499A  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
US-08-127-499A-39

Query Match 40.0%; Score 4; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTP 4  
Db 9 TQTP 12

RESULT 64  
US-08-482-847-36  
; Sequence 36, Application US/08482847  
; Patent No. 5556757  
; GENERAL INFORMATION:

```

; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-482-847-36

```

```

Query Match 40.0%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No.1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 TQTP 4
Db 9 TQTP 12

```

```

RESULT 65
US-08-482-847-39
; Sequence 39, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-482-847-39

```

```

Query Match 40.0%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No.1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 TQTP 4
Db 9 TQTP 12

```

```

RESULT 66
US-08-480-190-128
; Sequence 128, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906

```

TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 128:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-480-190-128

Query Match 40.0%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 VVVP 8  
Db 9 VVVP 12

RESULT 67  
US-08-488-379-128  
; Sequence 128, Application US/08488379  
; Patent No. 5880103  
; GENERAL INFORMATION:

APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,379  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 128:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-488-379-128

Query Match 40.0%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 VVVP 8

Db 9 VVVP 12

RESULT 68  
US-09-261-855-46  
; Sequence 46, Application US/09261855A  
; Patent No. 6255055  
; GENERAL INFORMATION:

APPLICANT: Ross, Jeffrey  
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
FILE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE  
FILE REFERENCE: 960296.95131  
CURRENT APPLICATION NUMBER: US/09/261.855A  
CURRENT FILING DATE: 1999-03-03  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 46  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-261-855-46

Query Match 40.0%; Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 VVVP 8  
Db 11 VVVP 14

RESULT 69  
US-08-475-399A-128  
; Sequence 128, Application US/08475399A  
; Patent No. 6509033  
; GENERAL INFORMATION:

APPLICANT: Urban, Robert G.  
APPLICANT: Chiciz, Roman M.  
APPLICANT: Vignali, Dario A.A.  
APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,399A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00246/168003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 128:

SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-128

Query Match 40.0%; Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 VVVP 8  
|||

Db 9 VVVP 12

# RESULT 70

PCT-US93-07545-128  
Sequence 128, Application PC/TUS9307545

GENERAL INFORMATION:

APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 of 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07545  
FILING DATE: 19930811

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 128:

SEQUENCE CHARACTERISTICS:

LENGTH: 14

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

PCT-US93-07545-128

Query Match 40.0%; Score 4; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 VVVP 8  
|||

Db 9 VVVP 12

# RESULT 71

US-08-331-398A-68  
Sequence 68, Application US/08331398A

Patent No. 5608039

GENERAL INFORMATION:

APPLICANT: Pastan, Ira

APPLICANT: Willingham, Mark

APPLICANT: FitzGerald, David

APPLICANT: Brinkmann, Ulrich

APPLICANT: Pai, Lee

TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins

TITLE OF INVENTION: and their Uses (as amended)

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew

STREET: One Market Plaza, Steuart Street Plaza

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/331.398A

FILING DATE: 28-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/767,331

FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/596,289

FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 015280-126110US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-331-398A-68

Query Match 40.0%; Score 4; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TQTP 4  
|||

Db 5 TQTP 8

# RESULT 72

US-08-480-190-129

Sequence 129, Application US/08480190

Patent No. 5827516

GENERAL INFORMATION:

APPLICANT: Robert G. Urban

APPLICANT: Roman M. Chicz

APPLICANT: Dario A. A. Vignali

APPLICANT: Mary L. Hedley

APPLICANT: Lawrence J. Stern

APPLICANT: Jack L. Strominger

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480.190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-480-190-129

Query Match 40.0%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8
Db 9 VVVP 12

RESULT 73
US-08-488-379-129
; Sequence 129, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Darlo A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488.379
; FILING DATE:

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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-488-379-129

Query Match 40.0%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VVVP 8
Db 9 VVVP 12

RESULT 74
US-08-997-080-15
; Sequence 15, Application US/08997080
; Patent No. 5988524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Other

LOCATION: 2..2

OTHER INFORMATION: Residue can be either Gly or Ala

NAME/KEY: Other

LOCATION: 15...15

OTHER INFORMATION: Residue can be either Pro or Ala

US-08-997-080-15

Query Match 40.0%; Score 4; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VVPP 9

Db 3 VVPP 6

#### RESULT 75

US-08-331-397B-68

; Sequence 68, Application US/08331397B

; Patent No. 5981726

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira

; APPLICANT: Benhar, Itai

; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-

; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses

; TITLE OF INVENTION: Thereof

; NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Street Plaza

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105-1492

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/331,397B

; FILING DATE: 28-OCT-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/767,331

; FILING DATE: 30-SEP-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/596,289

; FILING DATE: 12-OCT-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Hunter, Tom

; REGISTRATION NUMBER: 38,498

; REFERENCE/DOCKET NUMBER: 015280-126120US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 543-9600

; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-331-397B-68

Query Match

Best Local Similarity 40.0%; Score 4; DB 2; Length 15;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

i<sup>3</sup> TQTP 4

Db 5 TQTP 8

Search completed: November 25, 2003, 20:16:17

Job time : 11.9043 secs